OM protein - protein search, using sw model

Run on: August 18, 2004, 15:50:07 ; Search time 19 Seconds
(without alignments)
910.247 Million cell updates/sec

Title: US-10-063-549-46
Perfect score: 335
Sequence: 1 MAGSPTCLTLIYILWQLTGS.....PHSLLTMPDTPRLFAYENVI 335

Scoring table: OLIGO
Gapop 60.0 , Gapext 60.0

Searched: 389414 seqs, 51625971 residues

Word size : 0

Total number of hits satisfying chosen parameters: 389414

Minimum DB seq length: 0
Maximum DB seq length: 2000000000

Post-processing: Listing first 700 summaries

Database : Issued_Patents_AA:*
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Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	% Query Match	Length	DB	ID	Description
1	8	2.4	360	4	US-09-907-794A-213	Sequence 213, App
2	8	2.4	360	4	US-09-905-125A-213	Sequence 213, App
3	8	2.4	360	4	US-09-902-775A-213	Sequence 213, App
4	8	2.4	410	4	US-09-252-991A-31174	Sequence 31174, A
5	7	2.1	63	4	US-09-646-691B-10	Sequence 10, Appl
6	7	2.1	67	4	US-09-543-681A-4733	Sequence 4733, Ap
7	7	2.1	97	4	US-09-886-319A-29	Sequence 29, Appl
8	7	2.1	98	3	US-08-613-822-4	Sequence 4, Appli
9	7	2.1	98	3	US-08-852-212-2	Sequence 2, Appli
10	7	2.1	98	4	US-09-479-729B-4	Sequence 4, Appli
11	7	2.1	98	4	US-09-261-201A-4	Sequence 4, Appli
12	7	2.1	98	4	US-09-717-209-4	Sequence 4, Appli
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14	7	2.1	192	3	US-08-486-099-107	Sequence 107, App
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86	7	2.1	964	4	US-09-543-681A-5035	Sequence 5035, Ap
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248	6	1.8	125	4	US-09-543-681A-4730	Sequence 4730, Ap
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259	6	1.8	149	3	US-08-836-075A-30	Sequence 30, Appl
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265	6	1.8	156	4	US-09-148-545-136	Sequence 136, App
266	6	1.8	157	3	US-08-872-855-6	Sequence 6, Appli
267	6	1.8	157	3	US-08-981-392-68	Sequence 68, Appl
268	6	1.8	157	4	US-09-252-991A-22516	Sequence 22516, A
269	6	1.8	158	4	US-09-252-991A-26205	Sequence 26205, A
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271	6	1.8	166	3	US-08-916-576B-6	Sequence 6, Appli
272	6	1.8	166	4	US-09-213-293D-18	Sequence 18, Appl
273	6	1.8	168	1	US-08-193-977-9	Sequence 9, Appli
274	6	1.8	170	4	US-09-205-258-1011	Sequence 1011, Ap
275	6	1.8	171	4	US-09-646-028-9	Sequence 9, Appli
276	6	1.8	172	4	US-09-252-991A-23876	Sequence 23876, A
277	6	1.8	172	4	US-09-198-452A-1195	Sequence 1195, Ap
278	6	1.8	174	2	US-08-768-964-13	Sequence 13, Appl
279	6	1.8	174	3	US-09-005-299-13	Sequence 13, Appl
280	6	1.8	174	3	US-09-515-431-13	Sequence 13, Appl
281	6	1.8	176	3	US-09-309-317-2	Sequence 2, Appli
282	6	1.8	177	4	US-09-252-991A-20614	Sequence 20614, A
283	6	1.8	182	4	US-09-107-532A-5701	Sequence 5701, Ap
284	6	1.8	183	4	US-08-858-207A-401	Sequence 401, App
285	6	1.8	191	4	US-08-671-548C-30	Sequence 30, Appl
286	6	1.8	193	4	US-08-671-548C-20	Sequence 20, Appl
287	6	1.8	193	4	US-08-671-548C-36	Sequence 36, Appl
288	6	1.8	194	4	US-08-671-548C-26	Sequence 26, Appl
289	6	1.8	196	3	US-08-981-392-35	Sequence 35, Appl
290	6	1.8	196	4	US-09-328-352-5098	Sequence 5098, Ap
291	6	1.8	199	2	US-08-768-964-12	Sequence 12, Appl
292	6	1.8	199	3	US-09-005-299-12	Sequence 12, Appl
293	6	1.8	199	3	US-09-515-431-12	Sequence 12, Appl
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298	6	1.8	206	4	US-09-562-737-55	Sequence 55, Appl
299	6	1.8	206	4	US-09-562-737-56	Sequence 56, Appl
300	6	1.8	206	4	US-09-562-737-57	Sequence 57, Appl
301	6	1.8	206	4	US-09-562-737-58	Sequence 58, Appl
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303	6	1.8	209	3	US-08-235-836C-32	Sequence 32, Appl
304	6	1.8	210	4	US-09-697-367-10	Sequence 10, Appl
305	6	1.8	210	4	US-09-134-001C-4790	Sequence 4790, Ap
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309	6	1.8	212	2	US-08-878-957-34	Sequence 34, Appl
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311	6	1.8	212	3	US-08-209-603E-11	Sequence 11, Appl
312	6	1.8	212	3	US-08-235-836C-34	Sequence 34, Appl
313	6	1.8	212	4	US-09-216-066-1	Sequence 1, Appli
314	6	1.8	212	4	US-09-711-546-11	Sequence 11, Appl
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317	6	1.8	214	4	US-09-187-789-9	Sequence 9, Appli
318	6	1.8	216	4	US-09-489-039A-7265	Sequence 7265, Ap
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322	6	1.8	218	1	US-08-465-388-92	Sequence 92, Appl
323	6	1.8	222	4	US-09-589-733C-11	Sequence 11, Appl
324	6	1.8	223	2	US-08-394-189B-22	Sequence 22, Appl
325	6	1.8	223	4	US-09-465-901-12	Sequence 12, Appl
326	6	1.8	227	4	US-09-593-887-16	Sequence 16, Appl
327	6	1.8	230	4	US-09-187-789-7	Sequence 7, Appli
328	6	1.8	231	4	US-09-252-991A-25675	Sequence 25675, A
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332	6	1.8	232	3	US-08-811-757-2	Sequence 2, Appli
333	6	1.8	232	3	US-09-249-230-2	Sequence 2, Appli
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338	6	1.8	238	3	US-09-515-431-7	Sequence 7, Appli
339	6	1.8	238	4	US-09-149-476-485	Sequence 485, App
340	6	1.8	241	4	US-09-489-039A-7888	Sequence 7888, Ap
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342	6	1.8	242	4	US-09-252-991A-24652	Sequence 24652, A
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345	6	1.8	245	4	US-08-426-630-20	Sequence 20, Appl
346	6	1.8	246	4	US-09-198-452A-22	Sequence 22, Appl
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348	6	1.8	252	4	US-09-252-991A-17553	Sequence 17553, A
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365	6	1.8	266	3	US-09-557-917-11	Sequence 11, Appl
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481	6	1.8	371	4	US-09-148-545-259	Sequence 259, App
482	6	1.8	371	5	PCT-US95-04353-8	Sequence 8, Appli
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496	6	1.8	387	1	US-08-483-278-10	Sequence 10, Appl
497	6	1.8	387	1	US-08-483-278-12	Sequence 12, Appl
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535	6	1.8	415	1	US-08-442-281-5	Sequence 5, Appli
536	6	1.8	415	2	US-08-939-727-5	Sequence 5, Appli
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ALIGNMENTS

RESULT 1
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; Sequence 213, Application US/09907794A
; Patent No. 6635468
; GENERAL INFORMATION:
; APPLICANT: Genentech, Inc.
; APPLICANT: Ashkenazi, Avi
; APPLICANT: Botstein, David
; APPLICANT: Desnoyers, Luc
; APPLICANT: Eaton, Dan L.
; APPLICANT: Ferrara, Napoleone
; APPLICANT: Filvaroff, Ellen
; APPLICANT: Fong, Sherman
; APPLICANT: Gao, Wei-Qiang
; APPLICANT: Gerber, Hanspeter
; APPLICANT: Gerritsen, Mary E.
; APPLICANT: Goddard, A.
; APPLICANT: Godowski, Paul J.
; APPLICANT: Grimaldi, Christopher J.
; APPLICANT: Gurney, Austin L.
; APPLICANT: Hillan, Kenneth, J.
; APPLICANT: Kljavin, Ivar J.
; APPLICANT: Mather, Jennie P.
; APPLICANT: Pan, James
; APPLICANT: Paoni, Nicholas F.
; APPLICANT: Roy, Margaret Ann
; APPLICANT: Stewart, Timothy A.
; APPLICANT: Tumas, Daniel
; APPLICANT: Williams, P. Mickey
; APPLICANT: Wood, William, I.
; TITLE OF INVENTION: Secreted and Transmembrane Polypeptides and Nucleic
; TITLE OF INVENTION: Acids Encoding the Same
; FILE REFERENCE: 10466-14
; CURRENT APPLICATION NUMBER: US/09/907,794A
; CURRENT FILING DATE: 2001-07-17
; PRIOR APPLICATION NUMBER: PCT/US00/04414
; PRIOR FILING DATE: 2000-02-22
; PRIOR APPLICATION NUMBER: US 60/143,048
; PRIOR FILING DATE: 1999-07-07
; PRIOR APPLICATION NUMBER: US 60/145,698
; PRIOR FILING DATE: 1999-07-26
; PRIOR APPLICATION NUMBER: US 60/146,222
; PRIOR FILING DATE: 1999-07-28
; PRIOR APPLICATION NUMBER: PCT/US99/20594
; PRIOR FILING DATE: 1999-09-08
; PRIOR APPLICATION NUMBER: PCT/US99/20944
; PRIOR FILING DATE: 1999-09-13
; PRIOR APPLICATION NUMBER: PCT/US99/21090
; PRIOR FILING DATE: 1999-09-15
; PRIOR APPLICATION NUMBER: PCT/US99/21547
; PRIOR FILING DATE: 1999-09-15
; PRIOR APPLICATION NUMBER: PCT/US99/23089
; PRIOR FILING DATE: 1999-10-05
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; PRIOR APPLICATION NUMBER: PCT/US99/28313
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; PRIOR FILING DATE: 1999-12-02
; PRIOR APPLICATION NUMBER: PCT/US99/28565
; PRIOR FILING DATE: 1999-12-02
; PRIOR APPLICATION NUMBER: PCT/US99/30095
; PRIOR FILING DATE: 1999-12-16
; PRIOR APPLICATION NUMBER: PCT/US99/30911
; PRIOR FILING DATE: 1999-12-20
; PRIOR APPLICATION NUMBER: PCT/US99/30999
; PRIOR FILING DATE: 1999-12-20
; PRIOR APPLICATION NUMBER: PCT/US00/00219
; PRIOR FILING DATE: 2000-01-05
; NUMBER OF SEQ ID NOS: 423
; SEQ ID NO 213
; LENGTH: 360
; TYPE: PRT
; ORGANISM: Homo sapiens
US-09-907-794A-213

Query Match 2.4%; Score 8; DB 4; Length 360;
Best Local Similarity 100.0%; Pred. No. 16;
Matches 8; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

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; GENERAL INFORMATION:
; APPLICANT: Genentech, Inc.
; APPLICANT: Ashkenazi, Avi
; APPLICANT: Botstein, David
; APPLICANT: Desnoyers, Luc
; APPLICANT: Eaton, Dan L.
; APPLICANT: Ferrara, Napoleone
; APPLICANT: Filvaroff, Ellen
; APPLICANT: Fong, Sherman
; APPLICANT: Gao, Wei-Qiang
; APPLICANT: Gerber, Hanspeter
; APPLICANT: Gerritsen, Mary E.
; APPLICANT: Goddard, A.
; APPLICANT: Godowski, Paul J.
; APPLICANT: Grimaldi, Christopher J.
; APPLICANT: Gurney, Austin L.
; APPLICANT: Hillan, Kenneth, J.
; APPLICANT: Kljavin, Ivar J.
; APPLICANT: Mather, Jennie P.
; APPLICANT: Pan, James
; APPLICANT: Paoni, Nicholas F.
; APPLICANT: Roy, Margaret Ann
; APPLICANT: Stewart, Timothy A.
; APPLICANT: Tumas, Daniel
; APPLICANT: Williams, P. Mickey
; APPLICANT: Wood, William, I.
; TITLE OF INVENTION: Secreted and Transmembrane Polypeptides and Nucleic
; TITLE OF INVENTION: Acids Encoding the Same
; FILE REFERENCE: 10466-14
; CURRENT APPLICATION NUMBER: US/09/905,125A
; CURRENT FILING DATE: 2001-07-12
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; PRIOR FILING DATE: 2000-02-22
; PRIOR APPLICATION NUMBER: US 60/143,048
; PRIOR FILING DATE: 1999-07-07
; PRIOR APPLICATION NUMBER: US 60/145,698

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;  PRIOR FILING DATE: 1999-07-26
;  PRIOR APPLICATION NUMBER: US 60/146,222
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;  PRIOR APPLICATION NUMBER: PCT/US99/23089
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;  PRIOR FILING DATE: 1999-11-30
;  PRIOR APPLICATION NUMBER: PCT/US99/28564
;  PRIOR FILING DATE: 1999-12-02
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US-09-905-125A-213

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; GENERAL INFORMATION:
;  APPLICANT: Genentech, Inc.
;  APPLICANT:  Ashkenazi, Avi
;  APPLICANT:  Botstein, David
;  APPLICANT:  Desnoyers, Luc
;  APPLICANT:  Eaton, Dan L.
;  APPLICANT:  Ferrara, Napoleone
;  APPLICANT:  Filvaroff, Ellen
;  APPLICANT:  Fong, Sherman
;  APPLICANT:  Gao, Wei-Qiang
;  APPLICANT:  Gerber, Hanspeter
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;  APPLICANT:  Goddard, A.
;  APPLICANT:  Godowski, Paul J.
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;  APPLICANT:  Pan, James
;  APPLICANT:  Paoni, Nicholas F.
;  APPLICANT:  Roy, Margaret Ann
;  APPLICANT:  Stewart, Timothy A.
;  APPLICANT:  Tumas, Daniel
;  APPLICANT:  Williams, P. Mickey
;  APPLICANT:  Wood, William, I.
;  TITLE OF INVENTION: Secreted and Transmembrane Polypeptides and Nucleic
;  TITLE OF INVENTION:  Acids Encoding the Same
;  FILE REFERENCE: 10466-14
;  CURRENT APPLICATION NUMBER: US/09/902,775A
;  CURRENT FILING DATE:  2001-07-10
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;  PRIOR FILING DATE: 1999-12-02
;  PRIOR APPLICATION NUMBER: PCT/US99/30095
;  PRIOR FILING DATE: 1999-12-16
;  PRIOR APPLICATION NUMBER: PCT/US99/30911
;  PRIOR FILING DATE: 1999-12-20
;  PRIOR APPLICATION NUMBER: PCT/US99/30999
;  PRIOR FILING DATE: 1999-12-20
;  PRIOR APPLICATION NUMBER: PCT/US00/00219
;  PRIOR FILING DATE: 2000-01-05
;  NUMBER OF SEQ ID NOS: 423
; SEQ ID NO 213
;   LENGTH: 360
;   TYPE: PRT
;   ORGANISM: Homo sapiens
US-09-902-775A-213

  Query Match              2.4%;  Score 8;  DB 4;  Length 360;
  Best Local Similarity   100.0%;  Pred. No. 16;
  Matches    8;  Conservative    0;  Mismatches    0;  Indels    0;  Gaps    0;

Qy        231 LLLVPLLL 238
              ||||||||
Db          4 LLLVPLLL 11


RESULT 4
US-09-252-991A-31174
; Sequence 31174, Application US/09252991A
; Patent No. 6551795
; GENERAL INFORMATION:
;  APPLICANT:  Marc J. Rubenfield et al.
;  TITLE OF INVENTION:  NUCLEIC ACID AND AMINO ACID SEQUENCES RELATING TO PSEUDOMONAS
;  TITLE OF INVENTION:  AERUGINOSA FOR DIAGNOSTICS AND THERAPEUTICS
;  FILE REFERENCE:  107196.136
;  CURRENT APPLICATION NUMBER: US/09/252,991A
;  CURRENT FILING DATE:  1999-02-18
;  PRIOR APPLICATION NUMBER:  US 60/074,788
;  PRIOR FILING DATE:  1998-02-18
;  PRIOR APPLICATION NUMBER:  US 60/094,190
;  PRIOR FILING DATE:  1998-07-27
;  NUMBER OF SEQ ID NOS:  33142
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; SEQ ID NO 31174
; LENGTH: 410
; TYPE: PRT
; ORGANISM: Pseudomonas aeruginosa
US-09-252-991A-31174

Query Match 2.4%; Score 8; DB 4; Length 410;
Best Local Similarity 100.0%; Pred. No. 18;
Matches 8; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 29 LVGSVGGA 36
||||||||
Db 312 LVGSVGGA 319

RESULT 5
US-09-646-691B-10
; Sequence 10, Application US/09646691B
; Patent No. 6642353
; GENERAL INFORMATION:
; APPLICANT: McCONNELL, Stephen, J. and SPINELLA, Dominic, G.
; TITLE OF INVENTION: PEPTIDE LIGANDS FOR THE ERYTHROPOIETIN
; RECEPTOR
; NUMBER OF SEQUENCES: 90
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: Gen-Probe Incorporated
; STREET: 10210 Genetic Center Drive
; CITY: San Diego
; STATE: CA
; COUNTRY: USA
; ZIP: 92121
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Diskette
; COMPUTER: IBM Compatible
; OPERATING SYSTEM: DOS
; SOFTWARE: FastSEQ for Windows Version 2.0
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/09/646,691B
; FILING DATE: 20-Sep-2000
; CLASSIFICATION: <Unknown>
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: <Unknown>
; FILING DATE: <Unknown>
; ATTORNEY/AGENT INFORMATION:
; NAME: Gritzmacher, Christine A
; REGISTRATION NUMBER: 40,627
; REFERENCE/DOCKET NUMBER: CB9701-A01
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: 619-410-8926
; TELEFAX: 619-410-8928
; TELEX: <Unknown>
; INFORMATION FOR SEQ ID NO: 10:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 63 amino acids
; TYPE: amino acid
; STRANDEDNESS: single
; TOPOLOGY: linear
; MOLECULE TYPE: No. 6642353e
; SEQUENCE DESCRIPTION: SEQ ID NO: 10:
US-09-646-691B-10

Query Match 2.1%; Score 7; DB 4; Length 63;
Best Local Similarity 100.0%; Pred. No. 31;
Matches 7; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 18 TGSAASG 24
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Db 37 TGSAASG 43

RESULT 6
US-09-543-681A-4733
; Sequence 4733, Application US/09543681A
; Patent No. 6605709
; GENERAL INFORMATION:
; APPLICANT: GARY BRETON
; TITLE OF INVENTION: NUCLEIC ACID AND AMINO ACID SEQUENCES RELATING TO PROTEUS MIRABIL
; TITLE OF INVENTION: DIAGNOSTICS AND THERAPEUTICS
; FILE REFERENCE: 2709.1002-001
; CURRENT APPLICATION NUMBER: US/09/543,681A
; CURRENT FILING DATE: 2000-04-05
; PRIOR APPLICATION NUMBER: US 60/128,706
; PRIOR FILING DATE: 1999-04-09
; NUMBER OF SEQ ID NOS: 8344
; SEQ ID NO 4733
; LENGTH: 67
; TYPE: PRT
; ORGANISM: Proteus mirabilis
US-09-543-681A-4733

Query Match 2.1%; Score 7; DB 4; Length 67;
Best Local Similarity 100.0%; Pred. No. 33;
Matches 7; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 237 LLSLFVL 243
|||||||
Db 60 LLSLFVL 66

RESULT 7
US-09-886-319A-29
; Sequence 29, Application US/09886319A
; Patent No. 6586185
; GENERAL INFORMATION:
; APPLICANT: Wolf, Eckard
; APPLICANT: Werner, Sabine
; APPLICANT: Halle, Jorn-Peter
; APPLICANT: Regenbogen, Johannes
; APPLICANT: Goppelt, Andreas
; TITLE OF INVENTION: Use of Polypeptides or Nucleic Acids for
; TITLE OF INVENTION: the Diagnosis or Treatment of Skin Disorders and Wound
; TITLE OF INVENTION: Healing and for the Identification of Pharmacologically
; TITLE OF INVENTION: Active Substances
; FILE REFERENCE: 50125/014002
; CURRENT APPLICATION NUMBER: US/09/886,319A
; CURRENT FILING DATE: 2001-06-20
; PRIOR APPLICATION NUMBER: US 60/222,081
; PRIOR FILING DATE: 2000-08-01
; PRIOR APPLICATION NUMBER: DE 10030149.5
; PRIOR FILING DATE: 2000-06-20
; NUMBER OF SEQ ID NOS: 84
; SOFTWARE: FastSEQ for Windows Version 4.0
; SEQ ID NO 29
; LENGTH: 97
; TYPE: PRT
; ORGANISM: Mus musculus
US-09-886-319A-29

Query Match 2.1%; Score 7; DB 4; Length 97;
Best Local Similarity 100.0%; Pred. No. 45;
Matches 7; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 227 VLLCLLL 233
|||||||
Db 6 VLLCLLL 12

RESULT 8
US-08-613-822-4
; Sequence 4, Application US/08613822
; Patent No. 6174995
; GENERAL INFORMATION:
; APPLICANT: Li, Haodong
; TITLE OF INVENTION: Human Chemokine Polypeptides
; NUMBER OF SEQUENCES: 20
; CORRESPONDENCE ADDRESS:

```
;       ADDRESSEE:  Human Genome Sciences,Inc.
;       STREET:  9410 Key West Avenue
;       CITY:  Rockville
;       STATE:  MD
;       COUNTRY:  USA
;       ZIP:  20850
;     COMPUTER READABLE FORM:
;       MEDIUM TYPE:  Floppy disk
;       COMPUTER:  IBM PC compatible
;       OPERATING SYSTEM:  PC-DOS/MS-DOS
;       SOFTWARE:  PatentIn Release #1.0, Version #1.30
;     CURRENT APPLICATION DATA:
;       APPLICATION NUMBER:  US/08/613,822
;       FILING DATE:  23-FEB-1996
;       CLASSIFICATION:  435
;     ATTORNEY/AGENT INFORMATION:
;       NAME:  Millstein, Larry S
;       REGISTRATION NUMBER:  34,679
;     TELECOMMUNICATION INFORMATION:
;       TELEPHONE:  301-309-8504
;       TELEFAX:  301-309-8512
;   INFORMATION FOR SEQ ID NO:  4:
;     SEQUENCE CHARACTERISTICS:
;       LENGTH:  98 amino acids
;       TYPE:  amino acid
;       TOPOLOGY:  linear
;     MOLECULE TYPE:  protein
US-08-613-822-4

  Query Match             2.1%;  Score 7;  DB 3;  Length 98;
  Best Local Similarity   100.0%;  Pred. No. 46;
  Matches    7;  Conservative    0;  Mismatches    0;  Indels    0;  Gaps    0;

Qy        227 VLLCLLL 233
              |||||||
Db          6 VLLCLLL 12


RESULT 9
US-08-852-212-2
; Sequence 2, Application US/08852212
; Patent No. 6290948
; GENERAL INFORMATION:
;  APPLICANT: White et al.
;  TITLE OF INVENTION: Method of Treating Sepsis and ARDS using Chemokine Beta-10
;  FILE REFERENCE: PF501
;  CURRENT APPLICATION NUMBER: US/08/852,212
;  CURRENT FILING DATE: 1997-05-06
;  EARLIER APPLICATION NUMBER: 60/017,871
;  EARLIER FILING DATE: 1996-05-14
;  NUMBER OF SEQ ID NOS: 2
;  SOFTWARE: PatentIn Ver. 2.0
; SEQ ID NO 2
;   LENGTH: 98
;   TYPE: PRT
;   ORGANISM: Homo sapiens
US-08-852-212-2

  Query Match             2.1%;  Score 7;  DB 3;  Length 98;
  Best Local Similarity   100.0%;  Pred. No. 46;
  Matches    7;  Conservative    0;  Mismatches    0;  Indels    0;  Gaps    0;

Qy        227 VLLCLLL 233
              |||||||
Db          6 VLLCLLL 12


RESULT 10
US-09-479-729B-4
; Sequence 4, Application US/09479729B
; Patent No. 6391589
; GENERAL INFORMATION:
;  APPLICANT: Olsen, et al
;  TITLE OF INVENTION: Human Chemokine Beta-10 Mutant Polypeptides
;  FILE REFERENCE: PF504
;  CURRENT APPLICATION NUMBER: US/09/479,729B
;  CURRENT FILING DATE:  2000-01-07
;  PRIOR APPLICATION NUMBER: PCT/US94/09484
;  PRIOR FILING DATE: 1994-08-23
;  PRIOR APPLICATION NUMBER: 08/458,355
;  PRIOR FILING DATE: 1995-06-02
;  PRIOR APPLICATION NUMBER: 08/462,967
;  PRIOR FILING DATE: 1995-06-05
;  PRIOR APPLICATION NUMBER: 60/115,439
;  PRIOR FILING DATE: 1999-01-08
;  NUMBER OF SEQ ID NOS: 30
;  SOFTWARE: PatentIn version 3.0
; SEQ ID NO 4
;   LENGTH: 98
;   TYPE: PRT
;   ORGANISM: Homo sapiens
US-09-479-729B-4

  Query Match             2.1%;  Score 7;  DB 4;  Length 98;
  Best Local Similarity   100.0%;  Pred. No. 46;
  Matches    7;  Conservative    0;  Mismatches    0;  Indels    0;  Gaps    0;

Qy        227 VLLCLLL 233
              |||||||
Db          6 VLLCLLL 12


RESULT 11
US-09-261-201A-4
; Sequence 4, Application US/09261201A
; Patent No. 6458349
; GENERAL INFORMATION:
;  APPLICANT: Li et al.
;  TITLE OF INVENTION: Polynucleotides Encoding Chemokine B-4
;  FILE REFERENCE: PF132P1D1
;  CURRENT APPLICATION NUMBER: US/09/261,201A
;  CURRENT FILING DATE:  1999-03-03
;  PRIOR APPLICATION NUMBER: 08/458,355
;  PRIOR FILING DATE: 1995-06-02
;  PRIOR APPLICATION NUMBER: PCT/US94/09484
;  PRIOR FILING DATE: 1994-08-23
;  NUMBER OF SEQ ID NOS: 14
;  SOFTWARE: PatentIn version 3.1
; SEQ ID NO 4
;   LENGTH: 98
;   TYPE: PRT
;   ORGANISM: Homo sapiens
US-09-261-201A-4

  Query Match             2.1%;  Score 7;  DB 4;  Length 98;
  Best Local Similarity   100.0%;  Pred. No. 46;
  Matches    7;  Conservative    0;  Mismatches    0;  Indels    0;  Gaps    0;

Qy        227 VLLCLLL 233
              |||||||
Db          6 VLLCLLL 12


RESULT 12
US-09-717-209-4
; Sequence 4, Application US/09717209
; Patent No. 6673344
;  GENERAL INFORMATION:
;    APPLICANT:  Li, Haodong
;    TITLE OF INVENTION:  Human Chemokine Polypeptides
;    NUMBER OF SEQUENCES:  20
;    CORRESPONDENCE ADDRESS:
;      ADDRESSEE:  Human Genome Sciences,Inc.
;      STREET:  9410 Key West Avenue
;      CITY:  Rockville
;      STATE:  MD
```

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;       COUNTRY:  USA
;       ZIP:  20850
;     COMPUTER READABLE FORM:
;       MEDIUM TYPE:  Floppy disk
;       COMPUTER:  IBM PC compatible
;       OPERATING SYSTEM:  PC-DOS/MS-DOS
;       SOFTWARE:  PatentIn Release #1.0, Version #1.30
;     CURRENT APPLICATION DATA:
;       APPLICATION NUMBER:  US/09/717,209
;       FILING DATE:
;       CLASSIFICATION:
;     PRIOR APPLICATION DATA:
;       APPLICATION NUMBER:  US/08/613,822
;       FILING DATE:  23-FEB-1996
;     ATTORNEY/AGENT INFORMATION:
;       NAME:  Millstein, Larry S
;       REGISTRATION NUMBER:  34,679
;     TELECOMMUNICATION INFORMATION:
;       TELEPHONE:  301-309-8504
;       TELEFAX:  301-309-8512
;   INFORMATION FOR SEQ ID NO:  4:
;     SEQUENCE CHARACTERISTICS:
;       LENGTH:  98 amino acids
;       TYPE:  amino acid
;       TOPOLOGY:  linear
;     MOLECULE TYPE:  protein
US-09-717-209-4

  Query Match             2.1%;  Score 7;  DB 4;  Length 98;
  Best Local Similarity   100.0%;  Pred. No. 46;
  Matches    7;  Conservative    0;  Mismatches    0;  Indels    0;  Gaps    0;

Qy        227 VLLCLLL 233
              |||||||
Db          6 VLLCLLL 12


RESULT 13
US-09-545-894-2
; Sequence 2, Application US/09545894
; Patent No. 6673915
;  GENERAL INFORMATION:
;       APPLICANT: Luster, Andrew D.
;                  Garcia-Zepeda, Eduardo A.
;                  Sarafi, Mindy N.
;       TITLE OF INVENTION: MCP-4 AND MCP-5: NOVEL CHEMOKINES
;       NUMBER OF SEQUENCES: 30
;       CORRESPONDENCE ADDRESS:
;            ADDRESSEE: Clark & Elbing LLP
;            STREET: 176 Federal Street
;            CITY: Boston
;            STATE: MA
;            COUNTRY: USA
;            ZIP: 02110
;       COMPUTER READABLE FORM:
;            MEDIUM TYPE: Diskette
;            COMPUTER: IBM Compatible
;            OPERATING SYSTEM: DOS
;            SOFTWARE: FastSEQ for Windows Version 2.0
;       CURRENT APPLICATION DATA:
;            APPLICATION NUMBER: US/09/545,894
;            FILING DATE: 07-Apr-2000
;            CLASSIFICATION: <Unknown>
;       PRIOR APPLICATION DATA:
;            APPLICATION NUMBER: US/08/940,687
;            FILING DATE: 30-SEP-1997
;            APPLICATION NUMBER: 60/027,128
;            FILING DATE: 30-SEP-1996
;       ATTORNEY/AGENT INFORMATION:
;            NAME: Bieker-Brady, Kristina
;            REGISTRATION NUMBER: 39,109
;            REFERENCE/DOCKET NUMBER: 00786/293002
;       TELECOMMUNICATION INFORMATION:
;            TELEPHONE: 617-428-0200
;            TELEFAX: 617-428-7045
;            TELEX: <Unknown>
;   INFORMATION FOR SEQ ID NO: 2:
;       SEQUENCE CHARACTERISTICS:
;            LENGTH: 98 amino acids
;            TYPE: amino acid
;            STRANDEDNESS: unknown
;            TOPOLOGY: linear
;       MOLECULE TYPE: protein
;       SEQUENCE DESCRIPTION: SEQ ID NO: 2:
US-09-545-894-2

  Query Match             2.1%;  Score 7;  DB 4;  Length 98;
  Best Local Similarity   100.0%;  Pred. No. 46;
  Matches    7;  Conservative    0;  Mismatches    0;  Indels    0;  Gaps    0;

Qy        227 VLLCLLL 233
              |||||||
Db          6 VLLCLLL 12


RESULT 14
US-08-486-099-107
; Sequence 107, Application US/08486099
; Patent No. 6013263
;  GENERAL INFORMATION:
;    APPLICANT:  Bolognesi, Dani P.
;    APPLICANT:  Matthews, Thomas J.
;    APPLICANT:  Wild, Carl T.
;    APPLICANT:  Barney, Shawn O.
;    APPLICANT:  Lambert, Dennis M.
;    APPLICANT:  Petteway, Stephen R.
;    APPLICANT:  Langlois, Alphonse J.
;    TITLE OF INVENTION:  COMPOSITIONS FOR INHIBITION OF
;    TITLE OF INVENTION:  MEMBRANE FUSION-ASSOCIATED EVENTS, INCLUDING HEPATITIS
;    TITLE OF INVENTION:  B VIRUS TRANSMISSION
;    NUMBER OF SEQUENCES:  209
;    CORRESPONDENCE ADDRESS:
;      ADDRESSEE:  Pennie & Edmonds
;      STREET:  1155 Avenue of the Americas
;      CITY:  New York
;      STATE:  New York
;      COUNTRY:  USA
;      ZIP:  10036-2711
;    COMPUTER READABLE FORM:
;      MEDIUM TYPE:  Floppy disk
;      COMPUTER:  IBM PC compatible
;      OPERATING SYSTEM:  PC-DOS/MS-DOS
;      SOFTWARE:  PatentIn Release #1.0, Version #1.30
;    CURRENT APPLICATION DATA:
;      APPLICATION NUMBER:  US/08/486,099
;      FILING DATE:  07-JUN-1995
;      CLASSIFICATION:  435
;    ATTORNEY/AGENT INFORMATION:
;      NAME:  Coruzzi, Laura A.
;      REGISTRATION NUMBER:  30,742
;      REFERENCE/DOCKET NUMBER:  7872-031
;    TELECOMMUNICATION INFORMATION:
;      TELEPHONE:  (212) 790-9090
;      TELEFAX:  (212) 869-9741/8864
;      TELEX:  66141 PENNIE
;  INFORMATION FOR SEQ ID NO:  107:
;    SEQUENCE CHARACTERISTICS:
;      LENGTH:  192 amino acids
;      TYPE:  amino acid
;      STRANDEDNESS:
;      TOPOLOGY:  unknown
;    MOLECULE TYPE:  protein
US-08-486-099-107

  Query Match             2.1%;  Score 7;  DB 3;  Length 192;
  Best Local Similarity   100.0%;  Pred. No. 83;
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  Matches    7;  Conservative    0;  Mismatches    0;  Indels    0;  Gaps    0;

Qy        228 LLCLLLV 234
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Db        139 LLCLLLV 145


RESULT 15
US-08-360-107A-117
; Sequence 117, Application US/08360107A
; Patent No. 6017536
;  GENERAL INFORMATION:
;    APPLICANT:  Bolognesi, Dani P.
;    APPLICANT:  Matthews, Thomas J.
;    APPLICANT:  Wild, Carl T.
;    APPLICANT:  Barney, Shawn O.
;    APPLICANT:  Lambert, Dennis M.
;    APPLICANT:  Petteway, Stephen R.
;    APPLICANT:  Langlois, Alphonse J.
;    TITLE OF INVENTION:  METHODS AND COMPOSITIONS FOR INHIBITION
;    TITLE OF INVENTION:  OF MEMBRANE FUSION-ASSOCIATED EVENTS, INCLUDING HIV
;    TITLE OF INVENTION:  TRANSMISSION
;    NUMBER OF SEQUENCES:  149
;    CORRESPONDENCE ADDRESS:
;      ADDRESSEE:  Pennie & Edmonds
;      STREET:  1155 Avenue of the Americas
;      CITY:  New York
;      STATE:  New York
;      COUNTRY:  USA
;      ZIP:  10036-2711
;    COMPUTER READABLE FORM:
;      MEDIUM TYPE:  Floppy disk
;      COMPUTER:  IBM PC compatible
;      OPERATING SYSTEM:  PC-DOS/MS-DOS
;      SOFTWARE:  PatentIn Release #1.0, Version #1.30
;    CURRENT APPLICATION DATA:
;      APPLICATION NUMBER:  US/08/360,107A
;      FILING DATE:  20-DEC-1994
;      CLASSIFICATION:  435
;    ATTORNEY/AGENT INFORMATION:
;      NAME:  Coruzzi, Laura A.
;      REGISTRATION NUMBER:  30,742
;      REFERENCE/DOCKET NUMBER:  7872-013
;    TELECOMMUNICATION INFORMATION:
;      TELEPHONE:  (212) 790-9090
;      TELEFAX:  (212) 869-9741/8864
;      TELEX:  66141 PENNIE
;  INFORMATION FOR SEQ ID NO:  117:
;    SEQUENCE CHARACTERISTICS:
;      LENGTH:  192 amino acids
;      TYPE:  amino acid
;      STRANDEDNESS:
;      TOPOLOGY:  unknown
;    MOLECULE TYPE:  protein
US-08-360-107A-117

  Query Match             2.1%;  Score 7;  DB 3;  Length 192;
  Best Local Similarity   100.0%;  Pred. No. 83;
  Matches    7;  Conservative    0;  Mismatches    0;  Indels    0;  Gaps    0;

Qy        228 LLCLLLV 234
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Db        139 LLCLLLV 145


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Title: US-10-063-549-46
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Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	% Query Match	Length	DB	ID	Description
1	335	100.0	335	9	US-09-732-524-2	Sequence 2, Appli
2	335	100.0	335	9	US-09-989-722-253	Sequence 253, App
3	335	100.0	335	9	US-09-989-723-253	Sequence 253, App
4	335	100.0	335	9	US-09-989-279-253	Sequence 253, App
5	335	100.0	335	9	US-09-989-727-253	Sequence 253, App
6	335	100.0	335	9	US-09-989-731-253	Sequence 253, App
7	335	100.0	335	9	US-09-989-732-253	Sequence 253, App
8	335	100.0	335	9	US-09-745-605-4	Sequence 4, Appli
9	335	100.0	335	9	US-09-991-073-253	Sequence 253, App
10	335	100.0	335	9	US-09-990-442-253	Sequence 253, App
11	335	100.0	335	9	US-09-991-163-253	Sequence 253, App
12	335	100.0	335	9	US-09-993-604-253	Sequence 253, App
13	335	100.0	335	9	US-09-990-456-253	Sequence 253, App
14	335	100.0	335	9	US-09-989-721-253	Sequence 253, App
15	335	100.0	335	9	US-09-992-598-253	Sequence 253, App
16	335	100.0	335	9	US-09-989-293A-253	Sequence 253, App
17	335	100.0	335	9	US-09-989-735-253	Sequence 253, App
18	335	100.0	335	9	US-09-990-444-253	Sequence 253, App
19	335	100.0	335	9	US-09-991-181-253	Sequence 253, App
20	335	100.0	335	9	US-09-989-730-253	Sequence 253, App
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22	335	100.0	335	9	US-09-993-687-253	Sequence 253, App
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681	335	100.0	335	14	US-10-063-659-46	Sequence 46, Appl
682	335	100.0	335	14	US-10-063-661-46	Sequence 46, Appl
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689	335	100.0	335	14	US-10-063-592-46	Sequence 46, Appl
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691	335	100.0	335	14	US-10-063-602-46	Sequence 46, Appl
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693	335	100.0	335	14	US-10-063-609-46	Sequence 46, Appl
694	335	100.0	335	14	US-10-063-611-46	Sequence 46, Appl
695	335	100.0	335	14	US-10-063-614-46	Sequence 46, Appl
696	335	100.0	335	14	US-10-063-639-46	Sequence 46, Appl
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698	335	100.0	335	14	US-10-063-646-46	Sequence 46, Appl
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700	335	100.0	335	15	US-10-205-506-192	Sequence 192, App

ALIGNMENTS

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RESULT 1
US-09-732-524-2
; Sequence 2, Application US/09732524
; Patent No. US20020004193A1
; GENERAL INFORMATION:
;    APPLICANT:  Khodadoust, Mehran
;    TITLE OF INVENTION:  NOVEL MP-7 PROTEIN AND NUCLEIC ACID MOLECULES
;    TITLE OF INVENTION:  AND USES THEREOF
;    NUMBER OF SEQUENCES:  7
;    CORRESPONDENCE ADDRESS:
;      ADDRESSEE:  LAHIVE & COCKFIELD, LLP
;      STREET:  28 State Street
;      CITY:  Boston
;      STATE:  Massachusetts
;      COUNTRY:  USA
;      ZIP:  02109
;    COMPUTER READABLE FORM:
;      MEDIUM TYPE:  Floppy disk
;      COMPUTER:  IBM PC compatible
;      OPERATING SYSTEM:  PC-DOS/MS-DOS
;      SOFTWARE:  PatentIn Release #1.0, Version #1.25
;    CURRENT APPLICATION DATA:
;      APPLICATION NUMBER:  US/09/732,524
;      FILING DATE:
;      CLASSIFICATION:
;    PRIOR APPLICATION DATA:
;      APPLICATION NUMBER:  09/261,759
;      FILING DATE:
;    PRIOR APPLICATION DATA:
;      APPLICATION NUMBER:  60/090,579
;      FILING DATE:  1998-JUN-25
;    ATTORNEY/AGENT INFORMATION:
;      NAME:  Mandragouras, Amy E.
;      REGISTRATION NUMBER:  36,207
;      REFERENCE/DOCKET NUMBER:  MNI-048CP
;    TELECOMMUNICATION INFORMATION:
;      TELEPHONE:  (617)227-7400
;      TELEFAX:  (617)742-4214
;  INFORMATION FOR SEQ ID NO:  2:
;    SEQUENCE CHARACTERISTICS:
;      LENGTH:  335 amino acids
;      TYPE:  amino acid
;      TOPOLOGY:  linear
;    MOLECULE TYPE:  protein
US-09-732-524-2

  Query Match             100.0%;  Score 335;  DB 9;  Length 335;
  Best Local Similarity   100.0%;  Pred. No. 1.3e-305;
  Matches  335;  Conservative    0;  Mismatches    0;  Indels    0;  Gaps    0;

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Qy        121 VLHVYEHLSKPKVTMGLQSNKNGTCVTNLTCCMEHGEEDVIYTWKALGQAANESHNGSIL 180
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RESULT 2
US-09-989-722-253
; Sequence 253, Application US/09989722
; Patent No. US20020072067A1
; GENERAL INFORMATION:
;  APPLICANT: Ashkenazi,Avi J.
;  APPLICANT:  Baker,Kevin P.
;  APPLICANT:  Botstein,David
;  APPLICANT:  Desnoyers,Luc
;  APPLICANT:  Eaton,Dan L.
;  APPLICANT:  Ferrara,Napoleone
;  APPLICANT:  Fong,Sherman
;  APPLICANT:  Gerber,Hanspeter
;  APPLICANT:  Gerritsen,Mary E.
;  APPLICANT:  Goddard,Audrey
;  APPLICANT:  Godowski,Paul J.
;  APPLICANT:  Grimaldi,J.Christopher
;  APPLICANT:  Gurney,Austin L.
;  APPLICANT:  Kljavin,Ivar J.
;  APPLICANT:  Napier,Mary A.
;  APPLICANT:  Pan,James
;  APPLICANT:  Paoni,Nicholas F.
;  APPLICANT:  Roy, Margaret Ann
;  APPLICANT:  Stewart, Timothy A.
;  APPLICANT:  Tumas, Daniel
;  APPLICANT:  Watanabe, Colin K.
;  APPLICANT:  Williams, P. Mickey
;  APPLICANT:  Wood, William I.
;  APPLICANT:  Zhang, Zemin
;  TITLE OF INVENTION: Secreted and Transmembrane Polypeptides and Nucleic
;  TITLE OF INVENTION:  Acids Encoding the Same
;  FILE REFERENCE: P2730P1C63
;  CURRENT APPLICATION NUMBER: US/09/989,722
;  CURRENT FILING DATE:  2001-11-19
;  PRIOR APPLICATION NUMBER: 60/049787
;  PRIOR FILING DATE: 1997-06-16
;  PRIOR APPLICATION NUMBER: 60/062250
;  PRIOR FILING DATE: 1997-10-17
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; PRIOR APPLICATION NUMBER: 60/065186
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; PRIOR FILING DATE: 1997-11-13
; PRIOR APPLICATION NUMBER: 60/066770
; PRIOR FILING DATE: 1997-11-24
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; PRIOR FILING DATE: 1998-02-25
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; PRIOR APPLICATION NUMBER: 60/091978
; PRIOR FILING DATE: 1998-07-07
; PRIOR APPLICATION NUMBER: 60/091982
; PRIOR FILING DATE: 1998-07-07
; PRIOR APPLICATION NUMBER: 60/092182
; PRIOR FILING DATE: 1998-07-09

Query Match 100.0%; Score 335; DB 9; Length 335;
Best Local Similarity 100.0%; Pred. No. 1.3e-305;
Matches 335; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

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Qy          1 MAGSPTCLTLIYILWQLTGSAASGPVKELVGSVGGAVTFPLKSKVKQVDSIVWTFNTTPL 60
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Qy         61 VTIQPEGGTIIVTQNRNRERVDFPDGGYSLKLSKLKKNDSGIYYVGIYSSSLQQPSTQEY 120
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Db         61 VTIQPEGGTIIVTQNRNRERVDFPDGGYSLKLSKLKKNDSGIYYVGIYSSSLQQPSTQEY 120

Qy        121 VLHVYEHLSKPKVTMGLQSNKNGTCVTNLTCCMEHGEEDVIYTWKALGQAANESHNGSIL 180
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Db        121 VLHVYEHLSKPKVTMGLQSNKNGTCVTNLTCCMEHGEEDVIYTWKALGQAANESHNGSIL 180

Qy        181 PISWRWGESDMTFICVARNPVSRNFSSPILARKLCEGAADDPDSSMVLLCLLLVPLLLSL 240
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Db        181 PISWRWGESDMTFICVARNPVSRNFSSPILARKLCEGAADDPDSSMVLLCLLLVPLLLSL 240

Qy        241 FVLGLFLWFLKRERQEEYIEEKKRVDICRETPNICPHSGENTEYDTIPHTNRTILKEDPA 300
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Db        241 FVLGLFLWFLKRERQEEYIEEKKRVDICRETPNICPHSGENTEYDTIPHTNRTILKEDPA 300

Qy        301 NTVYSTVEIPKKMENPHSLLTMPDTPRLFAYENVI 335
              |||||||||||||||||||||||||||||||||||
Db        301 NTVYSTVEIPKKMENPHSLLTMPDTPRLFAYENVI 335
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RESULT 3
US-09-989-723-253
; Sequence 253, Application US/09989723
; Patent No. US20020072092A1
; GENERAL INFORMATION:
; APPLICANT: Ashkenazi,Avi J.
; APPLICANT: Baker,Kevin P.
; APPLICANT: Botstein,David
; APPLICANT: Desnoyers,Luc
; APPLICANT: Eaton,Dan L.
; APPLICANT: Ferrara,Napoleone
; APPLICANT: Fong,Sherman
; APPLICANT: Gerber,Hanspeter
; APPLICANT: Gerritsen,Mary E.
; APPLICANT: Goddard,Audrey
; APPLICANT: Godowski,Paul J.
; APPLICANT: Grimaldi,J.Christopher
; APPLICANT: Gurney,Austin L.
; APPLICANT: Kljavin,Ivar J.
; APPLICANT: Napier,Mary A.
; APPLICANT: Pan,James
; APPLICANT: Paoni,Nicholas F.
; APPLICANT: Roy, Margaret Ann
; APPLICANT: Stewart, Timothy A.
; APPLICANT: Tumas, Daniel
; APPLICANT: Watanabe, Colin K.
; APPLICANT: Williams, P. Mickey
; APPLICANT: Wood, William I.
; APPLICANT: Zhang, Zemin
; TITLE OF INVENTION: Secreted and Transmembrane Polypeptides and Nucleic
; TITLE OF INVENTION: Acids Encoding the Same
; FILE REFERENCE: P2730P1C62
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; PRIOR FILING DATE: 1998-07-07
; PRIOR APPLICATION NUMBER: 60/092182
; PRIOR FILING DATE: 1998-07-09

Query Match 100.0%; Score 335; DB 9; Length 335;
Best Local Similarity 100.0%; Pred. No. 1.3e-305;
Matches 335; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

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RESULT 4
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; Patent No. US20020072496A1
; GENERAL INFORMATION:
; APPLICANT: Ashkenazi,Avi J.
; APPLICANT: Baker,Kevin P.
; APPLICANT: Botstein,David
; APPLICANT: Desnoyers,Luc
; APPLICANT: Eaton,Dan L.
; APPLICANT: Ferrara,Napoleone
; APPLICANT: Fong,Sherman

; APPLICANT: Gerber,Hanspeter
; APPLICANT: Gerritsen,Mary E.
; APPLICANT: Goddard,Audrey
; APPLICANT: Godowski,Paul J.
; APPLICANT: Grimaldi,J.Christopher
; APPLICANT: Gurney,Austin L.
; APPLICANT: Kljavin,Ivar J.
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; APPLICANT: Roy, Margaret Ann
; APPLICANT: Stewart, Timothy A.
; APPLICANT: Tumas, Daniel
; APPLICANT: Watanabe, Colin K.
; APPLICANT: Williams, P. Mickey
; APPLICANT: Wood, William I.
; APPLICANT: Zhang, Zemin
; TITLE OF INVENTION: Secreted and Transmembrane Polypeptides and Nucleic
; TITLE OF INVENTION: Acids Encoding the Same
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; PRIOR FILING DATE: 1998-07-09

Query Match 100.0%; Score 335; DB 9; Length 335;
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; APPLICANT: Ashkenazi,Avi J.
; APPLICANT: Baker,Kevin P.
; APPLICANT: Botstein,David
; APPLICANT: Desnoyers,Luc
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; APPLICANT: Watanabe, Colin K.
; APPLICANT: Williams, P. Mickey
; APPLICANT: Wood, William I.
; APPLICANT: Zhang, Zemin
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; TITLE OF INVENTION: Acids Encoding the Same
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; PRIOR APPLICATION NUMBER: 60/091978
; PRIOR FILING DATE: 1998-07-07
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; PRIOR FILING DATE: 1998-07-07
; PRIOR APPLICATION NUMBER: 60/092182
; PRIOR FILING DATE: 1998-07-09

Query Match 100.0%; Score 335; DB 9; Length 335;
Best Local Similarity 100.0%; Pred. No. 1.3e-305;
Matches 335; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

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Db        301 NTVYSTVEIPKKMENPHSLLTMPDTPRLFAYENVI 335
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RESULT 6
US-09-989-731-253
; Sequence 253, Application US/09989731
; Patent No. US20020103125A1
; GENERAL INFORMATION:
; APPLICANT: Ashkenazi,Avi J.
; APPLICANT: Baker,Kevin P.
; APPLICANT: Botstein,David
; APPLICANT: Desnoyers,Luc
; APPLICANT: Eaton,Dan L.
; APPLICANT: Ferrara,Napoleone
; APPLICANT: Fong,Sherman
; APPLICANT: Gerber,Hanspeter
; APPLICANT: Gerritsen,Mary E.
; APPLICANT: Goddard,Audrey
; APPLICANT: Godowski,Paul J.
; APPLICANT: Grimaldi,J.Christopher
; APPLICANT: Gurney,Austin L.
; APPLICANT: Kljavin,Ivar J.
; APPLICANT: Napier,Mary A.
; APPLICANT: Pan,James
; APPLICANT: Paoni,Nicholas F.
; APPLICANT: Roy, Margaret Ann
; APPLICANT: Stewart, Timothy A.
; APPLICANT: Tumas, Daniel
; APPLICANT: Watanabe, Colin K.
; APPLICANT: Williams, P. Mickey
; APPLICANT: Wood, William I.
; APPLICANT: Zhang, Zemin
; TITLE OF INVENTION: Secreted and Transmembrane Polypeptides and Nucleic
; TITLE OF INVENTION: Acids Encoding the Same
; FILE REFERENCE: P2730P1C70
; CURRENT APPLICATION NUMBER: US/09/989,731
; CURRENT FILING DATE: 2001-11-20
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; PRIOR FILING DATE: 1997-06-16
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; PRIOR APPLICATION NUMBER: 60/092182
; PRIOR FILING DATE: 1998-07-09

Query Match 100.0%; Score 335; DB 9; Length 335;
Best Local Similarity 100.0%; Pred. No. 1.3e-305;

Matches 335; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

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Qy        121 VLHVYEHLSKPKVTMGLQSNKNGTCVTNLTCCMEHGEEDVIYTWKALGQAANESHNGSIL 180
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RESULT 7
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; APPLICANT: Ashkenazi,Avi J.
; APPLICANT: Baker,Kevin P.
; APPLICANT: Botstein,David
; APPLICANT: Desnoyers,Luc
; APPLICANT: Eaton,Dan L.
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; APPLICANT: Gerritsen,Mary E.
; APPLICANT: Goddard,Audrey
; APPLICANT: Godowski,Paul J.
; APPLICANT: Grimaldi,J.Christopher
; APPLICANT: Gurney,Austin L.
; APPLICANT: Kljavin,Ivar J.
; APPLICANT: Napier,Mary A.
; APPLICANT: Pan,James
; APPLICANT: Paoni,Nicholas F.
; APPLICANT: Roy, Margaret Ann
; APPLICANT: Stewart, Timothy A.
; APPLICANT: Tumas, Daniel
; APPLICANT: Watanabe, Colin K.
; APPLICANT: Williams, P. Mickey
; APPLICANT: Wood, William I.
; APPLICANT: Zhang, Zemin
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; TITLE OF INVENTION: Acids Encoding the Same
; FILE REFERENCE: P2730P1C57
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; CURRENT FILING DATE: 2001-11-19
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; PRIOR FILING DATE: 1998-07-01
; PRIOR APPLICATION NUMBER: 60/091478
; PRIOR FILING DATE: 1998-07-02
; PRIOR APPLICATION NUMBER: 60/091544
; PRIOR FILING DATE: 1998-07-01
; PRIOR APPLICATION NUMBER: 60/091519
; PRIOR FILING DATE: 1998-07-02

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;  PRIOR APPLICATION NUMBER: 60/091626
;  PRIOR FILING DATE: 1998-07-02
;  PRIOR APPLICATION NUMBER: 60/091633
;  PRIOR FILING DATE: 1998-07-02
;  PRIOR APPLICATION NUMBER: 60/091978
;  PRIOR FILING DATE: 1998-07-07
;  PRIOR APPLICATION NUMBER: 60/091982
;  PRIOR FILING DATE: 1998-07-07
;  PRIOR APPLICATION NUMBER: 60/092182
;  PRIOR FILING DATE: 1998-07-09

  Query Match             100.0%;  Score 335;  DB 9;  Length 335;
  Best Local Similarity   100.0%;  Pred. No. 1.3e-305;
  Matches  335;  Conservative    0;  Mismatches    0;  Indels    0;  Gaps    0;

Qy          1 MAGSPTCLTLIYILWQLTGSAASGPVKELVGSVGGAVTFPLKSKVKQVDSIVWTFNTTPL 60
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Db          1 MAGSPTCLTLIYILWQLTGSAASGPVKELVGSVGGAVTFPLKSKVKQVDSIVWTFNTTPL 60

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Db         61 VTIQPEGGTIIVTQNRNRERVDFPDGGYSLKLSKLKKNDSGIYYVGIYSSSLQQPSTQEY 120

Qy        121 VLHVYEHLSKPKVTMGLQSNKNGTCVTNLTCCMEHGEEDVIYTWKALGQAANESHNGSIL 180
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Db        121 VLHVYEHLSKPKVTMGLQSNKNGTCVTNLTCCMEHGEEDVIYTWKALGQAANESHNGSIL 180

Qy        181 PISWRWGESDMTFICVARNPVSRNFSSPILARKLCEGAADDPDSSMVLLCLLLVPLLLSL 240
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Db        181 PISWRWGESDMTFICVARNPVSRNFSSPILARKLCEGAADDPDSSMVLLCLLLVPLLLSL 240

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Qy        301 NTVYSTVEIPKKMENPHSLLTMPDTPRLFAYENVI 335
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RESULT 8
US-09-745-605-4
; Sequence 4, Application US/09745605
; Patent No. US20020123617A1
; GENERAL INFORMATION:
;  APPLICANT: Starling, Gary C.
;  APPLICANT:  Finger, Joshua N.
;  TITLE OF INVENTION: NOVEL IMMUNOGLOBIN SUPERFAMILY MEMBERS APEX-1, APEX-2,
;  TITLE OF INVENTION:  AND APEX-3 AND USES THEREOF
;  FILE REFERENCE: DB13NP
;  CURRENT APPLICATION NUMBER: US/09/745,605
;  CURRENT FILING DATE:  2000-12-22
;  PRIOR APPLICATION NUMBER: 60/172,025
;  PRIOR FILING DATE: 1999-12-23
;  NUMBER OF SEQ ID NOS: 44
;  SOFTWARE: PatentIn Ver. 2.0
; SEQ ID NO 4
;   LENGTH: 335
;   TYPE: PRT
;   ORGANISM: Homo sapiens
US-09-745-605-4

  Query Match             100.0%;  Score 335;  DB 9;  Length 335;
  Best Local Similarity   100.0%;  Pred. No. 1.3e-305;
  Matches  335;  Conservative    0;  Mismatches    0;  Indels    0;  Gaps    0;

Qy          1 MAGSPTCLTLIYILWQLTGSAASGPVKELVGSVGGAVTFPLKSKVKQVDSIVWTFNTTPL 60
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Qy        121 VLHVYEHLSKPKVTMGLQSNKNGTCVTNLTCCMEHGEEDVIYTWKALGQAANESHNGSIL 180
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RESULT 9
US-09-991-073-253
; Sequence 253, Application US/09991073
; Patent No. US20020127576A1
; GENERAL INFORMATION:
;  APPLICANT: Ashkenazi,Avi J.
;  APPLICANT:  Baker,Kevin P.
;  APPLICANT:  Botstein,David
;  APPLICANT:  Desnoyers,Luc
;  APPLICANT:  Eaton,Dan L.
;  APPLICANT:  Ferrara,Napoleone
;  APPLICANT:  Fong,Sherman
;  APPLICANT:  Gerber,Hanspeter
;  APPLICANT:  Gerritsen,Mary E.
;  APPLICANT:  Goddard,Audrey
;  APPLICANT:  Godowski,Paul J.
;  APPLICANT:  Grimaldi,J.Christopher
;  APPLICANT:  Gurney,Austin L.
;  APPLICANT:  Kljavin,Ivar J.
;  APPLICANT:  Napier,Mary A.
;  APPLICANT:  Pan,James
;  APPLICANT:  Paoni,Nicholas F.
;  APPLICANT:  Roy, Margaret Ann
;  APPLICANT:  Stewart, Timothy A.
;  APPLICANT:  Tumas, Daniel
;  APPLICANT:  Watanabe, Colin K.
;  APPLICANT:  Williams, P. Mickey
;  APPLICANT:  Wood, William I.
;  APPLICANT:  Zhang, Zemin
;  TITLE OF INVENTION: Secreted and Transmembrane Polypeptides and Nucleic
;  TITLE OF INVENTION:  Acids Encoding the Same
;  FILE REFERENCE: P2730P1C15
;  CURRENT APPLICATION NUMBER: US/09/991,073
;  CURRENT FILING DATE:  2001-11-14
;  PRIOR APPLICATION NUMBER: 60/049787
;  PRIOR FILING DATE: 1997-06-16
;  PRIOR APPLICATION NUMBER: 60/062250
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;  PRIOR FILING DATE: 1997-11-13
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;  PRIOR FILING DATE: 1997-11-24
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;  PRIOR FILING DATE: 1998-02-25
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; PRIOR APPLICATION NUMBER: 60/091982
; PRIOR FILING DATE: 1998-07-07
; PRIOR APPLICATION NUMBER: 60/092182

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;  PRIOR FILING DATE: 1998-07-09

  Query Match          100.0%;  Score 335;  DB 9;  Length 335;
  Best Local Similarity  100.0%;  Pred. No. 1.3e-305;
  Matches  335;  Conservative    0;  Mismatches    0;  Indels    0;  Gaps    0;

Qy          1 MAGSPTCLTLIYILWQLTGSAASGPVKELVGSVGGAVTFPLKSKVKQVDSIVWTFNTTPL 60
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Db          1 MAGSPTCLTLIYILWQLTGSAASGPVKELVGSVGGAVTFPLKSKVKQVDSIVWTFNTTPL 60

Qy         61 VTIQPEGGTIIVTQNRNRERVDFPDGGYSLKLSKLKKNDSGIYYVGIYSSSLQQPSTQEY 120
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Qy        121 VLHVYEHLSKPKVTMGLQSNKNGTCVTNLTCCMEHGEEDVIYTWKALGQAANESHNGSIL 180
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Db        121 VLHVYEHLSKPKVTMGLQSNKNGTCVTNLTCCMEHGEEDVIYTWKALGQAANESHNGSIL 180

Qy        181 PISWRWGESDMTFICVARNPVSRNFSSPILARKLCEGAADDPDSSMVLLCLLLVPLLLSL 240
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Qy        241 FVLGLFLWFLKRERQEEYIEEKKRVDICRETPNICPHSGENTEYDTIPHTNRTILKEDPA 300
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Db        241 FVLGLFLWFLKRERQEEYIEEKKRVDICRETPNICPHSGENTEYDTIPHTNRTILKEDPA 300

Qy        301 NTVYSTVEIPKKMENPHSLLTMPDTPRLFAYENVI 335
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RESULT 10
US-09-990-442-253
; Sequence 253, Application US/09990442
; Patent No. US20020132252A1
; GENERAL INFORMATION:
;  APPLICANT: Ashkenazi,Avi J.
;  APPLICANT:  Baker,Kevin P.
;  APPLICANT:  Botstein,David
;  APPLICANT:  Desnoyers,Luc
;  APPLICANT:  Eaton,Dan L.
;  APPLICANT:  Ferrara,Napoleone
;  APPLICANT:  Fong,Sherman
;  APPLICANT:  Gerber,Hanspeter
;  APPLICANT:  Gerritsen,Mary E.
;  APPLICANT:  Goddard,Audrey
;  APPLICANT:  Godowski,Paul J.
;  APPLICANT:  Grimaldi,J.Christopher
;  APPLICANT:  Gurney,Austin L.
;  APPLICANT:  Kljavin,Ivar J.
;  APPLICANT:  Napier,Mary A.
;  APPLICANT:  Pan,James
;  APPLICANT:  Paoni,Nicholas F.
;  APPLICANT:  Roy, Margaret Ann
;  APPLICANT:  Stewart, Timothy A.
;  APPLICANT:  Tumas, Daniel
;  APPLICANT:  Watanabe, Colin K.
;  APPLICANT:  Williams, P. Mickey
;  APPLICANT:  Wood, William I.
;  APPLICANT:  Zhang, Zemin
;  TITLE OF INVENTION: Secreted and Transmembrane Polypeptides and Nucleic
;  TITLE OF INVENTION:  Acids Encoding the Same
;  FILE REFERENCE: P2730P1C8
;  CURRENT APPLICATION NUMBER: US/09/990,442
;  CURRENT FILING DATE:  2001-11-14
;  PRIOR APPLICATION NUMBER: 60/049787
;  PRIOR FILING DATE: 1997-06-16
;  PRIOR APPLICATION NUMBER: 60/062250
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; PRIOR APPLICATION NUMBER: 60/091978
; PRIOR FILING DATE: 1998-07-07
; PRIOR APPLICATION NUMBER: 60/091982
; PRIOR FILING DATE: 1998-07-07
; PRIOR APPLICATION NUMBER: 60/092182
; PRIOR FILING DATE: 1998-07-09

Query Match 100.0%; Score 335; DB 9; Length 335;
Best Local Similarity 100.0%; Pred. No. 1.3e-305;
Matches 335; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

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Qy        181 PISWRWGESDMTFICVARNPVSRNFSSPILARKLCEGAADDPDSSMVLLCLLLVPLLLSL 240
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RESULT 11
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; Patent No. US20020132253A1
; GENERAL INFORMATION:
; APPLICANT: Ashkenazi,Avi J.
; APPLICANT: Baker,Kevin P.
; APPLICANT: Botstein,David
; APPLICANT: Desnoyers,Luc
; APPLICANT: Eaton,Dan L.
; APPLICANT: Ferrara,Napoleone
; APPLICANT: Fong,Sherman
; APPLICANT: Gerber,Hanspeter
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; APPLICANT: Godowski,Paul J.
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; APPLICANT: Kljavin,Ivar J.
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; APPLICANT: Pan,James
; APPLICANT: Paoni,Nicholas F.
; APPLICANT: Roy, Margaret Ann
; APPLICANT: Stewart, Timothy A.
; APPLICANT: Tumas, Daniel
; APPLICANT: Watanabe, Colin K.
; APPLICANT: Williams, P. Mickey
; APPLICANT: Wood, William I.
; APPLICANT: Zhang, Zemin

; TITLE OF INVENTION: Secreted and Transmembrane Polypeptides and Nucleic
; TITLE OF INVENTION: Acids Encoding the Same
; FILE REFERENCE: P2730P1C17
; CURRENT APPLICATION NUMBER: US/09/991,163
; CURRENT FILING DATE: 2001-11-14
; PRIOR APPLICATION NUMBER: 60/049787
; PRIOR FILING DATE: 1997-06-16
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; PRIOR APPLICATION NUMBER: 60/092182
; PRIOR FILING DATE: 1998-07-09

Query Match 100.0%; Score 335; DB 9; Length 335;
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Matches 335; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

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RESULT 12
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; APPLICANT: Ashkenazi,Avi J.
; APPLICANT: Baker,Kevin P.
; APPLICANT: Botstein,David
; APPLICANT: Desnoyers,Luc
; APPLICANT: Eaton,Dan L.
; APPLICANT: Ferrara,Napoleone
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; APPLICANT: Pan,James
; APPLICANT: Paoni,Nicholas F.
; APPLICANT: Roy, Margaret Ann
; APPLICANT: Stewart, Timothy A.
; APPLICANT: Tumas, Daniel
; APPLICANT: Watanabe, Colin K.
; APPLICANT: Williams, P. Mickey
; APPLICANT: Wood, William I.
; APPLICANT: Zhang, Zemin
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; TITLE OF INVENTION: Acids Encoding the Same
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; CURRENT FILING DATE: 2001-11-14
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Query Match 100.0%; Score 335; DB 9; Length 335;
Best Local Similarity 100.0%; Pred. No. 1.3e-305;
Matches 335; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

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RESULT 13
US-09-990-456-253
; Sequence 253, Application US/09990456

; Patent No. US20020137890A1
; GENERAL INFORMATION:
; APPLICANT: Ashkenazi,Avi J.
; APPLICANT: Baker,Kevin P.
; APPLICANT: Botstein,David
; APPLICANT: Desnoyers,Luc
; APPLICANT: Eaton,Dan L.
; APPLICANT: Ferrara,Napoleone
; APPLICANT: Fong,Sherman
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; APPLICANT: Kljavin,Ivar J.
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; APPLICANT: Roy, Margaret Ann
; APPLICANT: Stewart, Timothy A.
; APPLICANT: Tumas, Daniel
; APPLICANT: Watanabe, Colin K.
; APPLICANT: Williams, P. Mickey
; APPLICANT: Wood, William I.
; APPLICANT: Zhang, Zemin
; TITLE OF INVENTION: Secreted and Transmembrane Polypeptides and Nucleic
; TITLE OF INVENTION: Acids Encoding the Same
; FILE REFERENCE: P2730P1C22
; CURRENT APPLICATION NUMBER: US/09/990,456
; CURRENT FILING DATE: 2001-11-14
; PRIOR APPLICATION NUMBER: 60/049787
; PRIOR FILING DATE: 1997-06-16
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;  PRIOR FILING DATE: 1998-07-07
;  PRIOR APPLICATION NUMBER: 60/091982
;  PRIOR FILING DATE: 1998-07-07
;  PRIOR APPLICATION NUMBER: 60/092182
;  PRIOR FILING DATE: 1998-07-09

  Query Match           100.0%;  Score 335;  DB 9;  Length 335;
  Best Local Similarity  100.0%;  Pred. No. 1.3e-305;
  Matches  335;  Conservative    0;  Mismatches    0;  Indels    0;  Gaps    0;

Qy          1 MAGSPTCLTLIYILWQLTGSAASGPVKELVGSVGGAVTFPLKSKVKQVDSIVWTFNTTPL 60
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Db          1 MAGSPTCLTLIYILWQLTGSAASGPVKELVGSVGGAVTFPLKSKVKQVDSIVWTFNTTPL 60

Qy         61 VTIQPEGGTIIVTQNRNRERVDFPDGGYSLKLSKLKKNDSGIYYVGIYSSSLQQPSTQEY 120
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Qy        121 VLHVYEHLSKPKVTMGLQSNKNGTCVTNLTCCMEHGEEDVIYTWKALGQAANESHNGSIL 180
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Qy        181 PISWRWGESDMTFICVARNPVSRNFSSPILARKLCEGAADDPDSSMVLLCLLLVPLLLSL 240
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RESULT 14
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; Sequence 253, Application US/09989721
; Patent No. US20020142961A1
; GENERAL INFORMATION:
;  APPLICANT: Ashkenazi,Avi J.
;  APPLICANT:  Baker,Kevin P.
;  APPLICANT:  Botstein,David
;  APPLICANT:  Desnoyers,Luc
;  APPLICANT:  Eaton,Dan L.
;  APPLICANT:  Ferrara,Napoleone
;  APPLICANT:  Fong,Sherman
;  APPLICANT:  Gerber,Hanspeter
;  APPLICANT:  Gerritsen,Mary E.
;  APPLICANT:  Goddard,Audrey
;  APPLICANT:  Godowski,Paul J.
;  APPLICANT:  Grimaldi,J.Christopher
;  APPLICANT:  Gurney,Austin L.
;  APPLICANT:  Kljavin,Ivar J.
;  APPLICANT:  Napier,Mary A.
;  APPLICANT:  Pan,James
;  APPLICANT:  Paoni,Nicholas F.
;  APPLICANT:  Roy, Margaret Ann
;  APPLICANT:  Stewart, Timothy A.
;  APPLICANT:  Tumas, Daniel
;  APPLICANT:  Watanabe, Colin K.
;  APPLICANT:  Williams, P. Mickey
;  APPLICANT:  Wood, William I.
;  APPLICANT:  Zhang, Zemin
;  TITLE OF INVENTION: Secreted and Transmembrane Polypeptides and Nucleic
;  TITLE OF INVENTION:  Acids Encoding the Same
;  FILE REFERENCE: P2730P1C55
;  CURRENT APPLICATION NUMBER: US/09/989,721
;  CURRENT FILING DATE:  2001-11-19
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Matches 335; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

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RESULT 15
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; Patent No. US20020160384A1
; GENERAL INFORMATION:
;  APPLICANT: Ashkenazi,Avi J.
;  APPLICANT:  Baker,Kevin P.
;  APPLICANT:  Botstein,David
;  APPLICANT:  Desnoyers,Luc
;  APPLICANT:  Eaton,Dan L.
;  APPLICANT:  Ferrara,Napoleone
;  APPLICANT:  Fong,Sherman
;  APPLICANT:  Gerber,Hanspeter
;  APPLICANT:  Gerritsen,Mary E.
;  APPLICANT:  Goddard,Audrey
;  APPLICANT:  Godowski,Paul J.
;  APPLICANT:  Grimaldi,J.Christopher
;  APPLICANT:  Gurney,Austin L.
;  APPLICANT:  Kljavin,Ivar J.
;  APPLICANT:  Napier,Mary A.
;  APPLICANT:  Pan,James
;  APPLICANT:  Paoni,Nicholas F.
;  APPLICANT:  Roy, Margaret Ann
;  APPLICANT:  Stewart, Timothy A.
;  APPLICANT:  Tumas, Daniel
;  APPLICANT:  Watanabe, Colin K.
;  APPLICANT:  Williams, P. Mickey
;  APPLICANT:  Wood, William I.
;  APPLICANT:  Zhang, Zemin
;  TITLE OF INVENTION: Secreted and Transmembrane Polypeptides and Nucleic
;  TITLE OF INVENTION:  Acids Encoding the Same
;  FILE REFERENCE: P2730P1C20
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;  CURRENT FILING DATE:  2001-11-14
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; PRIOR FILING DATE: 1998-07-09

Query Match 100.0%; Score 335; DB 9; Length 335;
Best Local Similarity 100.0%; Pred. No. 1.3e-305;
Matches 335; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

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Qy         61 VTIQPEGGTIIVTQNRNRERVDFPDGGYSLKLSKLKKNDSGIYYVGIYSSSLQQPSTQEY 120
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Qy        121 VLHVYEHLSKPKVTMGLQSNKNGTCVTNLTCCMEHGEEDVIYTWKALGQAANESHNGSIL 180
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Qy        181 PISWRWGESDMTFICVARNPVSRNFSSPILARKLCEGAADDPDSSMVLLCLLLVPLLLSL 240
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Db        181 PISWRWGESDMTFICVARNPVSRNFSSPILARKLCEGAADDPDSSMVLLCLLLVPLLLSL 240

Qy        241 FVLGLFLWFLKRERQEEYIEEKKRVDICRETPNICPHSGENTEYDTIPHTNRTILKEDPA 300
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Db        241 FVLGLFLWFLKRERQEEYIEEKKRVDICRETPNICPHSGENTEYDTIPHTNRTILKEDPA 300

Qy        301 NTVYSTVEIPKKMENPHSLLTMPDTPRLFAYENVI 335
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Search completed: August 18, 2004, 15:58:09
Job time : 51 secs

GenCore version 5.1.6

OM protein - protein search, using sw model

Run on: August 18, 2004, 15:57:14 ; Search time 16 Seconds
(without alignments)'
2014.010 Million cell updates/sec

Title: US-10-063-549-46
Perfect score: 335
Sequence: 1 MAGSPTCLTLIYILWQLTGS.....PHSLLTMPDTPRLFAYENVI 335

Scoring table: OLIGO
Gapop 60.0 , Gapext 60.0

Searched: 283366 seqs, 96191526 residues

Word size : 0

Total number of hits satisfying chosen parameters: 283366

Minimum DB seq length: 0
Maximum DB seq length: 2000000000

Post-processing: Listing first 700 summaries

Database : PIR_78:*
1: pir1:*
2: pir2:*
3: pir3:*
4: pir4:*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	% Query Match	Length	DB	ID	Description
1	9	2.7	156	2	H72621	hypothetical prote
2	9	2.7	2464	1	QRMSP1	microtubule-associ
3	8	2.4	173	2	S76681	hypothetical prote
4	8	2.4	286	2	A82159	hypothetical prote
5	8	2.4	705	2	S18733	glutenin high mole
6	8	2.4	1117	2	S38673	desmoglein 2 - hum
7	7	2.1	105	2	T29918	hypothetical prote
8	7	2.1	161	2	E71866	hypothetical prote
9	7	2.1	170	2	AE1817	hypothetical prote
10	7	2.1	179	2	F97283	ribosomal protein
11	7	2.1	179	2	F83305	hypothetical prote
12	7	2.1	182	2	F97499	hypothetical prote
13	7	2.1	184	2	I40220	hypothetical prote
14	7	2.1	189	2	H70416	hypothetical prote
15	7	2.1	199	2	T45543	hypothetical prote
16	7	2.1	220	2	E75285	hypothetical prote
17	7	2.1	228	2	T47847	hypothetical prote
18	7	2.1	238	2	G69820	hypothetical prote
19	7	2.1	238	2	C82884	conserved hypothet
20	7	2.1	239	2	F69996	amino acid ABC tra
21	7	2.1	239	2	T51270	hypothetical prote
22	7	2.1	266	2	C87367	flagellar biosynth
23	7	2.1	274	2	G84218	cysteine synthase
24	7	2.1	290	2	A88616	protein T25C8.3 [i
25	7	2.1	301	2	T52549	probable thiosulfa
26	7	2.1	301	2	D83970	UDP-N-acetylenolpy
27	7	2.1	302	2	E75414	PecM-related prote
28	7	2.1	303	2	A43727	UDP-N-acetylenolpy
29	7	2.1	305	2	G96962	UDP-N-acetylenolpy
30	7	2.1	312	1	LPRTE	apolipoprotein E p
31	7	2.1	316	2	G95161	UDP-N-acetylenolpy
32	7	2.1	316	2	F98027	UDP-N-acetylmurama
33	7	2.1	331	2	C89469	protein F07G6.1 [i
34	7	2.1	348	2	E84299	hypothetical prote
35	7	2.1	351	2	C82755	conserved hypothet
36	7	2.1	356	2	S14396	cytochrome-c oxida
37	7	2.1	362	2	S68471	asparaginase (EC 3
38	7	2.1	367	2	S41024	hypothetical prote
39	7	2.1	369	2	T21392	hypothetical prote
40	7	2.1	377	2	H89717	protein C18B12.2 [
41	7	2.1	379	2	S49614	cycH protein - Rhi
42	7	2.1	381	2	T11776	ubiquinol-cytochro
43	7	2.1	381	2	T11312	ubiquinol-cytochro
44	7	2.1	410	2	B81744	poly(A) polymerase
45	7	2.1	413	2	T48089	hypothetical prote
46	7	2.1	418	2	F64059	tryptophan transpo
47	7	2.1	428	2	AD0675	membrane transport
48	7	2.1	433	2	S45856	probable membrane
49	7	2.1	443	2	AB2719	conserved hypothet
50	7	2.1	448	2	JC2305	gluconate permease
51	7	2.1	454	2	T19380	hypothetical prote
52	7	2.1	458	2	F69123	efflux pump antibi
53	7	2.1	463	2	A69905	conserved hypothet
54	7	2.1	464	2	AG1146	beta-glucosidase h
55	7	2.1	464	2	AG1505	beta-glucosidase h
56	7	2.1	467	2	A99498	hypothetical prote
57	7	2.1	475	2	T47480	hypothetical prote
58	7	2.1	480	2	F97500	tolerance to colic
59	7	2.1	492	2	D87606	sensor histidine k
60	7	2.1	501	2	H95859	probable ABC trans
61	7	2.1	508	2	E96804	probable thioredox
62	7	2.1	513	2	B84391	DNA damage-inducib
63	7	2.1	572	2	AB2671	cytochrome-c oxida
64	7	2.1	586	1	VCLJMP	env polyprotein -
65	7	2.1	587	1	VCLJSA	env polyprotein -
66	7	2.1	591	2	B54354	calnexin precursor
67	7	2.1	591	2	C54354	calnexin precursor
68	7	2.1	605	2	S52253	copper resistance
69	7	2.1	643	2	B72602	hypothetical prote
70	7	2.1	646	2	D82493	conserved hypothet
71	7	2.1	675	2	T22323	hypothetical prote
72	7	2.1	730	2	T13792	NADH2 dehydrogenas
73	7	2.1	732	1	JC4655	acylaminoacyl-pept
74	7	2.1	797	2	T50072	hypothetical prote
75	7	2.1	799	2	H71255	probable cell divi
76	7	2.1	829	2	T40239	probable helicase
77	7	2.1	914	2	I40529	penicillin-binding
78	7	2.1	943	2	F95021	excinuclease ABC,
79	7	2.1	943	2	C97893	excinuclease ABC c
80	7	2.1	954	2	AF2756	glycine cleavage s
81	7	2.1	954	2	E97537	glycine cleavage s
82	7	2.1	957	2	F91100	glycine decarboxyl
83	7	2.1	957	2	B85946	hypothetical prote
84	7	2.1	957	2	S36834	glycine dehydrogen
85	7	2.1	957	2	AC0873	glycine dehydrogen
86	7	2.1	958	2	E82994	glycine cleavage s
87	7	2.1	959	2	AB0111	glycine dehydrogen
88	7	2.1	997	2	T32814	hypothetical prote
89	7	2.1	1002	2	S62035	isoleucine-tRNA li
90	7	2.1	1020	2	JN0124	glycine dehydrogen
91	7	2.1	1032	2	S53571	hypothetical prote
92	7	2.1	1070	2	T06733	kinesin homolog F2
93	7	2.1	1085	2	S55352	IFH1 protein - yea
94	7	2.1	1166	2	T15628	hypothetical prote
95	7	2.1	1268	2	A49674	flightless-I homol
96	7	2.1	1277	2	T15109	hypothetical prote
97	7	2.1	1290	2	T00018	period protein hom
98	7	2.1	1291	2	T00019	period protein hom
99	7	2.1	1312	2	S68593	DNA-directed DNA p
100	7	2.1	1345	2	T29090	surface layer-asso
101	7	2.1	1355	2	T22552	hypothetical prote
102	7	2.1	1487	2	S15904	alpha-1 proteinase

103	7	2.1	1552	2	T05408	hypothetical prote
104	7	2.1	1560	2	T02885	peroxisome prolife
105	7	2.1	1585	2	AE2916	NAD-glutamate dehy
106	7	2.1	1585	2	H97690	NAD-glutamate dehy
107	7	2.1	1620	2	S61535	nucleotide-binding
108	7	2.1	2787	2	S45416	TEL1 protein - yea
109	7	2.1	3973	2	B71612	hypothetical prote
110	7	2.1	4545	1	S25111	alpha-2-macroglobu
111	6	1.8	30	2	I57689	ubiquinol-cytochro
112	6	1.8	32	2	S21547	T-cell receptor al
113	6	1.8	36	2	H64607	hypothetical prote
114	6	1.8	39	2	C90523	hypothetical prote
115	6	1.8	52	2	C60232	T-cell surface gly
116	6	1.8	56	2	C69044	hypothetical prote
117	6	1.8	57	2	D95852	hypothetical prote
118	6	1.8	60	2	B28918	hypothetical prote
119	6	1.8	61	2	JQ1086	nodulin-14 precurs
120	6	1.8	66	2	C89925	hypothetical prote
121	6	1.8	70	2	A42155	GTP-binding regula
122	6	1.8	72	2	C83219	hypothetical prote
123	6	1.8	73	2	T26110	hypothetical prote
124	6	1.8	73	2	T13199	hypothetical prote
125	6	1.8	74	2	E95204	hypothetical prote
126	6	1.8	75	2	C95959	hypothetical prote
127	6	1.8	77	2	AG2343	hypothetical prote
128	6	1.8	82	2	C81350	hypothetical prote
129	6	1.8	83	2	JC7607	prolactin-releasin
130	6	1.8	86	2	AC2117	hypothetical prote
131	6	1.8	92	2	I64109	mercury reductase
132	6	1.8	93	2	T45245	hypothetical prote
133	6	1.8	95	2	S68231	FHG22 protein prec
134	6	1.8	95	2	T49793	hypothetical prote
135	6	1.8	96	1	A42281	symbionin symS - p
136	6	1.8	96	1	ZEBPG4	gene E protein - p
137	6	1.8	96	2	JC4518	heat-shock protein
138	6	1.8	96	2	B64076	chaperonin groES -
139	6	1.8	96	2	C82048	chaperonin, 10 Kd
140	6	1.8	96	2	A84932	10 kD chaperonin [
141	6	1.8	97	1	BVECGS	chaperonin groES -
142	6	1.8	97	2	A48093	monocytic cytokine
143	6	1.8	97	2	JC5770	chaperonin groES-1
144	6	1.8	97	2	A86110	chaperonin mopB [s
145	6	1.8	97	2	C91269	chaperonin GroES [
146	6	1.8	97	2	AD1045	GroES protein [imp
147	6	1.8	97	2	E97266	glu-tRNA amidotran
148	6	1.8	98	2	S41828	NADH2 dehydrogenas
149	6	1.8	98	2	S24920	NADH2 dehydrogenas
150	6	1.8	98	2	T11488	NADH2 dehydrogenas
151	6	1.8	99	1	A39296	monocyte chemoattr
152	6	1.8	99	2	JC5295	monocyte chemotact
153	6	1.8	99	2	JC2336	monocyte chemoattr
154	6	1.8	99	2	JC2136	monocyte chemoattr
155	6	1.8	99	2	A60299	monocyte chemoattr
156	6	1.8	99	2	JC2417	monocyte chemoattr
157	6	1.8	100	2	E64999	NADH2 dehydrogenas
158	6	1.8	100	2	C91024	NADH dehydrogenase
159	6	1.8	100	2	D85868	NADH dehydrogenase
160	6	1.8	100	2	AH0310	NADH2 dehydrogenas
161	6	1.8	100	2	AE0796	NADH2 dehydrogenas
162	6	1.8	100	2	E69846	hypothetical prote
163	6	1.8	101	2	S37068	NADH2 dehydrogenas
164	6	1.8	101	2	S64222	probable membrane
165	6	1.8	102	2	F87993	protein ZC334.3 [i
166	6	1.8	103	2	S72692	probable membrane
167	6	1.8	106	2	B97734	hypothetical prote
168	6	1.8	107	2	PH0987	Ig heavy chain V r
169	6	1.8	107	2	C70188	hypothetical prote
170	6	1.8	108	2	S73125	hypothetical prote
171	6	1.8	108	2	A55590	hypothetical prote
172	6	1.8	108	2	I40598	hypothetical prote
173	6	1.8	109	2	A54678	monocyte chemotact
174	6	1.8	109	2	H71142	hypothetical prote
175	6	1.8	111	2	G75009	hypothetical prote
176	6	1.8	111	2	G64650	ribosome-binding f
177	6	1.8	111	2	F71940	probable ribosome-
178	6	1.8	111	2	B83101	hypothetical prote
179	6	1.8	112	2	S48472	probable membrane
180	6	1.8	113	2	S26266	T-cell receptor be
181	6	1.8	113	2	S17385	T-cell receptor be
182	6	1.8	113	2	S26262	T-cell receptor be
183	6	1.8	113	2	S26263	T-cell receptor be
184	6	1.8	113	2	JC4143	molt-inhibiting ho
185	6	1.8	113	2	AD2868	hypothetical prote
186	6	1.8	114	2	AC3033	hypothetical prote
187	6	1.8	115	2	AG3279	hypothetical prote
188	6	1.8	115	2	S09751	hypothetical prote
189	6	1.8	116	2	T51028	hypothetical prote
190	6	1.8	118	2	A97639	hypothetical prote
191	6	1.8	118	2	AB2862	conserved hypothet
192	6	1.8	118	2	H97644	hypothetical prote
193	6	1.8	120	2	I48147	monocyte chemoattr
194	6	1.8	122	2	A05304	hemoglobin beta-1
195	6	1.8	122	2	A83283	hypothetical prote
196	6	1.8	123	2	E95940	conserved hypothet
197	6	1.8	123	2	I48192	surface antigen -
198	6	1.8	123	2	G75336	hypothetical prote
199	6	1.8	124	2	AI1647	hypothetical prote
200	6	1.8	125	2	I46857	monocyte chemoattr
201	6	1.8	125	2	T27519	hypothetical prote
202	6	1.8	126	2	S73081	hypothetical prote
203	6	1.8	126	2	S30707	hypothetical 14.5K
204	6	1.8	126	2	AE0918	probable membrane
205	6	1.8	126	2	C72650	hypothetical prote
206	6	1.8	128	2	C48552	hypothetical prote
207	6	1.8	128	2	D29504	hypothetical 14K p
208	6	1.8	128	2	C75462	hypothetical prote
209	6	1.8	128	2	AD1386	hypothetical prote
210	6	1.8	128	2	AF1761	hypothetical prote
211	6	1.8	129	2	F95987	conserved hypothet
212	6	1.8	132	2	C87431	hypothetical prote
213	6	1.8	132	2	H75335	hypothetical prote
214	6	1.8	132	2	B83956	hypothetical prote
215	6	1.8	133	2	S57876	T cell receptor CK
216	6	1.8	133	2	C36886	hypothetical prote
217	6	1.8	134	2	D87021	probable DNA-bindi
218	6	1.8	135	2	A70659	hypothetical prote
219	6	1.8	135	2	B83440	hypothetical prote
220	6	1.8	135	2	F87156	hypothetical prote
221	6	1.8	136	2	AD0630	probable exported
222	6	1.8	136	2	T22797	hypothetical prote
223	6	1.8	137	1	F64961	hypothetical prote
224	6	1.8	137	2	S03489	T-cell receptor be
225	6	1.8	137	2	C85815	hypothetical prote
226	6	1.8	137	2	D90967	hypothetical prote
227	6	1.8	137	2	A44031	probable membrane
228	6	1.8	139	2	S36296	T-cell receptor ga
229	6	1.8	140	2	C81176	hypothetical prote
230	6	1.8	140	2	A99253	hypothetical prote
231	6	1.8	141	2	E32998	chorion protein S1
232	6	1.8	141	2	D81309	probable acetyltra
233	6	1.8	142	2	T27965	hypothetical prote
234	6	1.8	143	2	D75617	response regulator
235	6	1.8	144	2	T27945	hypothetical prote
236	6	1.8	145	2	G82617	VirK protein XF194
237	6	1.8	146	2	S26408	T-cell receptor be
238	6	1.8	146	2	T45385	ribosomal protein
239	6	1.8	146	2	T27964	hypothetical prote
240	6	1.8	149	2	AD3431	hypothetical prote
241	6	1.8	150	2	S43955	probable NADH2 deh
242	6	1.8	150	2	A87714	hypothetical prote
243	6	1.8	151	2	S48958	hypothetical prote
244	6	1.8	151	2	A83784	acetyltransferase
245	6	1.8	152	2	S21826	T-cell receptor be
246	6	1.8	152	2	F86318	protein F15H18.2 [
247	6	1.8	153	1	A28406	gastric inhibitory
248	6	1.8	153	2	C64373	hypothetical prote

249	6	1.8	153	2	E87306	hypothetical prote
250	6	1.8	157	2	S57451	cysteine proteinas
251	6	1.8	157	2	T24917	hypothetical prote
252	6	1.8	158	2	H96900	probable HD superf
253	6	1.8	159	2	D90586	hypothetical prote
254	6	1.8	161	2	E72339	hypothetical prote
255	6	1.8	162	1	CFKKA	C-phycocyanin alph
256	6	1.8	162	1	CFMWA	C-phycocyanin alph
257	6	1.8	162	2	S30940	phycocyanin alpha
258	6	1.8	162	2	H72351	hypothetical prote
259	6	1.8	163	2	A29674	phycocyanin alpha
260	6	1.8	163	2	AH1872	phycocyanin alpha
261	6	1.8	165	2	G82910	peptide methionine
262	6	1.8	166	2	T11099	NADH2 dehydrogenas
263	6	1.8	170	2	T30570	hypothetical prote
264	6	1.8	171	2	E75562	MutT/nudix family
265	6	1.8	171	2	H87440	hypothetical prote
266	6	1.8	172	1	DERTN6	NADH2 dehydrogenas
267	6	1.8	172	2	H72077	ct006 hypothetical
268	6	1.8	172	2	C81590	conserved hypothet
269	6	1.8	172	2	H86545	CT006 hypothetical
270	6	1.8	174	2	T01486	hypothetical prote
271	6	1.8	176	2	S35949	edeA protein - tre
272	6	1.8	176	2	JC6152	orphanin FQ precur
273	6	1.8	177	2	S45364	ribosomal protein
274	6	1.8	177	2	B91248	hypothetical prote
275	6	1.8	178	2	S54190	outer surface prot
276	6	1.8	179	2	S36295	T-cell receptor ga
277	6	1.8	179	2	S54186	outer surface prot
278	6	1.8	179	2	S54187	outer surface prot
279	6	1.8	179	2	S54188	outer surface prot
280	6	1.8	179	2	T35439	probable integral
281	6	1.8	180	2	S54189	outer surface prot
282	6	1.8	180	2	S54191	outer surface prot
283	6	1.8	181	2	G89799	hypothetical prote
284	6	1.8	181	2	I40146	outer surface prot
285	6	1.8	181	2	AC0686	hypothetical prote
286	6	1.8	184	2	S73640	inorganic diphosph
287	6	1.8	185	2	AG2026	hypothetical prote
288	6	1.8	186	1	HHFF23	heat shock protein
289	6	1.8	186	2	T11384	ATPase subunit 6 -
290	6	1.8	186	2	B20647	heat shock protein
291	6	1.8	186	2	T47804	hypothetical prote
292	6	1.8	187	2	G95076	conserved hypothet
293	6	1.8	187	2	H70450	lipoprotein nlpD h
294	6	1.8	188	2	S50158	RER1 protein - yea
295	6	1.8	188	2	A69880	hypothetical prote
296	6	1.8	190	2	T33366	hypothetical prote
297	6	1.8	191	2	F82430	periplasmic nitrat
298	6	1.8	191	2	S70262	outer surface prot
299	6	1.8	192	2	S22981	T-cell surface gly
300	6	1.8	192	2	JC4663	T-cell receptor CD
301	6	1.8	193	2	S70259	outer surface prot
302	6	1.8	193	2	S70274	outer surface prot
303	6	1.8	193	2	S70286	outer surface prot
304	6	1.8	194	2	D97944	conserved hypothet
305	6	1.8	194	2	C83312	hypothetical prote
306	6	1.8	196	2	S54196	outer surface prot
307	6	1.8	197	2	E70642	probable ribosomal
308	6	1.8	197	2	C90671	hypothetical prote
309	6	1.8	197	2	G85521	hypothetical prote
310	6	1.8	197	2	B83768	hypothetical prote
311	6	1.8	200	2	E64756	membrane protein y
312	6	1.8	200	2	A81295	probable membrane
313	6	1.8	201	2	D86912	conserved hypothet
314	6	1.8	202	2	T10016	hypothetical prote
315	6	1.8	202	2	D69046	conserved hypothet
316	6	1.8	202	2	B83375	hypothetical prote
317	6	1.8	203	2	AC0620	hypothetical proph
318	6	1.8	203	2	S32799	hypothetical prote
319	6	1.8	204	2	H70648	probable regulator
320	6	1.8	204	2	B72370	hypothetical prote
321	6	1.8	204	2	T51012	hypothetical prote
322	6	1.8	205	2	S42406	protein phosphatas
323	6	1.8	205	2	S10497	hypothetical prote
324	6	1.8	206	2	AE0891	probable membrane
325	6	1.8	206	2	S61705	hypothetical prote
326	6	1.8	206	2	AE2222	hypothetical prote
327	6	1.8	207	2	A35535	23K calcium-bindin
328	6	1.8	209	2	H69552	hypothetical prote
329	6	1.8	209	2	S69926	outer surface prot
330	6	1.8	209	2	I40285	outer surface prot
331	6	1.8	210	2	T50713	urease accessory p
332	6	1.8	210	2	G97037	hypothetical prote
333	6	1.8	211	2	S69932	outer surface prot
334	6	1.8	211	2	C59091	hypothetical prote
335	6	1.8	212	2	B29010	alkylmercury lyase
336	6	1.8	212	2	S69921	outer surface prot
337	6	1.8	212	2	S20543	outer surface prot
338	6	1.8	213	2	S74247	CDP diacylglycerol
339	6	1.8	213	2	S07573	amine oxidase (fla
340	6	1.8	213	2	C70346	UDP-N-acetoenolpyr
341	6	1.8	214	1	S18729	adenylyl-sulfate k
342	6	1.8	214	2	T21585	hypothetical prote
343	6	1.8	215	2	G95170	hemolysin [importe
344	6	1.8	215	2	G98036	conserved hypothet
345	6	1.8	215	2	T48789	TFS1 related prote
346	6	1.8	216	2	H72277	hypothetical prote
347	6	1.8	216	2	T00192	hypothetical prote
348	6	1.8	217	2	S65830	alpha fucosidase p
349	6	1.8	217	2	S49578	trypsin inhibitor
350	6	1.8	217	2	H72390	dihydroorotate deh
351	6	1.8	217	2	F91246	PTS system, sorbos
352	6	1.8	218	2	B83862	endonuclease III (
353	6	1.8	218	2	G64673	DNA polymerase III
354	6	1.8	218	2	B71844	probable DNA poyme
355	6	1.8	218	2	S74867	hypothetical prote
356	6	1.8	219	2	S49428	hypothetical prote
357	6	1.8	221	1	S24328	glutathione peroxi
358	6	1.8	221	2	A47367	24K androgen-depen
359	6	1.8	221	2	B42719	O-methyltransferas
360	6	1.8	222	2	JC7697	beta-casein-like p
361	6	1.8	222	2	AD2999	thiol:disulfide in
362	6	1.8	222	2	E98284	thiol,disulfide in
363	6	1.8	223	2	S49492	histone H1 - mouse
364	6	1.8	224	2	F69444	conserved hypothet
365	6	1.8	225	2	G70721	hypothetical prote
366	6	1.8	227	2	F97276	CPSD/CAPA conserve
367	6	1.8	227	2	D84775	hypothetical prote
368	6	1.8	228	2	B90369	hypothetical prote
369	6	1.8	229	2	B90534	trna/rrna methyltr
370	6	1.8	229	2	T18629	hypothetical prote
371	6	1.8	230	2	D84215	hypothetical prote
372	6	1.8	230	2	T36263	probable transcrip
373	6	1.8	231	2	AF1798	probable N-acetylm
374	6	1.8	232	2	B69392	ABC transporter, A
375	6	1.8	233	2	B64525	trbI protein - Hel
376	6	1.8	235	2	S48924	hypothetical prote
377	6	1.8	236	2	D84961	orotidine-5'-phosp
378	6	1.8	236	2	C75516	hypothetical prote
379	6	1.8	236	2	E75337	hypothetical prote
380	6	1.8	237	2	S08073	cyclic nucleotide
381	6	1.8	237	2	S34727	listeriolysin regu
382	6	1.8	237	2	AH1424	a probable N-acety
383	6	1.8	237	2	T05249	hypothetical prote
384	6	1.8	239	2	A81437	probable integral
385	6	1.8	239	2	T31881	hypothetical prote
386	6	1.8	240	2	AD1950	hypothetical prote
387	6	1.8	240	2	T47589	synaptobrevin-like
388	6	1.8	240	2	AG0048	hypothetical prote
389	6	1.8	241	2	T33804	hypothetical prote
390	6	1.8	241	2	C86492	hypothetical prote
391	6	1.8	241	2	C72130	hypothetical prote
392	6	1.8	242	2	JC7517	caspase-14/a - hum
393	6	1.8	243	2	G81255	1-(5-phosphoribosy
394	6	1.8	244	2	T43764	ATPase chain 6 [im

395	6	1.8	245	2	D36145	precorrin-2 methyl
396	6	1.8	245	2	B75340	transcription regu
397	6	1.8	245	2	F83105	hypothetical prote
398	6	1.8	246	2	T00704	hypothetical prote
399	6	1.8	247	2	A75254	conserved hypothet
400	6	1.8	247	2	E86250	protein F25C20.16
401	6	1.8	247	2	S66064	conserved hypothet
402	6	1.8	248	2	D69094	phosphoribosylamin
403	6	1.8	249	2	S23902	genome polyprotein
404	6	1.8	249	2	C75156	hypothetical prote
405	6	1.8	250	2	H83213	hypothetical prote
406	6	1.8	250	2	T40977	cdp-diacylglycerol
407	6	1.8	250	2	E82821	NADH-ubiquinone ox
408	6	1.8	251	2	C84036	succinate dehydrog
409	6	1.8	251	2	AC2187	phospho-2-dehydro-
410	6	1.8	251	2	B64851	flagellar basal bo
411	6	1.8	251	2	G90810	flagellar rod prot
412	6	1.8	251	2	C85670	flagellar rod prot
413	6	1.8	251	2	E72578	hypothetical prote
414	6	1.8	252	2	H90212	enoyl CoA hydratas
415	6	1.8	252	2	B47188	MHC class II histo
416	6	1.8	253	2	S05029	H+-transporting tw
417	6	1.8	253	2	D88427	protein R07E5.15 [
418	6	1.8	253	2	T30928	hypothetical prote
419	6	1.8	254	1	VCCVTY	coat protein - tob
420	6	1.8	254	2	S25281	gltF protein precu
421	6	1.8	255	2	F84244	proteasome, subuni
422	6	1.8	256	2	T22715	hypothetical prote
423	6	1.8	256	2	T00165	repressor - Staphy
424	6	1.8	257	2	B70246	outer surface prot
425	6	1.8	257	2	AC0087	probable flagellar
426	6	1.8	259	1	ONGAOL	ovulation hormone
427	6	1.8	260	2	I51544	MHC class II beta-
428	6	1.8	260	2	I51542	MHC class II beta-
429	6	1.8	260	2	T33869	hypothetical prote
430	6	1.8	260	2	T29909	hypothetical prote
431	6	1.8	260	2	S60480	low temperature-in
432	6	1.8	261	2	AE3499	O-sialoglycoprotei
433	6	1.8	261	2	S10321	31K protein - frog
434	6	1.8	261	2	D95271	hypothetical prote
435	6	1.8	262	1	OTFF3	cytochrome-c oxida
436	6	1.8	262	2	A81504	conserved hypothet
437	6	1.8	262	2	B72037	ct598 hypothetical
438	6	1.8	262	2	E86588	CT598 hypothetical
439	6	1.8	263	1	S23009	insulin-like growt
440	6	1.8	263	2	E72675	hypothetical prote
441	6	1.8	263	2	C69064	conserved hypothet
442	6	1.8	264	2	H81720	conserved hypothet
443	6	1.8	265	2	S16592	chlorophyll a/b-bi
444	6	1.8	265	2	F69742	hypothetical prote
445	6	1.8	267	2	A86891	hypothetical prote
446	6	1.8	267	2	H82201	probable bax prote
447	6	1.8	267	2	T29500	hypothetical prote
448	6	1.8	267	2	C75131	hypothetical prote
449	6	1.8	267	2	S70291	hypothetical prote
450	6	1.8	268	2	A71086	hypothetical prote
451	6	1.8	269	2	A75397	probable signal pe
452	6	1.8	269	2	I51539	MHC class II beta-
453	6	1.8	269	2	I51540	MHC class II beta-
454	6	1.8	269	2	S73999	hypothetical prote
455	6	1.8	269	2	T04095	ribonuclease S hom
456	6	1.8	269	2	H98273	iron(III) dicitrat
457	6	1.8	270	2	I51543	MHC class II beta-
458	6	1.8	270	2	S57457	formylmethanofuran
459	6	1.8	271	2	D83059	phosphatidylserine
460	6	1.8	272	2	H87075	probable conserved
461	6	1.8	273	2	B64446	formylmethanofuran
462	6	1.8	274	2	A47639	OX-2 membrane glyc
463	6	1.8	274	2	D97653	hypothetical prote
464	6	1.8	274	2	AB2877	conserved hypothet
465	6	1.8	275	2	S74417	hypothetical prote
466	6	1.8	275	2	S03967	intercellular adhe
467	6	1.8	276	1	PWYBAA	H+-transporting tw
468	6	1.8	276	2	AI0565	lipoprotein [impor
469	6	1.8	276	2	E91117	hypothetical prote
470	6	1.8	276	2	F72342	conserved hypothet
471	6	1.8	276	2	T00923	hypothetical prote
472	6	1.8	276	2	JT0591	ALI1 protein - yea
473	6	1.8	277	2	T32460	hypothetical prote
474	6	1.8	277	2	B69479	conserved hypothet
475	6	1.8	278	1	TDRTOX	OX-2 membrane glyc
476	6	1.8	279	2	E75472	ROK family protein
477	6	1.8	280	2	T02004	chitinase (EC 3.2.
478	6	1.8	280	2	B81100	2-dehydro-3-deoxyp
479	6	1.8	280	2	G81840	2-dehydro-3-deoxy-
480	6	1.8	280	2	B45537	viral coat protein
481	6	1.8	280	2	T32747	hypothetical prote
482	6	1.8	280	2	B87547	transcription regu
483	6	1.8	281	1	D69030	MJ1225-related pro
484	6	1.8	281	2	B47092	copy control prote
485	6	1.8	281	2	B86820	conserved hypothet
486	6	1.8	282	1	SAVL64	middle surface ant
487	6	1.8	282	2	AC3084	shikimate 5-dehydr
488	6	1.8	283	2	AH0726	phosphotransferase
489	6	1.8	283	2	AC1340	maltodextrin ABC-t
490	6	1.8	283	2	AI1710	maltodextrin ABC-t
491	6	1.8	284	2	H64914	probable dimethyls
492	6	1.8	284	2	H90915	probable DMSO redu
493	6	1.8	284	2	E85764	probable DMSO redu
494	6	1.8	284	2	C72222	UDP-N-acetylenolpy
495	6	1.8	284	2	T36934	probable transport
496	6	1.8	285	2	E81388	probable succinate
497	6	1.8	285	2	C98105	hypothetical prote
498	6	1.8	285	2	B95241	conserved hypothet
499	6	1.8	286	1	WQECMM	phosphotransferase
500	6	1.8	286	2	A98945	mannose-specific P
501	6	1.8	286	2	D85793	PTS enzyme IID, ma
502	6	1.8	286	2	H64053	murein endopeptida
503	6	1.8	287	1	A45168	probable 3-oxoacyl
504	6	1.8	287	2	T04236	xyloglucan endo-1,
505	6	1.8	288	2	S36956	cytochrome-c oxida
506	6	1.8	288	2	S28029	gene PD-1 protein
507	6	1.8	288	2	S18438	sporulation protei
508	6	1.8	289	1	S25286	probable dehydroge
509	6	1.8	289	2	T41305	hypothetical prote
510	6	1.8	291	2	F98202	shikimate 5-dehydr
511	6	1.8	293	2	S04649	beta-lactamase (EC
512	6	1.8	293	2	T09171	ribosomal protein'
513	6	1.8	293	2	T09170	ribosomal protein
514	6	1.8	293	2	A83623	hypothetical prote
515	6	1.8	295	2	E84336	sugar kinase [impo
516	6	1.8	295	2	AC0214	PTS system, mannos
517	6	1.8	296	2	T45930	uracil phosphoribo
518	6	1.8	296	2	T00559	hypothetical prote
519	6	1.8	296	2	A36966	probable dTDP-rham
520	6	1.8	297	2	B91102	replication initia
521	6	1.8	297	2	F85947	replication intiti
522	6	1.8	297	2	S22098	replication intiti
523	6	1.8	297	2	AF0874	chromosome intitia
524	6	1.8	297	2	C96524	F11A17.4 [imported
525	6	1.8	297	2	F70572	hypothetical prote
526	6	1.8	297	2	A70347	UDP-N-acetylenolpy
527	6	1.8	298	2	T36900	probable integral
528	6	1.8	298	2	B35272	osteoinductive fac
529	6	1.8	298	2	T20841	hypothetical prote
530	6	1.8	299	2	T04669	serine O-acetyltra
531	6	1.8	299	2	AB0609	probable membrane
532	6	1.8	299	2	T20953	hypothetical prote
533	6	1.8	300	2	A84220	proteinase IV homo
534	6	1.8	301	2	D90224	spermidine synthas
535	6	1.8	301	2	T37031	hypothetical prote
536	6	1.8	302	2	AE0112	chromosome initiat
537	6	1.8	302	2	H87476	conserved hypothet
538	6	1.8	303	2	T30737	probable DNA-direc
539	6	1.8	303	2	AI0411	ferrichrome-bindin
540	6	1.8	303	2	S23440	hypothetical prote

541	6	1.8	304	2	T34271	hypothetical prote
542	6	1.8	304	2	A86614	UDP-N-acetylenolpy
543	6	1.8	304	2	T40316	conserved kin7-lik
544	6	1.8	304	2	E72010	udp-n-acetylenolpy
545	6	1.8	304	2	C81530	UDP-N-acetylenolpy
546	6	1.8	305	2	JN0647	hydrogenase expres
547	6	1.8	305	2	T35344	probable oxidoredu
548	6	1.8	305	2	AF2843	conserved hypothet
549	6	1.8	305	2	G97620	hypothetical prote
550	6	1.8	305	2	D88656	protein F56D6.4 [i
551	6	1.8	305	2	C84189	hypothetical prote
552	6	1.8	306	2	F83348	probable transcrip
553	6	1.8	306	2	S77062	hypothetical prote
554	6	1.8	307	2	B75120	phosphoglycerate d
555	6	1.8	307	2	E71011	probable phosphogl
556	6	1.8	307	2	C81862	conserved hypothet
557	6	1.8	307	2	D81082	conserved hypothet
558	6	1.8	308	1	CRHU6	carbonate dehydrat
559	6	1.8	308	2	AG3317	zinc proteinase (E
560	6	1.8	309	2	H75113	NADH2 dehydrogenas
561	6	1.8	309	2	H89832	hypothetical prote
562	6	1.8	310	2	T40802	conserved hypothet
563	6	1.8	311	2	S39661	menaquinone biosyn
564	6	1.8	311	2	E95178	inorganic pyrophos
565	6	1.8	311	2	D98045	manganese-dependen
566	6	1.8	311	2	AH3197	transmembrane sens
567	6	1.8	312	2	G84058	cysteine synthase
568	6	1.8	312	2	H89884	hypothetical prote
569	6	1.8	313	2	T09670	abscisic acid acti
570	6	1.8	313	2	AB3186	transcription regu
571	6	1.8	313	2	H84169	hypothetical prote
572	6	1.8	315	2	T37901	probable purine nu
573	6	1.8	315	2	JC5836	olfactory receptor
574	6	1.8	317	2	F82362	hydroxymethylbilan
575	6	1.8	317	2	B83039	probable permease
576	6	1.8	317	2	D89961	conserved hypothet
577	6	1.8	317	2	T21046	hypothetical prote
578	6	1.8	317	2	A95282	ABC transporter, p
579	6	1.8	319	2	S44746	C04D8.1 protein -
580	6	1.8	323	2	AE0324	probable membrane
581	6	1.8	324	2	A69648	2-keto-3-deoxygluc
582	6	1.8	324	2	B96606	probable nicotiana
583	6	1.8	326	2	PRMVJA	proteinase (EC 3.4
584	6	1.8	327	2	G70402	conserved hypothet
585	6	1.8	328	2	A70871	probable quinone o
586	6	1.8	328	2	B84545	hypothetical prote
587	6	1.8	328	2	D69452	conserved hypothet
588	6	1.8	328	2	C69358	reductase homolog
589	6	1.8	328	2	D72566	hypothetical prote
590	6	1.8	328	2	S57128	hypothetical prote
591	6	1.8	329	2	T10203	hypothetical prote
592	6	1.8	329	2	H71192	hypothetical prote
593	6	1.8	330	2	C71096	probable modificat
594	6	1.8	330	2	D95958	conserved hypothet
595	6	1.8	330	4	PS0079	probable naringeni
596	6	1.8	331	2	D83480	cytochrome o ubiqu
597	6	1.8	331	2	T32168	hypothetical prote
598	6	1.8	331	2	T32445	hypothetical prote
599	6	1.8	332	1	WMBP16	gene 16 protein -
600	6	1.8	332	1	WMBP26	gene 16 protein -
601	6	1.8	332	2	AI1691	oxidoreductases ho
602	6	1.8	332	2	AI1319	oxidoreductases ho
603	6	1.8	332	2	T23503	hypothetical prote
604	6	1.8	332	2	H82064	conserved hypothet
605	6	1.8	333	2	B86567	proteinase [import
606	6	1.8	333	2	G72058	proteinase IV, pro
607	6	1.8	334	2	D83750	pyridoxal phosphat
608	6	1.8	334	2	S44299	hypothetical prote
609	6	1.8	334	2	T27658	hypothetical prote
610	6	1.8	335	2	T25498	hypothetical prote
611	6	1.8	336	2	B49683	ptsH 3'-region pro
612	6	1.8	337	2	E83961	involved in fatty
613	6	1.8	337	2	B88957	protein ZK697.7 [i
614	6	1.8	338	2	AF3617	oligopeptide trans
615	6	1.8	338	2	T49998	hypothetical prote
616	6	1.8	339	2	S08981	malate dehydrogena
617	6	1.8	339	2	S73840	ribonucleotide red
618	6	1.8	340	2	C64225	ribonucleotide red
619	6	1.8	340	2	B96661	unknown protein, 8
620	6	1.8	340	2	T22010	hypothetical prote
621	6	1.8	341	2	S55627	hypothetical prote
622	6	1.8	341	2	C90579	hypothetical prote
623	6	1.8	342	2	S53663	hydrogenase-relate
624	6	1.8	342	2	E90772	periplasmic protei
625	6	1.8	342	2	A85635	part of regulation
626	6	1.8	342	2	H64840	torT protein precu
627	6	1.8	343	2	A84335	chloromuconate cyc
628	6	1.8	343	2	AC3403	general L-amino ac
629	6	1.8	344	2	E84376	Na+/Ca2+-exchangin
630	6	1.8	344	2	T34981	probable integral
631	6	1.8	345	2	S28140	gas vesicle protei
632	6	1.8	345	2	A98251	hypothetical prote
633	6	1.8	345	2	AB3035	conserved hypothet
634	6	1.8	347	2	T11338	NADH2 dehydrogenas
635	6	1.8	347	2	T11481	NADH2 dehydrogenas
636	6	1.8	347	2	B75610	probable 3-hydroxy
637	6	1.8	347	2	JC5788	tsec-1 protein (A
638	6	1.8	349	2	H95421	probable ABC trans
639	6	1.8	350	2	B82777	conserved hypothet
640	6	1.8	350	2	JC7188	REIC protein - hum
641	6	1.8	351	2	S25480	heat shock transcr
642	6	1.8	351	2	JQ2166	spindle body prote
643	6	1.8	352	2	S24559	Wnt-2 protein - fr
644	6	1.8	352	2	T08209	matrix protein - H
645	6	1.8	352	2	T49432	Ribonuclease III r
646	6	1.8	353	1	A45052	L-iditol 2-dehydro
647	6	1.8	353	2	A87643	hypothetical prote
648	6	1.8	354	2	C71368	probable UDP-N-ace
649	6	1.8	354	2	A90012	hypothetical prote
650	6	1.8	354	2	B47065	phosphate starvati
651	6	1.8	354	2	B85647	hypothetical prote
652	6	1.8	354	2	B90787	ATP-binding pho re
653	6	1.8	354	2	T22274	hypothetical prote
654	6	1.8	355	1	S22181	gamma-1-microglobu
655	6	1.8	355	2	T03785	L-lactate dehydrog
656	6	1.8	356	2	C70249	hypothetical prote
657	6	1.8	356	2	S58529	alpha-complex prot
658	6	1.8	356	2	JQ2352	glycoprotein I - t
659	6	1.8	357	2	AD3491	hypothetical membr
660	6	1.8	358	2	D89823	hypothetical prote
661	6	1.8	359	2	H95892	probable oxidoredu
662	6	1.8	359	2	D83385	hypothetical prote
663	6	1.8	359	2	T26813	hypothetical prote
664	6	1.8	359	2	G86290	hypothetical prote
665	6	1.8	359	2	AH3465	oxidoreductase (EC
666	6	1.8	360	2	T27694	hypothetical prote
667	6	1.8	360	2	B70863	hypothetical prote
668	6	1.8	360	2	T51870	hypothetical prote
669	6	1.8	361	2	S57182	probable polygalac
670	6	1.8	361	2	T31815	hypothetical prote
671	6	1.8	362	2	S29968	coat protein VP1 -
672	6	1.8	362	2	S78515	single-stranded nu
673	6	1.8	363	2	AC0244	conserved hypothet
674	6	1.8	364	2	F96603	hypothetical prote
675	6	1.8	365	2	JQ0879	NS5 protein - hepa
676	6	1.8	365	2	S42471	hnRNP protein E2 -
677	6	1.8	365	2	AI2940	acetyltransferase
678	6	1.8	366	2	E87457	conserved hypothet
679	6	1.8	366	2	A55525	carboxy-cis,cis-mu
680	6	1.8	366	2	T31933	hypothetical prote
681	6	1.8	367	2	B72644	probable transketo
682	6	1.8	368	2	S71190	heat shock protein
683	6	1.8	368	2	AH2694	MFS permease [impo
684	6	1.8	370	2	A60089	transforming prote
685	6	1.8	370	2	S29139	aggrecan - pig (fr
686	6	1.8	370	2	G90248	conserved hypothet

687	6	1.8	371	2	A90044	hypothetical prote
688	6	1.8	371	2	A53908	brevican precursor
689	6	1.8	371	2	JC5498	G protein-coupled
690	6	1.8	371	2	G84358	N2,N2-dimethylguan
691	6	1.8	372	1	QQBE88	glycoprotein I pre
692	6	1.8	372	2	PQ0138	dnaK-type molecula
693	6	1.8	372	2	E84856	hypothetical prote
694	6	1.8	372	2	A98342	rspF protein (AF14
695	6	1.8	374	2	S40756	hypothetical prote
696	6	1.8	375	2	AH0209	probable sugar ABC
697	6	1.8	375	2	AI2041	hypothetical prote
698	6	1.8	376	2	AG1410	cell division prot
699	6	1.8	376	2	G83290	hypothetical prote
700	6	1.8	376	2	JC6535	multiubiquitin-cha

ALIGNMENTS

RESULT 1
H72621
hypothetical protein APE1433 - Aeropyrum pernix (strain K1)
C;Species: Aeropyrum pernix
C;Date: 20-Aug-1999 #sequence_revision 20-Aug-1999 #text_change 20-Aug-1999
C;Accession: H72621
R;Kawarabayasi, Y.; Hino, Y.; Horikawa, H.; Yamazaki, S.; Haikawa, Y.; Jin-no, K.; Takah
awa, H.; Takamiya, M.; Masuda, S.; Funahashi, T.; Tanaka, T.; Kudoh, Y.; Yamazaki, J.; K
DNA Res. 6, 83-101, 1999
A;Title: Complete genome sequence of an aerobic hyper-thermophilic Crenarchaeon, Aeropyr
A;Reference number: A72450; MUID:99310339; PMID:10382966
A;Accession: H72621
A;Status: preliminary
A;Molecule type: DNA
A;Residues: 1-156 <KAW>
A;Cross-references: DDBJ:AP000061; NID:g5104821; PIDN:BAA80430.1; PID:d1044216; PID:g510
A;Experimental source: strain K1
C;Genetics:
A;Gene: APE1433

Query Match 2.7%; Score 9; DB 2; Length 156;
Best Local Similarity 100.0%; Pred. No. 0.45;
Matches 9; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 17 LTGSAASGP 25
||||||||| |
Db 105 LTGSAASGP 113

RESULT 2
QRMSP1
microtubule-associated protein MAP1B - mouse
N;Alternate names: microtubule-associated protein MAP1(X); microtubule-associated protei
C;Species: Mus musculus (house mouse)
C;Date: 30-Sep-1991 #sequence_revision 30-Sep-1991 #text_change 01-Sep-2000
C;Accession: S07549; S44387; A33645
R;Noble, M.; Lewis, S.A.; Cowan, N.J.
J. Cell Biol. 109, 3367-3376, 1989
A;Title: The microtubule binding domain of microtubule-associated protein MAP1B contains
A;Reference number: A33645; MUID:90094539; PMID:2480963
A;Accession: S07549
A;Molecule type: mRNA
A;Residues: 1-2464 <NOB>
A;Cross-references: EMBL:X51396; NID:g52999; PIDN:CAA35761.1; PID:g53000
R;Sanchez, C.; Padilla, R.; Paciucci, R.; Zabala, J.C.; Avila, J.
Arch. Biochem. Biophys. 310, 428-432, 1994
A;Title: Binding of heat-shock protein 70 (hsp70) to tubulin.
A;Reference number: S44387; MUID:94234720; PMID:8179328
A;Accession: S44387
A;Status: preliminary
A;Molecule type: protein
A;Residues: 653-663,'IC' <SAN>
C;Superfamily: microtubule-associated protein MAP1B
C;Keywords: microtubule binding; phosphoprotein; tandem repeat
F;589-786/Domain: microtubule binding #status experimental <MTB>
F;589-592,639-642,649-652,655-658,660-663,668-671,674-677,679-682,683-686,687-690,691-69
R-K-E/D-X)
F;1861-2064/Region: 17-residue repeats
F;91,116,351,888,1124,1153,1168,1208,1662,1877,1918,2003,2030,2054,2083/Binding site: ph
F;147,969,1336,1562,1563,1702,1708,1990,2057,2063,2419/Binding site: phosphate (Thr) (co
F;1953/Binding site: phosphate (Tyr) (covalent) #status predicted

Query Match 2.7%; Score 9; DB 1; Length 2464;
Best Local Similarity 100.0%; Pred. No. 4.6;
Matches 9; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 21 AASGPVKEL 29
||||||||| |
Db 812 AASGPVKEL 820

RESULT 3
S76681
hypothetical protein - Synechocystis sp. (strain PCC 6803)
C;Species: Synechocystis sp.
A;Variety: PCC 6803
C;Date: 25-Apr-1997 #sequence_revision 25-Apr-1997 #text_change 20-Jun-2000
C;Accession: S76681
R;Kaneko, T.; Sato, S.; Kotani, H.; Tanaka, A.; Asamizu, E.; Nakamura, Y.; Miyajima, N.,
o, K.; Okumura, S.; Shimpo, S.; Takeuchi, C.; Wada, T.; Watanabe, A.; Yamada, M.; Yasuda
DNA Res. 3, 109-136, 1996
A;Title: Sequence analysis of the genome of the unicellular cyanobacterium Synechocystis
s.
A;Reference number: S74322; MUID:97061201; PMID:8905231
A;Accession: S76681
A;Status: preliminary
A;Molecule type: DNA
A;Residues: 1-173 <KAN>
A;Cross-references: EMBL:D64004; GB:AB001339; NID:g1001701; PIDN:BAA10625.1; PID:g120845
A;Note: the nucleotide sequence was submitted to the EMBL Data Library, June 1996
C;Superfamily: cyanelle Cyanophora paradoxa hypothetical protein ycf36

Query Match 2.4%; Score 8; DB 2; Length 173;
Best Local Similarity 100.0%; Pred. No. 4.9;
Matches 8; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 236 LLLSLFVL 243
||||||||
Db 85 LLLSLFVL 92

RESULT 4
A82159
hypothetical protein VC1772 [imported] - Vibrio cholerae (strain N16961 serogroup O1)
C;Species: Vibrio cholerae
C;Date: 18-Aug-2000 #sequence_revision 20-Aug-2000 #text_change 02-Feb-2001
C;Accession: A82159
R;Heidelberg, J.F.; Eisen, J.A.; Nelson, W.C.; Clayton, R.A.; Gwinn, M.L.; Dodson, R.J.,
chardson, D.; Ermolaeva, M.D.; Vamathevan, J.; Bass, S.; Qin, H.; Dragoi, I.; Sellers, P
l, R.R.; Mekalanos, J.J.; Venter, J.C.; Fraser, C.M.
Nature 406, 477-483, 2000
A;Title: DNA Sequence of both chromosomes of the cholera pathogen Vibrio cholerae.
A;Reference number: A82035; MUID:20406833; PMID:10952301
A;Accession: A82159
A;Status: preliminary
A;Molecule type: DNA
A;Residues: 1-286 <HEI>
A;Cross-references: GB:AE004254; GB:AE003852; NID:g9656292; PIDN:AAF94921.1; GSPDB:GN001
A;Experimental source: serogroup O1; strain N16961; biotype El Tor
C;Genetics:
A;Gene: VC1772
A;Map position: 1

Query Match 2.4%; Score 8; DB 2; Length 286;
Best Local Similarity 100.0%; Pred. No. 7.6;
Matches 8; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

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Qy        261 EKKRVDIC 268
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Db        134 EKKRVDIC 141
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RESULT 5
S18733
glutenin high molecular weight chain 1By9 precursor - wheat
C;Species: Triticum aestivum (common wheat)
C;Date: 08-Jun-1994 #sequence_revision 10-Nov-1995 #text_change 20-Aug-1999
C;Accession: S18733
R;Halford, N.G.; Forde, J.; Anderson, O.D.; Greene, F.C.; Shewry, P.R.
Theor. Appl. Genet. 75, 117-126, 1987
A;Title: The nucleotide and deduced amino acid sequences of an HMW glutenin subunit gene
A and 1D.
A;Reference number: S18733
A;Accession: S18733
A;Status: preliminary
A;Molecule type: DNA
A;Residues: 1-705 <HAL>
A;Cross-references: EMBL:X61026; NID:g22089; PIDN:CAA43361.1; PID:g22090
C;Superfamily: glutenin

  Query Match 2.4%; Score 8; DB 2; Length 705;
  Best Local Similarity 100.0%; Pred. No. 16;
  Matches 8; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

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Qy        108 YSSSLQQP 115
              ||||||||
Db        496 YSSSLQQP 503
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RESULT 6
S38673
desmoglein 2 - human
N;Alternate names: desmoglein HDGC
C;Species: Homo sapiens (man)
C;Date: 20-Feb-1995 #sequence_revision 20-Feb-1995 #text_change 20-Aug-1999
C;Accession: S38673; B38872
R;Zimbelmann, R.
submitted to the EMBL Data Library, September 1993
A;Reference number: S38673
A;Accession: S38673
A;Status: preliminary
A;Molecule type: mRNA
A;Residues: 1-1117 <ZIM>
A;Cross-references: EMBL:Z26317; NID:g416177; PIDN:CAA81226.1; PID:g416178
R;Koch, P.J.; Goldschmidt, M.D.; Walsh, M.J.; Zimbelmann, R.; Franke, W.W.
Eur. J. Cell Biol. 55, 200-208, 1991
A;Title: Complete amino acid sequence of the epidermal desmoglein precursor polypeptide
A;Reference number: A38872; MUID:92037656; PMID:1935985
A;Accession: B38872
A;Molecule type: mRNA
A;Residues: 777-1117 <KOC>
A;Cross-references: GB:S64273
C;Genetics:
A;Gene: GDB:DSG2
A;Cross-references: GDB:128808; OMIM:125671
A;Map position: 18q12.1-18q12.2
C;Superfamily: cadherin; cadherin repeat homology
C;Keywords: calcium binding; cell adhesion; duplication; glycoprotein; membrane protein
F;51-158/Domain: cadherin repeat homology <CR1>
F;161-271/Domain: cadherin repeat homology <CR2>

  Query Match 2.4%; Score 8; DB 2; Length 1117;
  Best Local Similarity 100.0%; Pred. No. 24;
  Matches 8; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

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Qy        231 LLLVPLLL 238
              ||||||||
Db        624 LLLVPLLL 631
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RESULT 7
T29918
hypothetical protein ZC449.4 - Caenorhabditis elegans
C;Species: Caenorhabditis elegans
C;Date: 15-Oct-1999 #sequence_revision 15-Oct-1999 #text_change 04-Mar-2000
C;Accession: T29918
R;Latreille, P.; Gattung, S.
submitted to the EMBL Data Library, November 1995
A;Description: The sequence of C. elegans cosmid ZC449.
A;Reference number: Z20708
A;Accession: T29918
A;Status: preliminary; translated from GB/EMBL/DDBJ
A;Molecule type: DNA
A;Residues: 1-105 <LAT>
A;Cross-references: EMBL:U41510; PIDN:AAA82633.1; CESP:ZC449.4
C;Genetics:
A;Gene: CESP:ZC449.4
A;Introns: 26/3; 51/1; 87/3
C;Superfamily: Caenorhabditis elegans hypothetical protein ZC449.4

  Query Match 2.1%; Score 7; DB 2; Length 105;
  Best Local Similarity 100.0%; Pred. No. 33;
  Matches 7; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

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Qy        226 MVLLCLL 232
              |||||||
Db         63 MVLLCLL 69
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RESULT 8
E71866
hypothetical protein jhp0956 - Helicobacter pylori (strain J99)
C;Species: Helicobacter pylori
A;Variety: strain J99
C;Date: 12-Feb-1999 #sequence_revision 12-Feb-1999 #text_change 04-Mar-2000
C;Accession: E71866
R;Alm, R.A.; Ling, L.S.L.; Moir, D.T.; King, B.L.; Brown, E.D.; Doig, P.C.; Smith, D.R.,
; Ives, C.; Gibson, R.; Merberg, D.; Mills, S.D.; Jiang, Q.; Taylor, D.E.; Vovis, G.F.;
Nature 397, 176-180, 1999
A;Title: Genomic sequence comparison of two unrelated isolates of the human gastric pati
A;Reference number: A71800; MUID:99120557; PMID:9923682
A;Accession: E71866
A;Status: preliminary
A;Molecule type: DNA
A;Residues: 1-161 <ARN>
A;Cross-references: GB:AE001525; GB:AE001439; NID:g4155533; PIDN:AAD06530.1; PID:g415553
A;Experimental source: strain J99
C;Genetics:
A;Gene: jhp0956
C;Superfamily: Helicobacter pylori hypothetical protein jhp0956

  Query Match 2.1%; Score 7; DB 2; Length 161;
  Best Local Similarity 100.0%; Pred. No. 47;
  Matches 7; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

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Qy        235 PLLLSLF 241
              |||||||
Db        102 PLLLSLF 108
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RESULT 9
AE1817
hypothetical protein all0085 [imported] - Nostoc sp. (strain PCC 7120)
C;Species: Nostoc sp. PCC 7120
A;Note: Nostoc sp. strain PCC 7120 is a synonym of Anabaena sp. strain PCC 7120
C;Date: 14-Dec-2001 #sequence_revision 14-Dec-2001 #text_change 09-Dec-2002
C;Accession: AE1817
R;Kaneko, T.; Nakamura, Y.; Wolk, C.P.; Kuritz, T.; Sasamoto, S.; Watanabe, A.; Iriguchi
 Nakazaki, N.; Shimpo, S.; Sugimoto, M.; Takazawa, M.; Yamada, M.; Yasuda, M.; Tabata, S
DNA Res. 8, 205-213, 2001
A;Title: Complete Genomic Sequence of the Filamentous Nitrogen-fixing Cyanobacterium Ana
A;Reference number: AB1807; MUID:21595285; PMID:11759840
A;Accession: AE1817

A;Status: preliminary
A;Molecule type: DNA
A;Residues: 1-170 <KUR>
A;Cross-references: GB:BA000019; PIDN:BAB77609.1; PID:g17135063; GSPDB:GN00179
A;Experimental source: strain PCC 7120
C;Genetics:
A;Gene: all0085

Query Match 2.1%; Score 7; DB 2; Length 170;
Best Local Similarity 100.0%; Pred. No. 49;
Matches 7; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 227 VLLCLLL 233
||||||| |
Db 14 VLLCLLL 20

RESULT 10
F97283
ribosomal protein L6 [imported] - Clostridium acetobutylicum
C;Species: Clostridium acetobutylicum
C;Date: 14-Sep-2001 #sequence_revision 14-Sep-2001 #text_change 12-Jun-2003
C;Accession: F97283
R;Nolling, J.; Breton, G.; Omelchenko, M.V.; Markarova, K.S.; Zeng, Q.; Gibson, R.; Lee,
.; Daly, M.J.; Bennett, G.N.; Koonin, E.V.; Smith, D.R.
J. Bacteriol. 183, 4823-4838, 2001
A;Title: Genome Sequence and Comparative Analysis of the Solvent-Producing Bacterium Clo
A;Reference number: A96900; MUID:21359325; PMID:21359325
A;Accession: F97283
A;Status: preliminary
A;Molecule type: DNA
A;Residues: 1-179 <KUR>
A;Cross-references: GB:AE001437; PIDN:AAK81057.1; PID:g15026184; GSPDB:GN00168
A;Experimental source: Clostridium acetobutylicum ATCC824
C;Genetics:
A;Gene: CAC3118
C;Superfamily: ribosomal protein L6/L9

Query Match 2.1%; Score 7; DB 2; Length 179;
Best Local Similarity 100.0%; Pred. No. 51;
Matches 7; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 27 KELVGSV 33
||||||| |
Db 139 KELVGSV 145

RESULT 11
F83305
hypothetical protein PA2724 [imported] - Pseudomonas aeruginosa (strain PAO1)
C;Species: Pseudomonas aeruginosa
C;Date: 15-Sep-2000 #sequence_revision 15-Sep-2000 #text_change 31-Dec-2000
C;Accession: F83305
R;Stover, C.K.; Pham, X.Q.; Erwin, A.L.; Mizoguchi, S.D.; Warrener, P.; Hickey, M.J.; Br
adman, S.; Yuan, Y.; Brody, L.L.; Coulter, S.N.; Folger, K.R.; Kas, A.; Larbig, K.; Lim,
.; Lory, S.; Olson, M.V.
Nature 406, 959-964, 2000
A;Title: Complete genome sequence of Pseudomonas aeruginosa PA01, an opportunistic pathc
A;Reference number: A82950; MUID:20437337; PMID:10984043
A;Accession: F83305
A;Status: preliminary
A;Molecule type: DNA
A;Residues: 1-179 <STO>
A;Cross-references: GB:AE004700; GB:AE004091; NID:g9948792; PIDN:AAG06112.1; GSPDB:GN001
A;Experimental source: strain PAO1
C;Genetics:
A;Gene: PA2724

Query Match 2.1%; Score 7; DB 2; Length 179;
Best Local Similarity 100.0%; Pred. No. 51;
Matches 7; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 80 RVDFPDG 86
||||||| |
Db 42 RVDFPDG 48

RESULT 12
F97499
hypothetical protein AGR_C_2123 [imported] - Agrobacterium tumefaciens (strain C58, Cere
C;Species: Agrobacterium tumefaciens
C;Date: 30-Sep-2001 #sequence_revision 30-Sep-2001 #text_change 18-Nov-2002
C;Accession: F97499
R;Goodner, B.; Hinkle, G.; Gattung, S.; Miller, N.; Blanchard, M.; Qurollo, B.; Goldman,
A.; Liu, F.; Wollam, C.; Allinger, M.; Doughty, D.; Scott, C.; Lappas, C.; Markelz, B.,
Science 294, 2323-2328, 2001
A;Title: Genome Sequence of the Plant Pathogen and Biotechnology Agent Agrobacterium tum
A;Reference number: A97359; MUID:21608551; PMID:11743194
A;Accession: F97499
A;Status: preliminary
A;Molecule type: DNA
A;Residues: 1-182 <KUR>
A;Cross-references: GB:AE007869; PIDN:AAK86951.1; PID:g15156185; GSPDB:GN00169
C;Genetics:
A;Gene: AGR_C_2123
A;Map position: circular chromosome

Query Match 2.1%; Score 7; DB 2; Length 182;
Best Local Similarity 100.0%; Pred. No. 52;
Matches 7; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 237 LLSLFVL 243
||||||| |
Db 34 LLSLFVL 40

RESULT 13
I40220
hypothetical protein 2 - Bacillus licheniformis (fragment)
C;Species: Bacillus licheniformis
C;Date: 12-Aug-1996 #sequence_revision 12-Aug-1996 #text_change 15-Oct-1999
C;Accession: I40220
R;Harry, E.J.; Partridge, S.R.; Weiss, A.S.; Wake, R.G.
Gene 147, 85-89, 1994
A;Title: Conservation of the 168 divIB gene in Bacillus subtilis W23 and B. licheniformi
A;Reference number: I40220; MUID:94374713; PMID:8088553
A;Accession: I40220
A;Status: preliminary; translated from GB/EMBL/DDBJ
A;Molecule type: DNA
A;Residues: 1-184 <RES>
A;Cross-references: EMBL:U01958; NID:g404008; PIDN:AAA57244.1; PID:g404010

Query Match 2.1%; Score 7; DB 2; Length 184;
Best Local Similarity 100.0%; Pred. No. 52;
Matches 7; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 31 GSVGGAV 37
||||||| |
Db 9 GSVGGAV 15

RESULT 14
H70416
hypothetical protein aq_1348 - Aquifex aeolicus
C;Species: Aquifex aeolicus
C;Date: 08-May-1998 #sequence_revision 08-May-1998 #text_change 24-Nov-1999
C;Accession: H70416
R;Deckert, G.; Warren, P.V.; Gaasterland, T.; Young, W.G.; Lenox, A.L.; Graham, D.E.; Ov
V.
Nature 392, 353-358, 1998
A;Title: The complete genome of the hyperthermophilic bacterium Aquifex aeolicus.
A;Reference number: A70300; MUID:98196666; PMID:9537320
A;Accession: H70416
A;Status: preliminary; nucleic acid sequence not shown; translation not shown
A;Molecule type: DNA
A;Residues: 1-189 <AQF>

A;Cross-references: GB:AE000736; NID:g2983763; PIDN:AAC07334.1; PID:g2983775; GB:AE00065
A;Experimental source: strain VF5
C;Genetics:
A;Gene: aq_1348
C;Superfamily: Aquifex aeolicus hypothetical protein aq_1348

Query Match 2.1%; Score 7; DB 2; Length 189;
Best Local Similarity 100.0%; Pred. No. 54;
Matches 7; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 244 GLFLWFL 250
|||||||
Db 142 GLFLWFL 148

RESULT 15
T45543
hypothetical protein 2 [imported] - Klebsiella pneumoniae transposon Tn5711
C;Species: Klebsiella pneumoniae
C;Date: 31-Jan-2000 #sequence_revision 31-Jan-2000 #text_change 17-Mar-2000
C;Accession: T45543
R;Albiger, B.; Hubert, J.C.; Lett, M.C.
submitted to the EMBL Data Library, October 1998
A;Description: Composite transposons Tn5708 and Tn5709 are based on a Tn3-like element T
A;Reference number: Z23003
A;Accession: T45543
A;Status: preliminary; translated from GB/EMBL/DDBJ
A;Molecule type: DNA
A;Residues: 1-199 <ALB>
A;Cross-references: EMBL:AJ011907; PIDN:CAA09858.1
A;Experimental source: strain KIIIA
C;Genetics:
A;Mobile element: transposon Tn5711
C;Superfamily: bacitracin transport permease; glucose-6-phosphatase catalytic domain hom

Query Match 2.1%; Score 7; DB 2; Length 199;
Best Local Similarity 100.0%; Pred. No. 56;
Matches 7; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 236 LLLSLFV 242
|||||||
Db 132 LLLSLFV 138

Search completed: August 18, 2004, 16:00:57
Job time : 19 secs

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GenCore version 5.1.6

OM protein - protein search, using sw model

Run on: August 18, 2004, 15:53:29 ; Search time 13 Seconds
(without alignments)
1341.808 Million cell updates/sec

Title: US-10-063-549-46
Perfect score: 335
Sequence: 1 MAGSPTCLTLIYILWQLTGS.....PHSLLTMPDTPRLFAYENVI 335

Scoring table: OLIGO
Gapop 60.0 , Gapext 60.0

Searched: 141681 seqs, 52070155 residues

Word size : 0

Total number of hits satisfying chosen parameters: 141681

Minimum DB seq length: 0
Maximum DB seq length: 2000000000

Post-processing: Listing first 700 summaries

Database : SwissProt_42:*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	% Query Match	Length	DB	ID	Description
1	9	2.7	2464	1	MAPB_MOUSE	P14873 mus musculu
2	8	2.4	669	1	BGAL_FELCA	O19015 felis silve
3	8	2.4	1117	1	DSG2_HUMAN	Q14126 homo sapien
4	8	2.4	1122	1	DSG2_MOUSE	O55111 mus musculu
5	7	2.1	75	1	MTRF_METKA	Q8tva7 methanopyru
6	7	2.1	97	1	SY08_MOUSE	Q9z121 mus musculu
7	7	2.1	98	1	SY13_HUMAN	Q99616 homo sapien
8	7	2.1	177	1	RL1X_SPOFR	Q8wqi7 spodoptera
9	7	2.1	184	1	MURB_BACLI	Q45305 bacillus li
10	7	2.1	189	1	YD48_AQUAE	O67363 aquifex aeo
11	7	2.1	228	1	UT11_ARATH	Q9m223 arabidopsis
12	7	2.1	239	1	YTML_BACSU	O34315 bacillus su
13	7	2.1	266	1	FLIP_CAUCR	Q45980 caulobacter
14	7	2.1	293	1	CFXQ_GUITH	O78450 guillardia
15	7	2.1	300	1	MURB_STRA3	Q8e553 streptococc
16	7	2.1	301	1	MURB_BACHD	Q9k9t1 bacillus ha
17	7	2.1	303	1	MURB_BACSU	P18579 bacillus su
18	7	2.1	305	1	MURB_CLOAB	Q97lp4 clostridium
19	7	2.1	312	1	APE_RAT	P02650 rattus norv
20	7	2.1	316	1	MURB_STRPN	Q97q41 streptococc
21	7	2.1	356	1	COX2_BACSU	P24011 bacillus su
22	7	2.1	362	1	ASG2_YEAST	P11163 saccharomyc
23	7	2.1	367	1	GLNA_CAEEL	P34497 caenorhabdi
24	7	2.1	381	1	CYB_ISUPA	P34871 isurus pauc
25	7	2.1	381	1	CYB_SCYCA	O79413 scyliorhinu
26	7	2.1	381	1	CYCH_RHIME	P45400 rhizobium m
27	7	2.1	418	1	MTR_HAEIN	P44614 haemophilus
28	7	2.1	433	1	YBL4_YEAST	P38211 saccharomyc
29	7	2.1	448	1	GNTP_BACLI	P46832 bacillus li
30	7	2.1	507	1	D7A1_MALDO	Q9zpb7 malus domes
31	7	2.1	508	1	PDI2_ARATH	Q9srg3 arabidopsis
32	7	2.1	515	1	SIR2_CANAL	O59923 candida alb
33	7	2.1	539	1	RIK2_MOUSE	P58801 mus musculu
34	7	2.1	540	1	RIK2_HUMAN	O43353 h receptor-
35	7	2.1	586	1	ENV_MPMV	P07575 simian maso
36	7	2.1	587	1	ENV_SRV1	P04027 simian retr
37	7	2.1	591	1	CALX_MOUSE	P35564 mus musculu
38	7	2.1	591	1	CALX_RAT	P35565 rattus norv
39	7	2.1	604	1	PGH2_CAVPO	P70682 cavia porce
40	7	2.1	605	1	PCOA_ECOLI	Q47452 escherichia
41	7	2.1	650	1	LIB1_HUMAN	Q8nhl6 h leukocyte
42	7	2.1	675	1	HPPA_XANAC	Q8ph20 xanthomonas
43	7	2.1	675	1	HPPA_XANCP	Q8p5m6 xanthomonas
44	7	2.1	732	1	ACPH_HUMAN	P13798 homo sapien
45	7	2.1	799	1	FTSK_TREPA	O83964 treponema p
46	7	2.1	914	1	PBPA_BACSU	P39793 bacillus su
47	7	2.1	943	1	UVRA_STRPN	Q97sx7 streptococc
48	7	2.1	954	1	GCSP_AGRT5	Q8ufd6 agrobacteri
49	7	2.1	954	1	GCSP_RHIME	Q92q11 rhizobium m
50	7	2.1	954	1	GCSP_SYNEL	Q8dii3 synechococc
51	7	2.1	954	1	GCSP_VIBPA	Q87i05 vibrio para
52	7	2.1	954	1	GCSP_VIBVU	Q8d7g7 vibrio vuln
53	7	2.1	956	1	GCSP_ECO57	Q8xd33 escherichia
54	7	2.1	956	1	GCSP_ECOL6	Q8fe67 escherichia
55	7	2.1	956	1	GCSP_ECOLI	P33195 escherichia
56	7	2.1	956	1	GCSP_SALTI	Q8z3x0 salmonella
57	7	2.1	956	1	GCSP_SALTY	Q8zm76 salmonella
58	7	2.1	957	1	GCP2_PSEPK	Q88ci9 pseudomonas
59	7	2.1	958	1	GCP2_PSEAE	Q9htx7 pseudomonas
60	7	2.1	958	1	GCSP_YERPE	Q8zhi8 yersinia pe
61	7	2.1	963	1	TRES_THETH	O06458 thermus the
62	7	2.1	975	1	GCSP_XANCP	Q8pbk7 xanthomonas
63	7	2.1	977	1	GCSP_XANAC	Q8pn59 xanthomonas
64	7	2.1	979	1	PTPN_BOVIN	P56722 bos taurus
65	7	2.1	982	1	GCSP_RALSO	Q8xu98 ralstonia s
66	7	2.1	1002	1	SYIM_YEAST	P48526 saccharomyc
67	7	2.1	1012	1	OFD1_HUMAN	O75665 homo sapien
68	7	2.1	1020	1	GCSP_HUMAN	P23378 homo sapien
69	7	2.1	1025	1	GCSP_MOUSE	Q91w43 mus musculu
70	7	2.1	1032	1	MT18_YEAST	P40469 saccharomyc
71	7	2.1	1085	1	IFH1_YEAST	P39520 saccharomyc
72	7	2.1	1210	1	PER3_HUMAN	P56645 homo sapien
73	7	2.1	1269	1	FLIH_HUMAN	Q13045 homo sapien
74	7	2.1	1290	1	PER1_HUMAN	O15534 homo sapien
75	7	2.1	1291	1	PER1_MOUSE	O35973 mus musculu
76	7	2.1	1312	1	DPOL_PYRSD	Q51334 pyrococcus
77	7	2.1	1581	1	PPRB_HUMAN	Q15648 h peroxisom
78	7	2.1	2787	1	TEL1_YEAST	P38110 saccharomyc
79	6	1.8	49	1	LHA7_RHOAC	P35093 rhodopseudo
80	6	1.8	52	1	CD3E_BOVIN	Q28073 bos taurus
81	6	1.8	61	1	NO14_PEA	P26415 pisum sativ
82	6	1.8	70	1	GBG1_DROME	P38040 drosophila
83	6	1.8	83	1	PRRP_RAT	P81278 rattus norv
84	6	1.8	84	1	RL27_CHLTE	Q8kcb7 chlorobium
85	6	1.8	92	1	YA50_HAEIN	P71365 haemophilus
86	6	1.8	95	1	CH10_ALTHA	Q9akt2 alteromonas
87	6	1.8	96	1	CH10_ACTAC	P46399 actinobacil
88	6	1.8	96	1	CH10_ACTPL	P94165 actinobacil
89	6	1.8	96	1	CH10_BUCAI	P25749 buchnera ap
90	6	1.8	96	1	CH10_BUCAP	Q59176 buchnera ap
91	6	1.8	96	1	CH10_BUCMP	O51831 buchnera ap
92	6	1.8	96	1	CH10_HAEIN	P43734 haemophilus
93	6	1.8	96	1	CH10_PASMU	Q59686 pasteurella
94	6	1.8	96	1	CH10_SHEON	Q8cx49 shewanella
95	6	1.8	96	1	CH11_VIBCH	Q9knr6 vibrio chol
96	6	1.8	96	1	CH11_VIBPA	Q87kx3 vibrio para
97	6	1.8	96	1	CH11_VIBVU	Q8cwl1 vibrio vuln
98	6	1.8	96	1	VGE_BPG4	P03640 bacteriopha
99	6	1.8	97	1	CH10_BUCBP	P59525 buchnera ap
100	6	1.8	97	1	CH10_BUCGU	Q9f4f4 buchnera ap
101	6	1.8	97	1	CH10_BUCPP	Q9f4f2 buchnera ap
102	6	1.8	97	1	CH10_BUCPS	Q9f4f0 buchnera ap
103	6	1.8	97	1	CH10_BUCTC	Q9f4e8 buchnera ap
104	6	1.8	97	1	CH10_BUCTS	Q9f4e4 buchnera ap
105	6	1.8	97	1	CH10_BUCTT	Q9f4e6 buchnera ap
106	6	1.8	97	1	CH10_ECOLI	P05380 escherichia

107	6	1.8	97	1	CH10_ENTAE	Q93fu7	enterobacte
108	6	1.8	97	1	CH10_SALTY	Q9lc51	salmonella
109	6	1.8	97	1	CH10_WIGBR	Q9ans0	wiggleswort
110	6	1.8	97	1	CH10_XANMA	P95801	xanthomonas
111	6	1.8	97	1	GAC2_CLOAB	Q97ex7	clostridium
112	6	1.8	97	1	SY07_MOUSE	Q03366	mus musculu
113	6	1.8	98	1	NULM_BALMU	P41301	balaenopter
114	6	1.8	98	1	NULM_BALPH	P24976	balaenopter
115	6	1.8	98	1	NULM_RABIT	O79435	oryctolagus
116	6	1.8	98	1	PRRP_BOVIN	P81264	bos taurus
117	6	1.8	99	1	MCPA_BOVIN	P28291	bos taurus
118	6	1.8	99	1	SY02_HUMAN	P13500	homo sapien
119	6	1.8	99	1	SY02_MACFA	Q9myn4	macaca fasc
120	6	1.8	99	1	SY02_PIG	P42831	sus scrofa
121	6	1.8	99	1	SY07_HUMAN	P80098	homo sapien
122	6	1.8	99	1	SY08_BOVIN	Q09141	bos taurus
123	6	1.8	99	1	SY08_HUMAN	P80075	homo sapien
124	6	1.8	99	1	SY08_PIG	P49873	sus scrofa
125	6	1.8	100	1	NUOK_ECOLI	P33606	escherichia
126	6	1.8	100	1	YJCE_BACSU	O31627	bacillus su
127	6	1.8	101	1	SY02_CANFA	P52203	canis famil
128	6	1.8	101	1	YGV4_YEAST	P53089	saccharomyc
129	6	1.8	102	1	CH11_VIBHA	Q83wi9	vibrio harv
130	6	1.8	104	1	SY12_MOUSE	Q62401	mus musculu
131	6	1.8	108	1	YC54_PORPU	P51204	porphyra pu
132	6	1.8	111	1	RBFA_HELPJ	Q9zm45	helicobacte
133	6	1.8	111	1	RBFA_HELPY	O25688	helicobacte
134	6	1.8	113	1	MIH_CALSI	P55321	callinectes
135	6	1.8	115	1	IR02_HCMVA	P16802	human cytom
136	6	1.8	118	1	VAG1_PANTR	Q862z6	pan troglod
137	6	1.8	118	1	VAG2_HUMAN	O95670	homo sapien
138	6	1.8	118	1	VAG2_MOUSE	Q9wtt4	mus musculu
139	6	1.8	118	1	VAG2_PIG	Q9tsv6	sus scrofa
140	6	1.8	120	1	SY02_CAVPO	Q08782	cavia porce
141	6	1.8	120	1	YMG6_RHIME	Q92ug5	rhizobium m
142	6	1.8	123	1	YII9_RHIME	Q92vb9	rhizobium m
143	6	1.8	124	1	APC4_RABIT	P55057	oryctolagus
144	6	1.8	124	1	KAB1_OLDAF	P56254	oldenlandia
145	6	1.8	125	1	SY02_RABIT	P28292	oryctolagus
146	6	1.8	126	1	NUOA_BUCAP	Q8k9y7	buchnera ap
147	6	1.8	126	1	YIGF_ECOLI	P27842	escherichia
148	6	1.8	126	1	YIGF_SALTY	P31139	salmonella
149	6	1.8	128	1	MERT_STAAU	P08656	staphylococ
150	6	1.8	128	1	U384_HSVMG	Q05102	marek's dis
151	6	1.8	128	1	Y739_PASMU	Q9cms3	pasteurella
152	6	1.8	130	1	YQ26_BACAN	Q9rn06	bacillus an
153	6	1.8	136	1	YEDX_SALTI	Q8z7q6	salmonella
154	6	1.8	136	1	YEDX_SALTY	Q8zq52	salmonella
155	6	1.8	137	1	YEDX_ECO57	Q8xb75	escherichia
156	6	1.8	137	1	YEDX_ECOLI	P76341	escherichia
157	6	1.8	141	1	CH16_DROSU	P24511	drosophila
158	6	1.8	141	1	LCA_RABIT	P00716	oryctolagus
159	6	1.8	141	1	RL9_HAECO	O02376	haemonchus
160	6	1.8	142	1	CST8_RAT	O88969	rattus norv
161	6	1.8	142	1	RUVX_MYCPE	Q8eur7	mycoplasma
162	6	1.8	143	1	IL4_MERUN	P47966	meriones un
163	6	1.8	145	1	SJ2B_HUMAN	P57105	homo sapien
164	6	1.8	146	1	HBB1_UROHA	P18991	uromastyx h
165	6	1.8	146	1	RL15_MYCLE	O33002	mycobacteri
166	6	1.8	146	1	YS55_CAEEL	Q09664	caenorhabdi
167	6	1.8	151	1	YHR6_YEAST	P38824	saccharomyc
168	6	1.8	153	1	GIP_HUMAN	P09681	homo sapien
169	6	1.8	153	1	Y587_METJA	Q58007	methanococc
170	6	1.8	158	1	IPYR_COREF	Q8fmf8	corynebacte
171	6	1.8	158	1	IPYR_CORGL	Q8nm79	corynebacte
172	6	1.8	160	1	RSBW_BACLI	O50231	bacillus li
173	6	1.8	161	1	5H1B_CANFA	P79250	canis famil
174	6	1.8	162	1	PHCA_AGLNE	P28557	aglaothamni
175	6	1.8	162	1	PHCA_GALSU	P00306	galdieria s
176	6	1.8	162	1	PHCA_MASLA	P00307	mastigoclad
177	6	1.8	163	1	PHCA_ANASP	P07121	anabaena sp
178	6	1.8	164	1	CGHB_CALJA	P51500	callithrix
179	6	1.8	165	1	MSRA_UREPA	Q9pqk2	ureaplasma
180	6	1.8	166	1	NU6M_DINSE	O79557	dinodon sem
181	6	1.8	171	1	FABA_RHILO	Q98bh8	rhizobium l
182	6	1.8	171	1	Y079_DEIRA	Q9ry71	deinococcus
183	6	1.8	172	1	NU6M_RAT	P03926	rattus norv
184	6	1.8	172	1	Y442_CHLPN	Q9z8a1	chlamydia p
185	6	1.8	176	1	PNOC_BOVIN	O62647	bos taurus
186	6	1.8	176	1	PNOC_HUMAN	Q13519	homo sapien
187	6	1.8	176	1	PRND_HUMAN	Q9uky0	homo sapien
188	6	1.8	177	1	RL1X_DROME	P41093	drosophila
189	6	1.8	184	1	IPYR_MYCPN	P75250	mycoplasma
190	6	1.8	185	1	DEF2_NITEU	Q82tc8	nitrosomona
191	6	1.8	186	1	FAPR_STAEP	Q8csv2	staphylococ
192	6	1.8	186	1	HS23_DROME	P02516	drosophila
193	6	1.8	188	1	FAPR_BACSU	O34835	bacillus su
194	6	1.8	188	1	RER1_YEAST	P25560	saccharomyc
195	6	1.8	192	1	CD3E_SHEEP	P29328	ovis aries
196	6	1.8	196	1	SOMA_FUGRU	O12980	fugu rubrip
197	6	1.8	197	1	RL22_MYCTU	P95054	mycobacteri
198	6	1.8	197	1	YKGB_ECOLI	P75685	escherichia
199	6	1.8	202	1	Y038_MYCLE	Q50191	mycobacteri
200	6	1.8	204	1	IPP2_HUMAN	P41236	homo sapien
201	6	1.8	205	1	SEGE_BPT4	P18060	bacteriopha
202	6	1.8	206	1	SJ2B_RAT	Q9wvj4	rattus norv
203	6	1.8	207	1	CB23_TETTH	P20473	tetrahymena
204	6	1.8	207	1	IL6_CANFA	P41323	canis famil
205	6	1.8	209	1	YO23_ARCFU	O30248	archaeoglob
206	6	1.8	212	1	MERB_ECOLI	P77072	escherichia
207	6	1.8	212	1	MERB_RHIME	Q91un2	rhizobium m
208	6	1.8	212	1	MERB_SERMA	P08664	serratia ma
209	6	1.8	212	1	OSC2_BORBU	Q08137	borrelia bu
210	6	1.8	213	1	PIS_HUMAN	O14735	homo sapien
211	6	1.8	213	1	PIS_RAT	P70500	rattus norv
212	6	1.8	214	1	CYC2_PSEAE	P29811	pseudomonas
213	6	1.8	215	1	EVA1_MOUSE	O70255	mus musculu
214	6	1.8	218	1	YF87_XANCP	Q8pa99	xanthomonas
215	6	1.8	221	1	GPX5_MOUSE	P21765	mus musculu
216	6	1.8	221	1	GPX5_RAT	P30710	rattus norv
217	6	1.8	221	1	MDMC_STRMY	Q00719	streptomyce
218	6	1.8	222	1	H15_MOUSE	P43276	mus musculu
219	6	1.8	225	1	YI30_MYCTU	Q50603	mycobacteri
220	6	1.8	229	1	AOFB_BOVIN	P56560	bos taurus
221	6	1.8	229	1	UCK_CAEEL	Q17413	caenorhabdi
222	6	1.8	230	1	MIP_COXBU	P51752	coxiella bu
223	6	1.8	231	1	NANE_LISIN	Q926v7	listeria in
224	6	1.8	233	1	ATPI_OCHNE	Q40607	ochrosphaer
225	6	1.8	235	1	YHE4_YEAST	P38727	saccharomyc
226	6	1.8	236	1	PYRF_BUCAI	P57358	buchnera ap
227	6	1.8	237	1	IPDE_DICDI	P22549	dictyosteli
228	6	1.8	237	1	NANE_LISMO	Q8y3n4	listeria mo
229	6	1.8	240	1	V727_ARATH	Q9m376	arabidopsis
230	6	1.8	241	1	PHZR_PSECL	P54303	pseudomonas
231	6	1.8	242	1	ICEE_HUMAN	P31944	homo sapien
232	6	1.8	243	1	HIS4_CAMJE	Q9pm74	campylobact
233	6	1.8	244	1	COBI_PSEDE	P21639	pseudomonas
234	6	1.8	245	1	KDSB_FUSNN	Q8rfa8	fusobacteri
235	6	1.8	246	1	SNXQ_HUMAN	O14559	homo sapien
236	6	1.8	247	1	YABB_BACSU	P37543	bacillus su
237	6	1.8	248	1	PUR7_METTH	O26272	methanobact
238	6	1.8	251	1	FLGF_ECOLI	P75938	escherichia
239	6	1.8	253	1	VATB_METTL	P20022	methanococc
240	6	1.8	254	1	COAT_TYDVA	P31616	tobacco yel
241	6	1.8	254	1	GLTP_ECOLI	P28721	escherichia
242	6	1.8	257	1	DPHB_THEAC	Q9hjt0	thermoplasm
243	6	1.8	259	1	OVUH_LYMST	P06308	lymnaea sta
244	6	1.8	260	1	DH10_ARATH	P42759	arabidopsis
245	6	1.8	261	1	VP31_FRG3V	P18178	frog virus
246	6	1.8	262	1	COX3_DROME	P00417	drosophila
247	6	1.8	262	1	DSVB_DESGI	P94694	desulfovibr
248	6	1.8	263	1	IBP1_BOVIN	P24591	bos taurus
249	6	1.8	265	1	CB23_PEA	P27520	pisum sativ
250	6	1.8	267	1	PPNK_LACPL	Q88v61	lactobacill
251	6	1.8	267	1	YAD7_YEAST	P39728	saccharomyc
252	6	1.8	267	1	ZDHC_HUMAN	Q96gr4	homo sapien

253	6	1.8	269	1	RIBF_MYCPN	P75587	mycoplasma
254	6	1.8	270	1	FWDC_METTM	Q59579	methanobact
255	6	1.8	273	1	FWDC_METJA	Q58571	methanococc
256	6	1.8	275	1	ICA2_HUMAN	P13598	homo sapien
257	6	1.8	276	1	ATP6_SYNY3	P27178	synechocyst
258	6	1.8	276	1	DHCA_MOUSE	P48758	mus musculu
259	6	1.8	276	1	NUGM_CANMA	Q00673	candida mal
260	6	1.8	278	1	OX2G_HUMAN	P41217	homo sapien
261	6	1.8	278	1	OX2G_MOUSE	O54901	mus musculu
262	6	1.8	278	1	OX2G_RAT	P04218	rattus norv
263	6	1.8	280	1	KDSA_NEIMA	Q9ju48	n 2-dehydro
264	6	1.8	280	1	KDSA_NEIMB	Q9jz55	n 2-dehydro
265	6	1.8	281	1	YQAC_LACLA	Q9cfb9	lactococcus
266	6	1.8	282	1	VMSA_WHVW6	P11293	woodchuck h
267	6	1.8	284	1	MURB_THEMA	Q9x239	thermotoga
268	6	1.8	284	1	YNFH_ECOLI	P76173	escherichia
269	6	1.8	286	1	MEPA_HAEIN	P44566	haemophilus
270	6	1.8	286	1	PTND_ECOLI	P08188	escherichia
271	6	1.8	287	1	XT14_ARATH	Q9zsu4	arabidopsis
272	6	1.8	288	1	PCD1_MOUSE	Q02242	mus musculu
273	6	1.8	288	1	PTR1_LEIMA	Q01782	leishmania
274	6	1.8	288	1	SP4G_BACSU	P26937	bacillus su
275	6	1.8	289	1	PTR1_LEITA	P42556	leishmania
276	6	1.8	290	1	NANA_FUSNN	Q8rdn6	fusobacteri
277	6	1.8	290	1	PRMA_PORGI	P60093	porphyromon
278	6	1.8	292	1	V226_FOWPV	Q9j509	fowlpox vir
279	6	1.8	293	1	BLAC_RHOCA	P14171	rhodobacter
280	6	1.8	293	1	RK4_SPIOL	O49937	spinacia ol
281	6	1.8	296	1	MURB_CHLCV	Q822b0	chlamydophi
282	6	1.8	296	1	RFBF_SHIFL	P37782	shigella fl
283	6	1.8	297	1	BXD1_CAEEL	Q9n3f0	caenorhabdi
284	6	1.8	297	1	ICIA_ECOLI	P24194	escherichia
285	6	1.8	297	1	ICIA_EDWIC	O52399	edwardsiell
286	6	1.8	297	1	ICIA_SALTI	P58508	salmonella
287	6	1.8	297	1	ICIA_SALTY	P58509	salmonella
288	6	1.8	297	1	MURB_AQUAE	O66805	aquifex aeo
289	6	1.8	298	1	MIME_HUMAN	P20774	homo sapien
290	6	1.8	298	1	YSMK_CAEEL	Q19408	caenorhabdi
291	6	1.8	299	1	T2R1_CERAE	Q8mju6	cercopithec
292	6	1.8	302	1	ICIA_YERPE	P58510	yersinia pe
293	6	1.8	302	1	MURB_LACPL	Q88yf4	lactobacill
294	6	1.8	303	1	HYPB_AZOVI	P31880	azotobacter
295	6	1.8	304	1	MURB_CHLPN	Q9z6s1	chlamydia p
296	6	1.8	305	1	HYPB_AZOCH	Q43949	azotobacter
297	6	1.8	307	1	MURB_OCEIH	Q8esr4	oceanobacil
298	6	1.8	308	1	CAH6_HUMAN	P23280	homo sapien
299	6	1.8	311	1	HEM3_VIBCH	Q9kvm1	vibrio chol
300	6	1.8	311	1	MENA_BACSU	P39582	bacillus su
301	6	1.8	311	1	PIX1_CHICK	P56673	gallus gall
302	6	1.8	311	1	PPAC_STRPN	Q97pr8	streptococc
303	6	1.8	313	1	SPY1_MOUSE	Q9qxv9	mus musculu
304	6	1.8	314	1	RLA0_THEAC	P57692	thermoplasm
305	6	1.8	315	1	O8J3_HUMAN	Q8ngg0	homo sapien
306	6	1.8	316	1	O8J1_HUMAN	Q8ngp2	homo sapien
307	6	1.8	318	1	KDGT_XANAC	Q8pqi6	xanthomonas
308	6	1.8	319	1	NU1M_VARFL	Q94vi4	varanus fla
309	6	1.8	324	1	KDGK_BACSU	P50845	bacillus su
310	6	1.8	324	1	NAS4_ARATH	Q9c7x5	arabidopsis
311	6	1.8	325	1	SYGA_RALSO	Q8y211	ralstonia s
312	6	1.8	326	1	VPRT_JSRV	P31625	sheep pulmo
313	6	1.8	327	1	CI30_HUMAN	Q9y375	homo sapien
314	6	1.8	327	1	YQ80_BACAN	Q9rmv5	bacillus an
315	6	1.8	328	1	YJ77_YEAST	P47145	saccharomyc
316	6	1.8	331	1	PLSX_CHLTE	Q8kap3	chlorobium
317	6	1.8	332	1	VG16_BPPH2	P11014	bacteriopha
318	6	1.8	332	1	VG16_BPPZA	P07541	bacteriopha
319	6	1.8	334	1	PDXA_BACHD	Q9rc88	bacillus ha
320	6	1.8	335	1	LEP4_MYXXA	O30387	myxococcus
321	6	1.8	335	1	Y7C9_BORBR	O06702	bordetella
322	6	1.8	336	1	YPH1_MYCCA	P45613	mycoplasma
323	6	1.8	337	1	GP26_HUMAN	Q8ndv2	homo sapien
324	6	1.8	337	1	GP26_MOUSE	Q8bza7	mus musculu
325	6	1.8	337	1	GP26_RAT	Q9qxi3	rattus norv
326	6	1.8	337	1	PLSX_BACHD	Q9ka01	bacillus ha
327	6	1.8	339	1	MDH_METFE	P16142	methanother
328	6	1.8	339	1	RIR2_MYCPN	P75461	mycoplasma
329	6	1.8	340	1	RIR2_MYCGE	P47471	mycoplasma
330	6	1.8	342	1	HUPV_AZOCH	Q43959	azotobacter
331	6	1.8	342	1	TORT_ECO57	P58358	escherichia
332	6	1.8	342	1	TORT_ECOLI	P38683	escherichia
333	6	1.8	344	1	GVN2_HALN1	Q9hhs9	halobacteri
334	6	1.8	345	1	GVN2_HALN2	P33965	halobacteri
335	6	1.8	347	1	FOS_CYPCA	P79702	cyprinus ca
336	6	1.8	347	1	NU2M_DUGDU	Q8w9n5	dugong dugo
337	6	1.8	347	1	NU2M_RABIT	O79428	oryctolagus
338	6	1.8	350	1	DKK3_HUMAN	Q9ubp4	homo sapien
339	6	1.8	350	1	GLCE_ECOLI	P52073	escherichia
340	6	1.8	350	1	HN3G_HUMAN	P55318	homo sapien
341	6	1.8	351	1	HSF3_LYCPE	P41152	lycopersico
342	6	1.8	351	1	SPIN_HAEPV	Q05894	heliothis a
343	6	1.8	352	1	DHSO_BACSU	Q06004	bacillus su
344	6	1.8	352	1	WNT2_DROME	P28465	drosophila
345	6	1.8	353	1	CKR8_MOUSE	P56484	mus musculu
346	6	1.8	354	1	MURB_TREPA	O83128	treponema p
347	6	1.8	354	1	PHOH_ECOLI	P31544	escherichia
348	6	1.8	355	1	AMBP_PLEPL	P36992	pleuronecte
349	6	1.8	356	1	PCB1_HUMAN	Q15365	homo sapien
350	6	1.8	356	1	PCB1_RABIT	O19048	oryctolagus
351	6	1.8	357	1	IDI2_CHLTE	Q8kfr5	chlorobium
352	6	1.8	358	1	ILVE_STAAM	Q99w55	staphylococ
353	6	1.8	358	1	ILVE_STAEP	Q8cq78	staphylococ
354	6	1.8	358	1	RF1_STRCO	Q9k4e4	streptomyce
355	6	1.8	360	1	YS03_CAEEL	Q09358	caenorhabdi
356	6	1.8	361	1	PGLR_YEAST	P47180	saccharomyc
357	6	1.8	361	1	RM45_DROME	Q9vcx3	drosophila
358	6	1.8	362	1	PCB2_MOUSE	Q61990	mus musculu
359	6	1.8	363	1	AROB_STRAW	Q827r8	streptomyce
360	6	1.8	363	1	AROB_STRCO	Q9kxq6	streptomyce
361	6	1.8	365	1	CMLE_NEUCR	P38677	neurospora
362	6	1.8	365	1	PCB2_HUMAN	Q15366	homo sapien
363	6	1.8	371	1	CML1_MOUSE	P97468	mus musculu
364	6	1.8	371	1	TRM1_HALN1	P57705	halobacteri
365	6	1.8	372	1	HS72_PARLI	P22623	paracentrot
366	6	1.8	372	1	MURG_CORGL	Q8nnn5	corynebacte
367	6	1.8	372	1	VGLI_HSV23	P06764	herpes simp
368	6	1.8	374	1	FXL8_HUMAN	Q96cd0	homo sapien
369	6	1.8	374	1	NIR_RHOSH	Q53239	rhodobacter
370	6	1.8	376	1	PSD4_MOUSE	O35226	mus musculu
371	6	1.8	377	1	PSD4_HUMAN	P55036	homo sapien
372	6	1.8	377	1	Y392_CHLTR	P36427	chlamydia t
373	6	1.8	379	1	CYB_GALMO	Q9g9j6	galago moho
374	6	1.8	380	1	DSVB_DESVH	P45575	desulfovibr
375	6	1.8	386	1	5H1B_MOUSE	P28334	mus musculu
376	6	1.8	386	1	5H1B_RAT	P28564	rattus norv
377	6	1.8	386	1	5H1B_SPAEH	P56496	spalax leuc
378	6	1.8	387	1	SGCA_HUMAN	Q16586	homo sapien
379	6	1.8	387	1	SGCA_MESAU	Q64255	mesocricetu
380	6	1.8	387	1	SGCA_MOUSE	P82350	mus musculu
381	6	1.8	387	1	SGCA_RABIT	Q28686	oryctolagus
382	6	1.8	388	1	5H1B_DIDMA	P35404	didelphis m
383	6	1.8	390	1	5H1B_HUMAN	P28222	homo sapien
384	6	1.8	390	1	5H1B_PANTR	P60020	pan troglod
385	6	1.8	390	1	5H1B_RABIT	P49144	oryctolagus
386	6	1.8	390	1	VGLI_HSV11	P06487	herpes simp
387	6	1.8	391	1	POLG_CYVV	P20177	clover yell
388	6	1.8	393	1	STAD_ELAGV	O24428	elaeis guin
389	6	1.8	394	1	PGCA_RABIT	Q28670	oryctolagus
390	6	1.8	396	1	HEM3_HALN1	Q9hmy5	halobacteri
391	6	1.8	396	1	Y111_METJA	Q57575	methanococc
392	6	1.8	397	1	ARGD_NEIMA	Q9jtx9	neisseria m
393	6	1.8	398	1	ARGD_NEIMB	Q9jyy4	neisseria m
394	6	1.8	398	1	FRHA_METVO	Q00390	methanococc
395	6	1.8	398	1	SHBG_RABIT	P15196	oryctolagus
396	6	1.8	399	1	METK_BACHD	Q9k7q9	bacillus ha
397	6	1.8	400	1	ISDF_AGRT5	Q8uff4	a ispd/ispf
398	6	1.8	400	1	TYRP_HAEIN	P44727	haemophilus

399	6	1.8	402	1	YJ93_PSEAE	Q9i2b6	pseudomonas
400	6	1.8	404	1	ALR_RICPR	Q9ze52	rickettsia
401	6	1.8	404	1	METK_PYRAB	Q9v1p7	pyrococcus
402	6	1.8	404	1	METK_PYRHO	O59488	pyrococcus
403	6	1.8	406	1	RL4B_ARATH	Q9sf40	arabidopsis
404	6	1.8	409	1	AA2A_CAVPO	P46616	cavia porce
405	6	1.8	409	1	MDP1_PIG	P22412	sus scrofa
406	6	1.8	409	1	Y774_METJA	Q58184	methanococc
407	6	1.8	412	1	AA2A_CANFA	P11617	canis famil
408	6	1.8	412	1	AA2A_HUMAN	P29274	homo sapien
409	6	1.8	413	1	ARGJ_STAAM	Q99x38	s arginine
410	6	1.8	413	1	ARGJ_STAAW	Q8nym7	s arginine
411	6	1.8	414	1	GAG2_DROME	P20828	drosophila
412	6	1.8	415	1	IL5R_MOUSE	P21183	mus musculu
413	6	1.8	415	1	SCB2_CAEEL	P53589	caenorhabdi
414	6	1.8	415	1	YZ07_METJA	Q60269	methanococc
415	6	1.8	416	1	AROA_ARCFU	O28775	archaeoglob
416	6	1.8	416	1	CRTC_BETVU	O81919	beta vulgar
417	6	1.8	417	1	IE63_HSVSA	P13199	herpesvirus
418	6	1.8	417	1	PGCB_FELCA	P41725	felis silve
419	6	1.8	419	1	KDAP_MOUSE	O09043	mus musculu
420	6	1.8	420	1	DYX1_MOUSE	Q8r368	mus musculu
421	6	1.8	420	1	FLA8_ARATH	O22126	arabidopsis
422	6	1.8	421	1	V1BR_MOUSE	Q9wu02	mus musculu
423	6	1.8	422	1	EXUT_BACSU	O34456	bacillus su
424	6	1.8	422	1	ZP3_MESAU	P23491	mesocricetu
425	6	1.8	424	1	NODC_RHILO	P17862	rhizobium l
426	6	1.8	426	1	VMSA_WHV1	P03143	woodchuck h
427	6	1.8	428	1	VMSA_HPBGS	P03144	ground squi
428	6	1.8	429	1	PEPB_VIBCH	Q9ktx5	vibrio chol
429	6	1.8	431	1	VMSA_WHV59	P12910	woodchuck h
430	6	1.8	431	1	VMSA_WHV7	P12909	woodchuck h
431	6	1.8	431	1	VMSA_WHV8	P06432	woodchuck h
432	6	1.8	431	1	VMSA_WHV8I	P17400	woodchuck h
433	6	1.8	432	1	PEPB_VIBPA	Q87s21	vibrio para
434	6	1.8	432	1	PEPB_YERPE	P58475	yersinia pe
435	6	1.8	436	1	MNTH_DEIRA	Q9rtp8	deinococcus
436	6	1.8	437	1	EF1A_AERPE	Q9yav0	aeropyrum p
437	6	1.8	438	1	RR45_MOUSE	Q9jhi7	m exosome c
438	6	1.8	442	1	CYS4_DICDI	P54639	dictyosteli
439	6	1.8	442	1	LEU2_BUCUS	Q9evi3	buchnera ap
440	6	1.8	443	1	LEU2_BUCUA	Q9evg5	buchnera ap
441	6	1.8	444	1	ASSY_HAEIN	P44315	haemophilus
442	6	1.8	445	1	ASSY_BRAJA	P59607	bradyrhizob
443	6	1.8	445	1	ASSY_PASMU	P57877	pasteurella
444	6	1.8	445	1	ASSY_RALSO	Q8xwc1	ralstonia s
445	6	1.8	446	1	ASSY_ECO57	Q8x9m0	escherichia
446	6	1.8	446	1	ASSY_ECOLI	P22767	escherichia
447	6	1.8	446	1	ASSY_SALTI	Q8z3h5	salmonella
448	6	1.8	446	1	ASSY_SALTY	Q8zlt0	salmonella
449	6	1.8	446	1	ASSY_SHIFL	P59609	shigella fl
450	6	1.8	446	1	Y612_METJA	Q58029	methanococc
451	6	1.8	447	1	ASSY_NEIMA	Q9jwm1	neisseria m
452	6	1.8	447	1	ASSY_NEIMB	Q9jxc1	neisseria m
453	6	1.8	449	1	GSBN_DROME	P09083	drosophila
454	6	1.8	449	1	QSEC_ECO57	Q8x524	escherichia
455	6	1.8	449	1	QSEC_ECOLI	P40719	escherichia
456	6	1.8	449	1	QSEC_SALTI	Q8z3p2	salmonella
457	6	1.8	449	1	QSEC_SALTY	Q8zlz9	salmonella
458	6	1.8	451	1	Y037_MYCPN	P75067	mycoplasma
459	6	1.8	453	1	YBU5_YEAST	P38255	saccharomyc
460	6	1.8	454	1	ASSY_YERPE	Q8zfv7	yersinia pe
461	6	1.8	459	1	AAPA_BACSU	O06005	bacillus su
462	6	1.8	459	1	ZPR1_SCHPO	O13724	schizosacch
463	6	1.8	460	1	IL6A_MOUSE	P22272	mus musculu
464	6	1.8	461	1	Y608_HAEIN	Q57486	haemophilus
465	6	1.8	462	1	CHI1_CANAL	P46876	candida alb
466	6	1.8	462	1	IL6A_RAT	P22273	rattus norv
467	6	1.8	463	1	CTXA_CARAL	Q9gnn8	carybdea al
468	6	1.8	466	1	FA7_HUMAN	P08709	homo sapien
469	6	1.8	468	1	T10A_HUMAN	O00220	homo sapien
470	6	1.8	470	1	RAN1_SCHPO	P08092	schizosacch
471	6	1.8	471	1	Y872_HAEIN	Q57491	haemophilus
472	6	1.8	472	1	KCCG_HUMAN	Q13555	homo sapien
473	6	1.8	473	1	MDM2_XENLA	P56273	xenopus lae
474	6	1.8	473	1	PSBC_MARPO	P06414	marchantia
475	6	1.8	474	1	NOEK_RHISN	P55356	rhizobium s
476	6	1.8	476	1	BM3B_RAT	P55108	rattus norv
477	6	1.8	476	1	NOEA_RHIME	Q52892	rhizobium m
478	6	1.8	477	1	HSS_RHOVI	O32323	rhodopseudo
479	6	1.8	478	1	RDP1_SCHPO	O13862	schizosacch
480	6	1.8	480	1	ASSY_STRCO	P24532	streptomyce
481	6	1.8	480	1	DJA3_HUMAN	Q96ey1	homo sapien
482	6	1.8	480	1	DJA3_MOUSE	Q99m87	mus musculu
483	6	1.8	481	1	ASSY_STRLA	Q06734	streptomyce
484	6	1.8	482	1	PTSB_VIBCH	Q9kvd9	vibrio chol
485	6	1.8	482	1	SYFA_THEVO	Q979u4	thermoplasm
486	6	1.8	484	1	UAP1_CAEEL	Q18493	caenorhabdi
487	6	1.8	488	1	DHAL_PSESP	P33008	pseudomonas
488	6	1.8	488	1	SYFA_AERPE	Q9y9i6	aeropyrum p
489	6	1.8	488	1	YA15_HAEIN	P71364	haemophilus
490	6	1.8	490	1	CPCD_RAT	P20814	rattus norv
491	6	1.8	491	1	YC70_CORGL	P42531	corynebacte
492	6	1.8	493	1	AMPA_CLOPE	Q8xhi3	clostridium
493	6	1.8	493	1	CHI1_RHINI	P29025	rhizopus ni
494	6	1.8	497	1	UDP2_HUMAN	Q16851	homo sapien
495	6	1.8	498	1	SYC_DEIRA	Q9rtt6	deinococcus
496	6	1.8	500	1	RASP_DROME	Q9vzu2	drosophila
497	6	1.8	501	1	YSV1_CAEEL	Q22566	caenorhabdi
498	6	1.8	503	1	CED3_CAEEL	P42573	caenorhabdi
499	6	1.8	503	1	SHS1_HUMAN	P78324	h protein-t
500	6	1.8	506	1	SHS1_BOVIN	O46631	bos taurus
501	6	1.8	507	1	UDP2_BOVIN	Q07130	bos taurus
502	6	1.8	507	1	UDP2_PIG	P79303	sus scrofa
503	6	1.8	507	1	YCGG_ECOLI	P75995	escherichia
504	6	1.8	509	1	AGP4_MOUSE	Q9wvh6	mus musculu
505	6	1.8	509	1	CPV1_BRARE	O42145	brachydanio
506	6	1.8	509	1	PAST_HUMAN	Q9y2w3	homo sapien
507	6	1.8	511	1	ACH2_RAT	P12389	rattus norv
508	6	1.8	513	1	HDAC_MAIZE	P56521	zea mays (m
509	6	1.8	513	1	SHS1_MOUSE	P97797	m protein-t
510	6	1.8	515	1	LEU1_BUCPS	P58898	buchnera ap
511	6	1.8	516	1	HS70_LEIMA	P14834	leishmania
512	6	1.8	518	1	CPV2_CARAU	O73686	carassius a
513	6	1.8	518	1	LEU1_BUCAP	O85063	buchnera ap
514	6	1.8	518	1	LEU1_BUCRP	P48571	buchnera ap
515	6	1.8	519	1	LEU1_BUCAI	Q9zey8	buchnera ap
516	6	1.8	520	1	AMPA_MYCSA	P47707	mycoplasma
517	6	1.8	522	1	MSAB_NEIMA	Q9jwm8	n peptide m
518	6	1.8	527	1	COX1_PEA	P12786	pisum sativ
519	6	1.8	527	1	COX1_SOYBN	P07506	glycine max
520	6	1.8	527	1	KCCG_RAT	P11730	rattus norv
521	6	1.8	527	1	TXK_HUMAN	P42681	homo sapien
522	6	1.8	527	1	TXK_MOUSE	P42682	mus musculu
523	6	1.8	529	1	KCCG_MOUSE	Q923t9	mus musculu
524	6	1.8	531	1	YTGF_LACLA	Q9cee2	lactococcus
525	6	1.8	532	1	P72_MYCMY	P55801	mycoplasma
526	6	1.8	535	1	PYRG_BACCR	Q814t2	bacillus ce
527	6	1.8	536	1	GAG_FSVMD	P03340	feline sarc
528	6	1.8	537	1	PGCA_PIG	Q29011	sus scrofa
529	6	1.8	537	1	PPOC_ARATH	P55826	arabidopsis
530	6	1.8	538	1	RO60_XENLA	P42700	xenopus lae
531	6	1.8	540	1	CH60_STRPN	Q97nv4	streptococc
532	6	1.8	541	1	IR18_HUMAN	Q13478	homo sapien
533	6	1.8	541	1	NU5M_ARTSF	Q37710	artemia san
534	6	1.8	542	1	CH60_LACLA	P37282	lactococcus
535	6	1.8	542	1	CH60_LACLC	Q9aep7	lactococcus
536	6	1.8	542	1	CH60_STRMU	Q8cww6	streptococc
537	6	1.8	542	1	CH60_STRP3	Q8k5m5	streptococc
538	6	1.8	542	1	CH60_STRP8	Q8nz56	streptococc
539	6	1.8	542	1	CH60_STRPY	P82485	streptococc
540	6	1.8	542	1	V155_FOWPV	Q9j5a7	fowlpox vir
541	6	1.8	544	1	SGPL_ARATH	Q9c509	arabidopsis
542	6	1.8	546	1	Y61B_MYCPN	P75040	mycoplasma
543	6	1.8	548	1	PPOC_TOBAC	O24163	nicotiana t
544	6	1.8	548	1	TCPQ_MOUSE	P42932	mus musculu

545	6	1.8	551	1	RN27_HUMAN	Q9bzr9	homo sapien
546	6	1.8	551	1	RN27_MOUSE	Q99pj2	mus musculu
547	6	1.8	552	1	ARRA_ARATH	O49397	arabidopsis
548	6	1.8	552	1	UBIB_XYLFA	Q9pce8	xylella fas
549	6	1.8	552	1	UBIB_XYLFT	Q87cn1	xylella fas
550	6	1.8	557	1	MAOX_ANAPL	P28227	anas platyr
551	6	1.8	557	1	MAOX_COLLI	P40927	columba liv
552	6	1.8	557	1	YU61_VIBMA	Q9ra11	vibrio mari
553	6	1.8	564	1	ARX_MOUSE	O35085	mus musculu
554	6	1.8	564	1	ASM1_CAEEL	Q10916	caenorhabdi
555	6	1.8	566	1	PILB_PSEAE	P22608	pseudomonas
556	6	1.8	567	1	CYDC_BACSU	P94366	bacillus su
557	6	1.8	567	1	FZD7_CHICK	O57329	gallus gall
558	6	1.8	568	1	TAPB_AERHY	P45792	aeromonas h
559	6	1.8	574	1	ENV_SRV2R	P51520	simian retr
560	6	1.8	574	1	ILD2_BRAJA	Q89ky5	bradyrhizob
561	6	1.8	576	1	ACH2_DROME	P17644	drosophila
562	6	1.8	576	1	HXT4_YEAST	P32467	saccharomyc
563	6	1.8	577	1	ALG8_YEAST	P40351	saccharomyc
564	6	1.8	579	1	PHOR_BACSU	P23545	bacillus su
565	6	1.8	585	1	DHSA_BACSU	P08065	bacillus su
566	6	1.8	588	1	C166_CHICK	P42292	gallus gall
567	6	1.8	590	1	HMDF_DROME	P07548	drosophila
568	6	1.8	591	1	FLGE_CAUCR	P35806	caulobacter
569	6	1.8	592	1	FTSZ_BARBA	O31314	bartonella
570	6	1.8	596	1	GPD2_ARATH	Q9fy99	arabidopsis
571	6	1.8	597	1	LEPA_VIBVU	Q8dc78	vibrio vuln
572	6	1.8	600	1	S133_MOUSE	Q91y63	mus musculu
573	6	1.8	600	1	S133_RAT	Q9z0z5	rattus norv
574	6	1.8	601	1	3BP1_MOUSE	P55194	mus musculu
575	6	1.8	603	1	C48B_ARATH	Q9zpr1	arabidopsis
576	6	1.8	603	1	PURL_THEMA	Q9x0x3	thermotoga
577	6	1.8	603	1	YD25_MYCTU	Q10637	mycobacteri
578	6	1.8	618	1	DNAK_CORGL	Q8nly6	corynebacte
579	6	1.8	619	1	DNAK_COREF	Q8fm78	corynebacte
580	6	1.8	620	1	KHL8_HUMAN	Q9p2g9	homo sapien
581	6	1.8	620	1	S6A6_BOVIN	Q9mz34	bos taurus
582	6	1.8	620	1	S6A6_CANFA	Q00589	canis famil
583	6	1.8	620	1	S6A6_HUMAN	P31641	homo sapien
584	6	1.8	621	1	LONH_ARCFU	O29883	archaeoglob
585	6	1.8	621	1	S6A6_MOUSE	O35316	mus musculu
586	6	1.8	621	1	S6A6_RAT	P31643	rattus norv
587	6	1.8	622	1	3BP1_HUMAN	Q9y3l3	homo sapien
588	6	1.8	622	1	COX1_BACSU	P24010	bacillus su
589	6	1.8	624	1	COX1_BACPF	Q04440	bacillus ps
590	6	1.8	625	1	XYNA_PIRSP	Q12667	piromyces s
591	6	1.8	626	1	RN17_MOUSE	Q99mv7	mus musculu
592	6	1.8	627	1	K2C1_MOUSE	P04104	mus musculu
593	6	1.8	629	1	SKIL_MOUSE	Q60665	mus musculu
594	6	1.8	630	1	MNT3_YEAST	P40549	saccharomyc
595	6	1.8	632	1	APS_HUMAN	O14492	homo sapien
596	6	1.8	634	1	GLGB_LACPL	Q890j1	lactobacill
597	6	1.8	636	1	YNR6_YEAST	P53882	saccharomyc
598	6	1.8	637	1	FTSH_BACSU	P37476	bacillus su
599	6	1.8	640	1	C5P1_ARATH	Q8h0v1	arabidopsis
600	6	1.8	640	1	HS7A_CAEEL	P09446	caenorhabdi
601	6	1.8	640	1	HS7C_DICDI	P36415	dictyosteli
602	6	1.8	641	1	NU5M_ALLMA	P50365	allomyces m
603	6	1.8	641	1	UGS2_SOLTU	P93568	solanum tub
604	6	1.8	643	1	HS71_SCHPO	Q10265	schizosacch
605	6	1.8	643	1	Y903_METJA	Q58313	methanococc
606	6	1.8	644	1	LON1_METTH	O26878	methanobact
607	6	1.8	648	1	S281_RAT	Q62674	rattus norv
608	6	1.8	649	1	HS70_PYRSA	P37899	pyrenomonas
609	6	1.8	650	1	AMPB_HUMAN	Q9h4a4	homo sapien
610	6	1.8	650	1	Y096_MYCGE	P47342	mycoplasma
611	6	1.8	652	1	HS70_LEIAM	Q07437	leishmania
612	6	1.8	653	1	HS70_LEIDO	P17804	leishmania
613	6	1.8	653	1	RN17_HUMAN	Q9bxt8	homo sapien
614	6	1.8	654	1	HS70_HYDMA	Q05944	hydra magni
615	6	1.8	654	1	YLH4_SCHPO	Q9hgq2	schizosacch
616	6	1.8	657	1	MM15_MOUSE	O54732	mus musculu
617	6	1.8	661	1	HS74_TRYBB	P11145	trypanosoma
618	6	1.8	661	1	WHI3_YEAST	P34761	saccharomyc
619	6	1.8	665	1	HS70_ECHGR	Q24789	echinococcu
620	6	1.8	665	1	KF22_HUMAN	Q14807	homo sapien
621	6	1.8	667	1	TKT2_ECOLI	P33570	escherichia
622	6	1.8	668	1	TKT_XANFL	P51010	xanthobacte
623	6	1.8	669	1	MM15_HUMAN	P51511	homo sapien
624	6	1.8	674	1	CIN_DROME	P39205	drosophila
625	6	1.8	674	1	YB66_YEAST	P38315	saccharomyc
626	6	1.8	682	1	E13B_BACCI	P23903	bacillus ci
627	6	1.8	682	1	S219_RAT	Q9jhi3	rattus norv
628	6	1.8	686	1	ATKB_MYXXA	Q93mv5	myxococcus
629	6	1.8	690	1	SYGB_BUCAI	P57235	buchnera ap
630	6	1.8	695	1	NU5C_CAPBA	Q31952	capsicum ba
631	6	1.8	695	1	NU5C_LYCES	Q32516	lycopersico
632	6	1.8	702	1	UMOB_PROMI	O86988	proteus mir
633	6	1.8	703	1	COAT_SMSV4	P36285	san miguel
634	6	1.8	704	1	MID2_SCHPO	Q9p7y8	schizosacch
635	6	1.8	707	1	GCVK_HCMVA	P16788	human cytom
636	6	1.8	710	1	PKN6_MYXXA	P54738	myxococcus
637	6	1.8	711	1	Z336_HUMAN	Q9h116	homo sapien
638	6	1.8	712	1	E2BE_YEAST	P32501	saccharomyc
639	6	1.8	713	1	CADD_HUMAN	P55290	homo sapien
640	6	1.8	715	1	UVRD_MYCPN	P75437	mycoplasma
641	6	1.8	723	1	DLL1_HUMAN	O00548	homo sapien
642	6	1.8	725	1	HS9B_BRARE	O57521	brachydanio
643	6	1.8	727	1	PEC1_MOUSE	Q08481	mus musculu
644	6	1.8	731	1	DAXX_RAT	Q8vib2	rattus norv
645	6	1.8	731	1	GOA5_HUMAN	Q8tba6	homo sapien
646	6	1.8	735	1	CIGB_DICDI	Q94481	dictyosteli
647	6	1.8	735	1	MCM5_XENLA	P55862	xenopus lae
648	6	1.8	738	1	DX_DROME	Q23985	drosophila
649	6	1.8	739	1	DAXX_MOUSE	O35613	mus musculu
650	6	1.8	740	1	NU5C_TOBAC	P06265	nicotiana t
651	6	1.8	743	1	BGAL_THEET	P77989	thermoanaer
652	6	1.8	754	1	Z287_HUMAN	Q9hbt7	homo sapien
653	6	1.8	759	1	Z287_MOUSE	Q9eqb9	mus musculu
654	6	1.8	761	1	METE_VIBCH	Q9krd8	vibrio chol
655	6	1.8	764	1	ICCR_DROME	Q08180	drosophila
656	6	1.8	766	1	GAP1_SCHPO	P33277	schizosacch
657	6	1.8	767	1	CC10_SCHPO	P01129	schizosacch
658	6	1.8	772	1	ELA1_HUMAN	Q14241	homo sapien
659	6	1.8	775	1	POT3_ARATH	Q9fe38	arabidopsis
660	6	1.8	775	1	REP_BPHP1	P51711	bacteriopha
661	6	1.8	779	1	MSS4_YEAST	P38994	saccharomyc
662	6	1.8	784	1	LON_RICPR	Q9zd92	rickettsia
663	6	1.8	787	1	OBP_HSV7J	P52379	human herpe
664	6	1.8	788	1	QOXM_SULAC	P39481	sulfolobus
665	6	1.8	790	1	ARNT_RABIT	O02748	oryctolagus
666	6	1.8	790	1	DNLI_ARATH	Q42572	arabidopsis
667	6	1.8	796	1	SEC6_CAEEL	Q19262	caenorhabdi
668	6	1.8	800	1	GUN_BACS1	P06564	bacillus sp
669	6	1.8	801	1	SC34_YEAST	P40094	saccharomyc
670	6	1.8	801	1	VP5_RDVA	P14583	rice dwarf
671	6	1.8	801	1	VP5_RDVF	Q85437	rice dwarf
672	6	1.8	803	1	SYFB_WIGBR	Q8d3b5	wiggleswort
673	6	1.8	804	1	DPP6_MOUSE	Q9z218	mus musculu
674	6	1.8	804	1	YBBP_ECOLI	P77504	escherichia
675	6	1.8	809	1	AL14_SCHPO	O94534	schizosacch
676	6	1.8	812	1	LON_BRUAB	O52605	brucella ab
677	6	1.8	812	1	LON_BRUME	Q8yhc6	brucella me
678	6	1.8	812	1	LON_BRUSU	Q8g0i7	brucella su
679	6	1.8	819	1	AD09_HUMAN	Q13443	homo sapien
680	6	1.8	828	1	PMFC_PROMI	P53514	proteus mir
681	6	1.8	828	1	YKR6_YEAST	P34239	saccharomyc
682	6	1.8	829	1	SC10_ARATH	Q8rvq5	arabidopsis
683	6	1.8	830	1	SREC_HUMAN	Q14162	homo sapien
684	6	1.8	836	1	GCS1_HUMAN	Q13724	homo sapien
685	6	1.8	842	1	ABC6_HUMAN	Q9np58	homo sapien
686	6	1.8	848	1	TOP1_BORBU	O51768	borrelia bu
687	6	1.8	852	1	YKM1_YEAST	P32330	saccharomyc
688	6	1.8	855	1	CNRC_BOVIN	P16586	bos taurus
689	6	1.8	856	1	AAP1_YEAST	P37898	saccharomyc
690	6	1.8	858	1	POT7_ARATH	Q9fy75	arabidopsis

691	6	1.8	863	1	MCM4_XENLA	P30664 xenopus lae
692	6	1.8	870	1	CSX2_SCHPO	Q9uue2 schizosacch
693	6	1.8	870	1	Y563_HUMAN	O60309 homo sapien
694	6	1.8	874	1	SYA_PSEAE	Q9i553 pseudomonas
695	6	1.8	877	1	P101_PIG	O02696 sus scrofa
696	6	1.8	877	1	SECA_GUITH	O78441 guillardia
697	6	1.8	880	1	BRC4_DROME	Q24206 drosophila
698	6	1.8	883	1	PGCB_MOUSE	Q61361 mus musculu
699	6	1.8	883	1	PGCB_RAT	P55068 rattus norv
700	6	1.8	887	1	MCM2_DROME	P49735 drosophila

ALIGNMENTS

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RESULT 1
MAPB_MOUSE
ID   MAPB_MOUSE     STANDARD;      PRT;  2464 AA.
AC   P14873;
DT   01-APR-1990 (Rel. 14, Created)
DT   01-APR-1990 (Rel. 14, Last sequence update)
DT   28-FEB-2003 (Rel. 41, Last annotation update)
DE   Microtubule-associated protein 1B (MAP 1B) (MAP1.2) (MAP1(X))
DE   [Contains: MAP1 light chain LC1].
GN   MAP1B OR MTAP1B OR MTAP5.
OS   Mus musculus (Mouse).
OC   Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC   Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus.
OX   NCBI_TaxID=10090;
RN   [1]
RP   SEQUENCE FROM N.A., AND DOMAIN.
RC   STRAIN=Swiss Webster; TISSUE=Brain;
RX   MEDLINE=90094539; PubMed=2480963;
RA   Noble M., Lewis S.A., Cowan N.J.;
RT   "The microtubule binding domain of microtubule-associated protein
RT   MAP1B contains a repeated sequence motif unrelated to that of MAP2
RT   and tau.";
RL   J. Cell Biol. 109:3367-3376(1989).
CC   -!- FUNCTION: The function of brain MAPS is essentially unknown.
CC       Phosphorylated MAP1B may play a role in the cytoskeletal changes
CC       that accompany neurite extension. Possibly MAP1B Binds to at least
CC       two tubulin subunits in the polymer, and this bridging of subunits
CC       might be involved in nucleating microtubule polymerization and in
CC       stabilizing microtubules.
CC   -!- SUBUNIT: 3 different light chains, LC1, LC2 and LC3, can associate
CC       with MAP1A and MAP1B proteins.
CC   -!- DOMAIN: Has a highly basic region with many copies of the sequence
CC       KKEE and KKEI/V, repeated but not at fixed intervals, which is
CC       responsible for the binding of MAP1B to microtubules.
CC   -!- PTM: LC1 is coexpressed with MAP1B. It is a polypeptide generated
CC       from MAP1B by proteolytic processing. It is free to associate with
CC       both MAP1A and MAP1B. It interacts with the amino-terminal region
CC       of MAP1B.
CC   -!- SIMILARITY: TO MAP1A.
CC   ---------------------------------------------------------------------
CC   This SWISS-PROT entry is copyright. It is produced through a collaboration
CC   between the Swiss Institute of Bioinformatics and the EMBL outstation -
CC   the European Bioinformatics Institute. There are no restrictions on its
CC   use by non-profit institutions as long as its content is in no way
CC   modified and this statement is not removed. Usage by and for commercial
CC   entities requires a license agreement (See http://www.isb-sib.ch/announce/
CC   or send an email to license@isb-sib.ch).
CC   ---------------------------------------------------------------------
DR   EMBL; X51396; CAA35761.1; -.
DR   PIR; S07549; QRMSP1.
DR   MGD; MGI:1306778; Mtap1b.
DR   GO; GO:0016358; P:dendrite morphogenesis; IMP.
DR   GO; GO:0001578; P:microtubule bundling; IMP.
DR   InterPro; IPR000102; MAP1B_neuraxin.
DR   Pfam; PF00414; MAP1B_neuraxin; 10.
DR   PROSITE; PS00230; MAP1B_NEURAXIN; 7.
KW   Microtubule; Repeat; Phosphorylation.
FT   CHAIN        ?    2464       MAP1 LIGHT CHAIN LC1.
FT   REPEAT      1874   1890       MAP1B 1.
FT   REPEAT      1891   1907       MAP1B 2.
FT   REPEAT      1908   1924       MAP1B 3.
FT   REPEAT      1925   1941       MAP1B 4.
FT   REPEAT      1942   1958       MAP1B 5.
FT   REPEAT      1959   1975       MAP1B 6.
FT   REPEAT      1993   2009       MAP1B 7.
FT   REPEAT      2010   2026       MAP1B 8.
FT   REPEAT      2027   2043       MAP1B 9.
FT   REPEAT      2044   2060       MAP1B 10.
FT   DOMAIN       589    787       LYS-RICH (HIGHLY BASIC, CONTAINS MANY
FT                                 KKEE AND KKEI/V REPEATS).
SQ   SEQUENCE   2464 AA;  270408 MW;  FBD3DD99CFDBDA87 CRC64;

  Query Match             2.7%;  Score 9;  DB 1;  Length 2464;
  Best Local Similarity   100.0%;  Pred. No. 3.7;
  Matches    9;  Conservative    0;  Mismatches    0;  Indels    0;  Gaps    0;

Qy         21 AASGPVKEL 29
              |||||||||
Db        812 AASGPVKEL 820


RESULT 2
BGAL_FELCA
ID   BGAL_FELCA     STANDARD;      PRT;   669 AA.
AC   O19015; O18898;
DT   15-DEC-1998 (Rel. 37, Created)
DT   15-DEC-1998 (Rel. 37, Last sequence update)
DT   30-MAY-2000 (Rel. 39, Last annotation update)
DE   Beta-galactosidase precursor (EC 3.2.1.23) (Lactase) (Acid beta-
DE   galactosidase).
GN   GLB1 OR BGAL.
OS   Felis silvestris catus (Cat).
OC   Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC   Mammalia; Eutheria; Carnivora; Fissipedia; Felidae; Felis.
OX   NCBI_TaxID=9685;
RN   [1]
RP   SEQUENCE FROM N.A.
RA   Varadarajan G.S., Smith B.F., Foureman P., Martin D.R.,
RA   Varadarajan U., Georgeson M., Baker H.J.;
RT   "The sequence of feline lysosomal beta-galactosidase.";
RL   Submitted (JUN-1997) to the EMBL/GenBank/DDBJ databases.
RN   [2]
RP   SEQUENCE FROM N.A.
RC   TISSUE=Brain;
RA   Smith B.F., Foureman P., Georgeson M., Martin D.R., Baker H.J.;
RT   "The mutation in feline beta-galactosidase deficiency (GM1
RT   gangliosidosis).";
RL   Submitted (OCT-1997) to the EMBL/GenBank/DDBJ databases.
CC   -!- FUNCTION: Cleaves beta-linked terminal galactosyl residues from
CC       gangliosides, glycoproteins, and glycosaminoglycans.
CC   -!- CATALYTIC ACTIVITY: Hydrolysis of terminal, non-reducing beta-D-
CC       galactose residues in beta-D-galactosides.
CC   -!- SUBCELLULAR LOCATION: Lysosomal.
CC   -!- SIMILARITY: Belongs to family 35 of glycosyl hydrolases.
CC   ---------------------------------------------------------------------
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CC   or send an email to license@isb-sib.ch).
CC   ---------------------------------------------------------------------
DR   EMBL; AF006749; AAB81350.1; -.
DR   EMBL; AF029974; AAB86405.1; -.
DR   InterPro; IPR001944; Glyco_hydro_35.
DR   Pfam; PF01301; Glyco_hydro_35; 1.
DR   PRINTS; PR00742; GLHYDRLASE35.
DR   PROSITE; PS01182; GLYCOSYL_HYDROL_F35; 1.
KW   Hydrolase; Glycosidase; Lysosome; Signal; Glycoprotein.
FT   SIGNAL        1     24       POTENTIAL.
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FT   PROPEP       25     29       BY SIMILARITY.
FT   CHAIN        30    669       BETA-GALACTOSIDASE.
FT   ACT_SITE    189    189       PROTON DONOR (BY SIMILARITY).
FT   ACT_SITE    269    269       NUCLEOPHILE (POTENTIAL).
FT   CARBOHYD     27     27       N-LINKED (GLCNAC. . .) (POTENTIAL).
FT   CARBOHYD    248    248       N-LINKED (GLCNAC. . .) (POTENTIAL).
FT   CARBOHYD    465    465       N-LINKED (GLCNAC. . .) (POTENTIAL).
FT   CARBOHYD    499    499       N-LINKED (GLCNAC. . .) (POTENTIAL).
FT   CARBOHYD    547    547       N-LINKED (GLCNAC. . .) (POTENTIAL).
FT   CARBOHYD    557    557       N-LINKED (GLCNAC. . .) (POTENTIAL).
FT   CONFLICT    483    483       R -> P (IN REF. 2).
SQ   SEQUENCE   669 AA;  75229 MW;  35B84933BB5E2F76 CRC64;

  Query Match             2.4%;  Score 8;  DB 1;  Length 669;
  Best Local Similarity   100.0%;  Pred. No. 12;
  Matches    8;  Conservative    0;  Mismatches    0;  Indels    0;  Gaps    0;

Qy        231 LLLVPLLL 238
              ||||||||
Db         12 LLLVPLLL 19


RESULT 3
DSG2_HUMAN
ID   DSG2_HUMAN     STANDARD;      PRT;  1117 AA.
AC   Q14126;
DT   01-NOV-1997 (Rel. 35, Created)
DT   01-NOV-1997 (Rel. 35, Last sequence update)
DT   10-OCT-2003 (Rel. 42, Last annotation update)
DE   Desmoglein 2 precursor (HDGC).
GN   DSG2.
OS   Homo sapiens (Human).
OC   Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC   Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
OX   NCBI_TaxID=9606;
RN   [1]
RP   SEQUENCE FROM N.A.
RC   TISSUE=Colon carcinoma;
RX   MEDLINE=94192736; PubMed=8143788;
RA   Schaefer S., Koch P.J., Franke W.W.;
RT   "Identification of the ubiquitous human desmoglein, Dsg2, and the
RT   expression catalogue of the desmoglein subfamily of desmosomal
RT   cadherins.";
RL   Exp. Cell Res. 211:391-399(1994).
RN   [2]
RP   SEQUENCE OF 777-1117 FROM N.A.
RX   MEDLINE=92037656; PubMed=1935985;
RA   Koch P.J., Goldschmidt M.D., Walsh M.J., Zimbelmann R., Franke W.W.;
RT   "Complete amino acid sequence of the epidermal desmoglein precursor
RT   polypeptide and identification of a second type of desmoglein gene.";
RL   Eur. J. Cell Biol. 55:200-208(1991).
RN   [3]
RP   CARBOHYDRATE-LINKAGE SITE ASN-111.
RX   MEDLINE=22660472; PubMed=12754519;
RA   Zhang H., Li X.-J., Martin D.B., Aebersold R.;
RT   "Identification and quantification of N-linked glycoproteins using
RT   hydrazide chemistry, stable isotope labeling and mass spectrometry.";
RL   Nat. Biotechnol. 21:660-666(2003).
CC   -!- FUNCTION: Component of intercellular desmosome junctions. Involved
CC       in the interaction of plaque proteins and intermediate filaments
CC       mediating cell-cell adhesion.
CC   -!- SUBCELLULAR LOCATION: Type I membrane protein (By similarity).
CC   -!- TISSUE SPECIFICITY: All of the tissues tested and carcinomas.
CC   -!- DOMAIN: Calcium may be bound by the cadherin-like repeats
CC       (Potential).
CC   -!- SIMILARITY: Contains 4 cadherin domains.
CC   ---------------------------------------------------------------------
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CC   or send an email to license@isb-sib.ch).
CC   ---------------------------------------------------------------------
DR   EMBL; Z26317; CAA81226.1; -.
DR   PIR; S38673; S38673.
DR   HSSP; P15116; 1NCI.
DR   Genew; HGNC:3049; DSG2.
DR   MIM; 125671; -.
DR   GO; GO:0005911; C:intercellular junction; TAS.
DR   InterPro; IPR002126; Cadherin.
DR   Pfam; PF00028; cadherin; 4.
DR   PRINTS; PR00205; CADHERIN.
DR   SMART; SM00112; CA; 4.
DR   PROSITE; PS00232; CADHERIN_1; 3.
DR   PROSITE; PS50268; CADHERIN_2; 4.
KW   Cell adhesion; Glycoprotein; Transmembrane; Repeat; Signal;
KW   Cytoskeleton; Calcium-binding.
FT   SIGNAL        1     23       POTENTIAL.
FT   PROPEP       24     48       POTENTIAL.
FT   CHAIN        49   1117       DESMOGLEIN 2.
FT   DOMAIN       49    608       EXTRACELLULAR (POTENTIAL).
FT   TRANSMEM    609    633       POTENTIAL.
FT   DOMAIN      634   1117       CYTOPLASMIC (POTENTIAL).
FT   DOMAIN       49    159       CADHERIN 1.
FT   DOMAIN      160    272       CADHERIN 2.
FT   DOMAIN      273    387       CADHERIN 3.
FT   DOMAIN      388    502       CADHERIN 4.
FT   REPEAT      880    911       DESMOGLEIN REPEAT 1.
FT   REPEAT      912    941       DESMOGLEIN REPEAT 2.
FT   REPEAT      942    967       DESMOGLEIN REPEAT 3.
FT   REPEAT      968    991       DESMOGLEIN REPEAT 4.
FT   REPEAT      992   1020       DESMOGLEIN REPEAT 5.
FT   REPEAT     1021   1050       DESMOGLEIN REPEAT 6.
FT   CARBOHYD    111    111       N-LINKED (GLCNAC. . .).
FT   CARBOHYD    181    181       N-LINKED (GLCNAC. . .) (POTENTIAL).
FT   CARBOHYD    308    308       N-LINKED (GLCNAC. . .) (POTENTIAL).
FT   CARBOHYD    461    461       N-LINKED (GLCNAC. . .) (POTENTIAL).
FT   CARBOHYD    513    513       N-LINKED (GLCNAC. . .) (POTENTIAL).
SQ   SEQUENCE   1117 AA;  122385 MW;  223B897FED70B289 CRC64;

  Query Match             2.4%;  Score 8;  DB 1;  Length 1117;
  Best Local Similarity   100.0%;  Pred. No. 18;
  Matches    8;  Conservative    0;  Mismatches    0;  Indels    0;  Gaps    0;

Qy        231 LLLVPLLL 238
              ||||||||
Db        624 LLLVPLLL 631


RESULT 4
DSG2_MOUSE
ID   DSG2_MOUSE     STANDARD;      PRT;  1122 AA.
AC   O55111; Q8K069; Q8R517;
DT   28-FEB-2003 (Rel. 41, Created)
DT   28-FEB-2003 (Rel. 41, Last sequence update)
DT   10-OCT-2003 (Rel. 42, Last annotation update)
DE   Desmoglein 2 precursor.
GN   DSG2.
OS   Mus musculus (Mouse).
OC   Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC   Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus.
OX   NCBI_TaxID=10090;
RN   [1]
RP   SEQUENCE FROM N.A.
RC   TISSUE=Pancreas;
RA   Zhuxiang N., Garrod D.R.;
RT   "Desmosomal cadherins mediate homophilic cell adhesion.";
RL   Submitted (SEP-2001) to the EMBL/GenBank/DDBJ databases.
RN   [2]
RP   SEQUENCE OF 348-1122 FROM N.A.
RC   STRAIN=C57BL/6J; TISSUE=Mammary gland;
RX   MEDLINE=22388257; PubMed=12477932;
RA   Strausberg R.L., Feingold E.A., Grouse L.H., Derge J.G.,
RA   Klausner R.D., Collins F.S., Wagner L., Shenmen C.M., Schuler G.D.,
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RA   Altschul S.F., Zeeberg B., Buetow K.H., Schaefer C.F., Bhat N.K.,
RA   Hopkins R.F., Jordan H., Moore T., Max S.I., Wang J., Hsieh F.,
RA   Diatchenko L., Marusina K., Farmer A.A., Rubin G.M., Hong L.,
RA   Stapleton M., Soares M.B., Bonaldo M.F., Casavant T.L., Scheetz T.E.,
RA   Brownstein M.J., Usdin T.B., Toshiyuki S., Carninci P., Prange C.,
RA   Raha S.S., Loquellano N.A., Peters G.J., Abramson R.D., Mullahy S.J.,
RA   Bosak S.A., McEwan P.J., McKernan K.J., Malek J.A., Gunaratne P.H.,
RA   Richards S., Worley K.C., Hale S., Garcia A.M., Gay L.J., Hulyk S.W.,
RA   Villalon D.K., Muzny D.M., Sodergren E.J., Lu X., Gibbs R.A.,
RA   Fahey J., Helton E., Ketteman M., Madan A., Rodrigues S., Sanchez A.,
RA   Whiting M., Madan A., Young A.C., Shevchenko Y., Bouffard G.G.,
RA   Blakesley R.W., Touchman J.W., Green E.D., Dickson M.C.,
RA   Rodriguez A.C., Grimwood J., Schmutz J., Myers R.M.,
RA   Butterfield Y.S.N., Krzywinski M.I., Skalska U., Smailus D.E.,
RA   Schnerch A., Schein J.E., Jones S.J.M., Marra M.A.;
RT   "Generation and initial analysis of more than 15,000 full-length
RT   human and mouse cDNA sequences.";
RL   Proc. Natl. Acad. Sci. U.S.A. 99:16899-16903(2002).
RN   [3]
RP   SEQUENCE OF 1042-1122 FROM N.A., AND TISSUE SPECIFICITY.
RX   MEDLINE=98067789; PubMed=9404003;
RA   King I.A., Angst B.D., Hunt D.M., Kruger M., Arnemann J., Buxton R.S.;
RT   "Hierarchical expression of desmosomal cadherins during stratified
RT   epithelial morphogenesis in the mouse.";
RL   Differentiation 62:83-96(1997).
CC   -!- FUNCTION: Component of intercellular desmosome junctions. Involved
CC       in the interaction of plaque proteins and intermediate filaments
CC       mediating cell-cell adhesion.
CC   -!- SUBCELLULAR LOCATION: Type I membrane protein (By similarity).
CC   -!- TISSUE SPECIFICITY: Expressed uniformly in all E12.5 epithelia,
CC       gradually becoming confined to the basal cell layers during
CC       epithelial stratification.
CC   -!- DOMAIN: Calcium may be bound by the cadherin-like repeats
CC       (Potential).
CC   -!- SIMILARITY: Contains 4 cadherin domains.
CC   ---------------------------------------------------------------------
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CC   ---------------------------------------------------------------------
DR   EMBL; AB072269; BAB86843.1; -.
DR   EMBL; BC034056; AAH34056.1; -.
DR   EMBL; AJ000328; CAA03995.1; -.
DR   MGD; MGI:1196466; Dsg2.
DR   GO; GO:0030057; C:desmosome; IDA.
DR   InterPro; IPR002126; Cadherin.
DR   Pfam; PF00028; cadherin; 4.
DR   PRINTS; PR00205; CADHERIN.
DR   SMART; SM00112; CA; 4.
DR   PROSITE; PS00232; CADHERIN_1; 3.
DR   PROSITE; PS50268; CADHERIN_2; 4.
KW   Cell adhesion; Glycoprotein; Transmembrane; Repeat; Signal;
KW   Cytoskeleton; Calcium-binding.
FT   SIGNAL        1     28       POTENTIAL.
FT   PROPEP       29     54       POTENTIAL.
FT   CHAIN        55   1122       DESMOGLEIN 2.
FT   DOMAIN       29    618       EXTRACELLULAR (POTENTIAL).
FT   TRANSMEM    619    639       POTENTIAL.
FT   DOMAIN      640   1122       CYTOPLASMIC (POTENTIAL).
FT   DOMAIN       54    164       CADHERIN 1.
FT   DOMAIN      165    277       CADHERIN 2.
FT   DOMAIN      278    398       CADHERIN 3.
FT   DOMAIN      397    504       CADHERIN 4.
FT   REPEAT      885    916       DESMOGLEIN REPEAT 1.
FT   REPEAT      917    945       DESMOGLEIN REPEAT 2.
FT   REPEAT      946    971       DESMOGLEIN REPEAT 3.
FT   REPEAT      972    995       DESMOGLEIN REPEAT 4.
FT   REPEAT      996   1024       DESMOGLEIN REPEAT 5.
FT   REPEAT     1025   1055       DESMOGLEIN REPEAT 6.
FT   CARBOHYD    117    117       N-LINKED (GLCNAC. . .) (POTENTIAL).
FT   CARBOHYD    314    314       N-LINKED (GLCNAC. . .) (POTENTIAL).
FT   CARBOHYD    467    467       N-LINKED (GLCNAC. . .) (POTENTIAL).
FT   CARBOHYD    519    519       N-LINKED (GLCNAC. . .) (POTENTIAL).
FT   CONFLICT    358    358       I -> L (IN REF. 2).
FT   CONFLICT    480    480       E -> D (IN REF. 2).
FT   CONFLICT    491    491       V -> I (IN REF. 2).
FT   CONFLICT    863    863       T -> R (IN REF. 2).
FT   CONFLICT    899    899       R -> H (IN REF. 2).
SQ   SEQUENCE   1122 AA;  122397 MW;  CEC0C489F858ED57 CRC64;

  Query Match           2.4%;  Score 8;  DB 1;  Length 1122;
  Best Local Similarity  100.0%;  Pred. No. 18;
  Matches    8;  Conservative    0;  Mismatches    0;  Indels    0;  Gaps    0;

Qy        231 LLLVPLLL 238
              ||||||||
Db        630 LLLVPLLL 637


RESULT 5
MTRF_METKA
ID   MTRF_METKA     STANDARD;      PRT;    75 AA.
AC   Q8TVA7;
DT   15-MAR-2004 (Rel. 43, Created)
DT   15-MAR-2004 (Rel. 43, Last sequence update)
DT   15-MAR-2004 (Rel. 43, Last annotation update)
DE   Tetrahydromethanopterin S-methyltransferase subunit F (EC 2.1.1.86)
DE   (N5-methyltetrahydromethanopterin--coenzyme M methyltransferase
DE   subunit F).
GN   MTRF OR MK1485.
OS   Methanopyrus kandleri.
OC   Archaea; Euryarchaeota; Methanopyri; Methanopyrales; Methanopyraceae;
OC   Methanopyrus.
OX   NCBI_TaxID=2320;
RN   [1]
RP   SEQUENCE FROM N.A.
RC   STRAIN=AV19 / DSM 6324 / JCM 9639;
RX   MEDLINE=21927647; PubMed=11930014;
RA   Slesarev A.I., Mezhevaya K.V., Makarova K.S., Polushin N.N.,
RA   Shcherbinina O.V., Shakhova V.V., Belova G.I., Aravind L.,
RA   Natale D.A., Rogozin I.B., Tatusov R.L., Wolf Y.I., Stetter K.O.,
RA   Malykh A.G., Koonin E.V., Kozyavkin S.A.;
RT   "The complete genome of hyperthermophile Methanopyrus kandleri AV19
RT   and monophyly of archaeal methanogens.";
RL   Proc. Natl. Acad. Sci. U.S.A. 99:4644-4649(2002).
CC   -!- FUNCTION: Part of a complex that catalyzes the formation of
CC       methyl-coenzyme M and tetrahydromethanopterin from coenzyme M and
CC       methyl-tetrahydromethanopterin. This is an energy-conserving,
CC       sodium-ion translocating step (By similarity).
CC   -!- CATALYTIC ACTIVITY: 5-methyl-5,6,7,8-tetrahydromethanopterin + 2-
CC       mercaptoethanesulfonate = 5,6,7,8-tetrahydromethanopterin + 2-
CC       (methylthio)ethanesulfonate.
CC   -!- PATHWAY: Methanogenesis from carbon dioxide; sixth step.
CC   -!- SUBUNIT: The complex is composed of 8 subunits; mtrA, mtrB, mtrC,
CC       mtrD, mtrE, mtrF, mtrG and mtrH (By similarity).
CC   -!- SUBCELLULAR LOCATION: Membrane-anchored (Potential).
CC   -!- MISCELLANEOUS: Unlike other orthologs, mtrF from M.kandleri is not
CC       located in the mtr operon.
CC   -!- SIMILARITY: Belongs to the mtrF family.
CC   ---------------------------------------------------------------------
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CC   ---------------------------------------------------------------------
DR   EMBL; AE010439; AAM02698.1; -.
DR   HAMAP; MF_01099; -; 1.
KW   Methanogenesis; One-carbon metabolism; Transferase; Methyltransferase;
KW   Transmembrane; Complete proteome.
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FT   TRANSMEM     53      73       POTENTIAL.
SQ   SEQUENCE   75 AA;  8130 MW;  0186C402CCFCEF28 CRC64;

  Query Match             2.1%;  Score 7;  DB 1;  Length 75;
  Best Local Similarity   100.0%;  Pred. No. 19;
  Matches    7;  Conservative    0;  Mismatches    0;  Indels    0;  Gaps    0;

Qy        232 LLVPLLL 238
              |||||||
Db         66 LLVPLLL 72


RESULT 6
SY08_MOUSE
ID   SY08_MOUSE     STANDARD;      PRT;    97 AA.
AC   Q9Z121;
DT   16-OCT-2001 (Rel. 40, Created)
DT   16-OCT-2001 (Rel. 40, Last sequence update)
DT   10-OCT-2003 (Rel. 42, Last annotation update)
DE   Small inducible cytokine A8 precursor (CCL8) (Monocyte chemotactic
DE   protein 2) (MCP-2) (Monocyte chemoattractant protein 2).
GN   CCL8 OR SCYA8 OR MCP2.
OS   Mus musculus (Mouse).
OC   Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC   Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus.
OX   NCBI_TaxID=10090;
RN   [1]
RP   SEQUENCE FROM N.A.
RC   STRAIN=C57BL/6J; TISSUE=Mammary gland;
RA   Nomiyama H.;
RL   Submitted (FEB-1999) to the EMBL/GenBank/DDBJ databases.
RN   [2]
RP   SEQUENCE FROM N.A.
RC   STRAIN=C57BL/6J; TISSUE=Pancreas;
RX   MEDLINE=21085660; PubMed=11217851;
RA   Kawai J., Shinagawa A., Shibata K., Yoshino M., Itoh M., Ishii Y.,
RA   Arakawa T., Hara A., Fukunishi Y., Konno H., Adachi J., Fukuda S.,
RA   Aizawa K., Izawa M., Nishi K., Kiyosawa H., Kondo S., Yamanaka I.,
RA   Saito T., Okazaki Y., Gojobori T., Bono H., Kasukawa T., Saito R.,
RA   Kadota K., Matsuda H.A., Ashburner M., Batalov S., Casavant T.,
RA   Fleischmann W., Gaasterland T., Gissi C., King B., Kochiwa H.,
RA   Kuehl P., Lewis S., Matsuo Y., Nikaido I., Pesole G., Quackenbush J.,
RA   Schriml L.M., Staubli F., Suzuki R., Tomita M., Wagner L., Washio T.,
RA   Sakai K., Okido T., Furuno M., Aono H., Baldarelli R., Barsh G.,
RA   Blake J., Boffelli D., Bojunga N., Carninci P., de Bonaldo M.F.,
RA   Brownstein M.J., Bult C., Fletcher C., Fujita M., Gariboldi M.,
RA   Gustincich S., Hill D., Hofmann M., Hume D.A., Kamiya M., Lee N.H.,
RA   Lyons P., Marchionni L., Mashima J., Mazzarelli J., Mombaerts P.,
RA   Nordone P., Ring B., Ringwald M., Rodriguez I., Sakamoto N.,
RA   Sasaki H., Sato K., Schoenbach C., Seya T., Shibata Y., Storch K.-F.,
RA   Suzuki H., Toyo-oka K., Wang K.H., Weitz C., Whittaker C., Wilming L.,
RA   Wynshaw-Boris A., Yoshida K., Hasegawa Y., Kawaji H., Kohtsuki S.,
RA   Hayashizaki Y.;
RT   "Functional annotation of a full-length mouse cDNA collection.";
RL   Nature 409:685-690(2001).
CC   -!- FUNCTION: Chemotactic factor that attracts monocytes. This protein
CC       can bind heparin (By similarity).
CC   -!- SIMILARITY: Belongs to the intercrine beta (chemokine CC) family.
CC   ---------------------------------------------------------------------
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CC   ---------------------------------------------------------------------
DR   EMBL; AB023418; BAA75014.1; -.
DR   EMBL; AK007942; BAB25365.1; -.
DR   HSSP; P51671; 1EOT.
DR   MGD; MGI:101878; Ccl8.
DR   InterPro; IPR000827; CC_chemkine_sml.
DR   InterPro; IPR001811; Chemokine_IL8.
DR   Pfam; PF00048; IL8; 1.
DR   SMART; SM00199; SCY; 1.
DR   PROSITE; PS00472; SMALL_CYTOKINES_CC; FALSE_NEG.
KW   Cytokine; Chemotaxis; Signal; Heparin-binding; Inflammatory response.
FT   SIGNAL        1     19       POTENTIAL.
FT   CHAIN        20     97       SMALL INDUCIBLE CYTOKINE A8.
FT   DISULFID     32     57       BY SIMILARITY.
FT   DISULFID     33     73       BY SIMILARITY.
SQ   SEQUENCE   97 AA;  11017 MW;  65BB3722F2F98D54 CRC64;

  Query Match             2.1%;  Score 7;  DB 1;  Length 97;
  Best Local Similarity   100.0%;  Pred. No. 23;
  Matches    7;  Conservative    0;  Mismatches    0;  Indels    0;  Gaps    0;

Qy        227 VLLCLLL 233
              |||||||
Db          6 VLLCLLL 12


RESULT 7
SY13_HUMAN
ID   SY13_HUMAN     STANDARD;      PRT;    98 AA.
AC   Q99616; O95689;
DT   15-JUL-1998 (Rel. 36, Created)
DT   15-JUL-1998 (Rel. 36, Last sequence update)
DT   15-MAR-2004 (Rel. 43, Last annotation update)
DE   Small inducible cytokine A13 precursor (CCL13) (Monocyte chemotactic
DE   protein 4) (MCP-4) (Monocyte chemoattractant protein 4) (CK-beta-10)
DE   (NCC-1).
GN   CCL13 OR SCYA13 OR MCP4 OR NCC1.
OS   Homo sapiens (Human).
OC   Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC   Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
OX   NCBI_TaxID=9606;
RN   [1]
RP   SEQUENCE FROM N.A.
RC   TISSUE=Heart;
RX   MEDLINE=97113354; PubMed=8955214;
RA   Garcia-Zepeda E.A., Combadiere C., Rothenberg M.E., Sarafi M.N.,
RA   Lavigne F., Hamid Q., Murphy P.M., Luster A.D.;
RT   "Human monocyte chemoattractant protein (MCP)-4 is a novel CC
RT   chemokine with activities on monocytes, eosinophils, and basophils
RT   induced in allergic and nonallergic inflammation that signals through
RT   the CC chemokine receptors (CCR)-2 and -3.";
RL   J. Immunol. 157:5613-5626(1996).
RN   [2]
RP   SEQUENCE FROM N.A., AND SEQUENCE OF 17-98.
RC   TISSUE=Fetal;
RX   MEDLINE=96235049; PubMed=8642349;
RA   Uguccioni M., Loetscher P., Forssmann U., Dewald B., Li H., Lima S.H.,
RA   Li Y., Kreider B., Garotta G., Thelen M., Baggiolini M.;
RT   "Monocyte chemotactic protein 4 (MCP-4), a novel structural and
RT   functional analogue of MCP-3 and eotaxin.";
RL   J. Exp. Med. 183:2379-2384(1996).
RN   [3]
RP   SEQUENCE FROM N.A., AND SEQUENCE OF 22-33.
RC   TISSUE=Fetal;
RX   MEDLINE=97341179; PubMed=9195948;
RA   Berkhout T.A., Sarau H.M., Moores K., White J.R., Elshourbagy N.,
RA   Appelbaum E., Reape T.J., Brawner M., Makwana J., Foley J.J.,
RA   Schmidt D.B., Imburgia C., Macnulty D., Matthews J., O'Donnell K.,
RA   O'Shannessy D., Scott M., Groot P.H.E., Macphee C.;
RT   "Cloning, in vitro expression, and functional characterization of a
RT   novel human CC chemokine of the monocyte chemotactic protein (MCP)
RT   family (MCP-4) that binds and signals through the CC chemokine
RT   receptor 2B.";
RL   J. Biol. Chem. 272:16404-16413(1997).
RN   [4]
RP   SEQUENCE FROM N.A.
RA   Dante M., Gibson A.;
RL   Submitted (AUG-1997) to the EMBL/GenBank/DDBJ databases.
RN   [5]
RP   SEQUENCE FROM N.A.
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RC   TISSUE=Lung;
RA   Power C.A., Meyer A., Rison S.C.G., Guye-Coulin F., Wells T.N.C.;
RL   Submitted (DEC-1997) to the EMBL/GenBank/DDBJ databases.
RN   [6]
RP   SEQUENCE FROM N.A.
RX   MEDLINE=97213770; PubMed=9060459;
RA   Godiska R., Chantry D., Raport C.J., Schweickart V.L., Trong H.L.,
RA   Gray P.W.;
RT   "Monocyte chemotactic protein-4: tissue-specific expression and
RT   signaling through CC chemokine receptor-2.";
RL   J. Leukoc. Biol. 61:353-360(1997).
RN   [7]
RP   SEQUENCE FROM N.A.
RC   TISSUE=Skin fibroblast;
RX   MEDLINE=99160888; PubMed=10049733;
RA   Hein H., Schluter C., Kulke R., Christophers E., Schroeder J.-M.,
RA   Bartels J.;
RT   "Genomic organization, sequence analysis and transcriptional
RT   regulation of the human MCP-4 chemokine gene (SCYA13) in dermal
RT   fibroblasts: a comparison to other eosinophilic beta-chemokines.";
RL   Biochem. Biophys. Res. Commun. 255:470-476(1999).
RN   [8]
RP   SEQUENCE FROM N.A.
RC   TISSUE=Brain;
RX   MEDLINE=22388257; PubMed=12477932;
RA   Strausberg R.L., Feingold E.A., Grouse L.H., Derge J.G.,
RA   Klausner R.D., Collins F.S., Wagner L., Shenmen C.M., Schuler G.D.,
RA   Altschul S.F., Zeeberg B., Buetow K.H., Schaefer C.F., Bhat N.K.,
RA   Hopkins R.F., Jordan H., Moore T., Max S.I., Wang J., Hsieh F.,
RA   Diatchenko L., Marusina K., Farmer A.A., Rubin G.M., Hong L.,
RA   Stapleton M., Soares M.B., Bonaldo M.F., Casavant T.L., Scheetz T.E.,
RA   Brownstein M.J., Usdin T.B., Toshiyuki S., Carninci P., Prange C.,
RA   Raha S.S., Loquellano N.A., Peters G.J., Abramson R.D., Mullahy S.J.,
RA   Bosak S.A., McEwan P.J., McKernan K.J., Malek J.A., Gunaratne P.H.,
RA   Richards S., Worley K.C., Hale S., Garcia A.M., Gay L.J., Hulyk S.W.,
RA   Villalon D.K., Muzny D.M., Sodergren E.J., Lu X., Gibbs R.A.,
RA   Fahey J., Helton E., Ketteman M., Madan A., Rodrigues S., Sanchez A.,
RA   Whiting M., Madan A., Young A.C., Shevchenko Y., Bouffard G.G.,
RA   Blakesley R.W., Touchman J.W., Green E.D., Dickson M.C.,
RA   Rodriguez A.C., Grimwood J., Schmutz J., Myers R.M.,
RA   Butterfield Y.S.N., Krzywinski M.I., Skalska U., Smailus D.E.,
RA   Schnerch A., Schein J.E., Jones S.J.M., Marra M.A.;
RT   "Generation and initial analysis of more than 15,000 full-length
RT   human and mouse cDNA sequences.";
RL   Proc. Natl. Acad. Sci. U.S.A. 99:16899-16903(2002).
RN   [9]
RP   SEQUENCE OF 17-95 FROM N.A.
RC   TISSUE=Foreskin;
RA   Bartels J.H., Schlueter C., Richter E., Noso N., Christophers E.,
RA   Schroeder J.-M.;
RT   "Expression of a MCP-4 like novel CC-chemokine in human dermal
RT   fibroblasts: molecular cloning and RT-PCR analysis.";
RL   Submitted (JUL-1996) to the EMBL/GenBank/DDBJ databases.
CC   -!- FUNCTION: Chemotactic factor that attracts monocytes, lymphocytes,
CC       basophils and eosinophils, but not neutrophils. Signals through
CC       CCR2B and CCR3 receptors. Plays a role in the accumulation of
CC       Leukocytes at both sides of allergic and nonallergic inflammation.
CC       May be involved in the recruitment of monocytes into the arterial
CC       wall during the disease process of artherosclerosis. May play a
CC       role in the monocyte attraction in tissues chronically exposed to
CC       exogenous pathogens.
CC   -!- SUBCELLULAR LOCATION: Secreted.
CC   -!- TISSUE SPECIFICITY: Widely expressed. Found in small intestine,
CC       thymus, colon, lung, trachea, stomach and lymph node. Low levels
CC       seen in the pulmonary artery smooth muscle cells.
CC   -!- INDUCTION: By interleukin-1 and TNF-alpha.
CC   -!- PTM: ONE MAJOR ISOFORM MCP-4, AND TWO MINOR ISOFORMS (LA)MCP-4 AND
CC       (FNPQGLA)MCP-4 ARE PRODUCED BY DIFFERENTIAL SIGNAL CLEAVAGE.
CC       (LA)MCP-4 IS ABOUT 30 FOLD LESS ACTIVE THAN MCP-4.
CC   -!- MASS SPECTROMETRY: MW=9314; MW_ERR=30; METHOD=MALDI; RANGE=17-98.
CC   -!- MASS SPECTROMETRY: MW=8760; MW_ERR=30; METHOD=MALDI; RANGE=22-98.
CC   -!- MASS SPECTROMETRY: MW=8575; MW_ERR=30; METHOD=MALDI; RANGE=24-98.
CC   -!- MISCELLANEOUS: This protein can bind heparin.
CC   -!- SIMILARITY: Belongs to the intercrine beta (chemokine CC) family.
CC   ---------------------------------------------------------------------
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CC   or send an email to license@isb-sib.ch).
CC   ---------------------------------------------------------------------
DR   EMBL; U46767; AAB38703.1; -.
DR   EMBL; AC002482; AAB67307.1; -.
DR   EMBL; X98306; CAA66950.1; -.
DR   EMBL; U59808; AAD09362.1; -.
DR   EMBL; AJ001634; CAA04888.1; -.
DR   EMBL; BC008621; AAH08621.1; -.
DR   EMBL; Z77650; CAB01111.1; -.
DR   HSSP; P51671; 1EOT.
DR   Genew; HGNC:10611; CCL13.
DR   MIM; 601391; -.
DR   GO; GO:0005615; C:extracellular space; TAS.
DR   GO; GO:0008009; F:chemokine activity; TAS.
DR   GO; GO:0005102; F:receptor binding; TAS.
DR   GO; GO:0006874; P:calcium ion homeostasis; TAS.
DR   GO; GO:0007267; P:cell-cell signaling; TAS.
DR   GO; GO:0006935; P:chemotaxis; TAS.
DR   GO; GO:0006954; P:inflammatory response; TAS.
DR   GO; GO:0007165; P:signal transduction; TAS.
DR   InterPro; IPR000827; CC_chemkine_sml.
DR   InterPro; IPR001811; Chemokine_IL8.
DR   InterPro; IPR008097; Fractalkine.
DR   Pfam; PF00048; IL8; 1.
DR   PRINTS; PR01721; FRACTALKINE.
DR   SMART; SM00199; SCY; 1.
DR   PROSITE; PS00472; SMALL_CYTOKINES_CC; 1.
KW   Cytokine; Chemotaxis; Signal; Glycoprotein; Inflammatory response;
KW   Pyrrolidone carboxylic acid.
FT   SIGNAL       1     16
FT   CHAIN       17     98       SMALL INDUCIBLE CYTOKINE A13, LONG FORM.
FT   CHAIN       24     98       SMALL INDUCIBLE CYTOKINE A13, SHORT FORM.
FT   MOD_RES     24     24       PYRROLIDONE CARBOXYLIC ACID.
FT   DISULFID    34     58       BY SIMILARITY.
FT   DISULFID    35     74       BY SIMILARITY.
FT   CARBOHYD    29     29       N-LINKED (GLCNAC. . .) (POTENTIAL).
FT   CONFLICT    93     98       AHTLKT -> LTP (IN REF. 9).
SQ   SEQUENCE   98 AA;  10986 MW;  612688DFCD308873 CRC64;

  Query Match             2.1%;  Score 7;  DB 1;  Length 98;
  Best Local Similarity   100.0%;  Pred. No. 24;
  Matches    7;  Conservative    0;  Mismatches    0;  Indels    0;  Gaps    0;

Qy        227 VLLCLLL 233
              |||||||
Db          6 VLLCLLL 12


RESULT 8
RL1X_SPOFR
ID   RL1X_SPOFR     STANDARD;      PRT;   177 AA.
AC   Q8WQI7;
DT   28-FEB-2003 (Rel. 41, Created)
DT   28-FEB-2003 (Rel. 41, Last sequence update)
DT   10-OCT-2003 (Rel. 42, Last annotation update)
DE   60S ribosomal protein L18a.
GN   RPL18A.
OS   Spodoptera frugiperda (Fall armyworm).
OC   Eukaryota; Metazoa; Arthropoda; Hexapoda; Insecta; Pterygota;
OC   Neoptera; Endopterygota; Lepidoptera; Glossata; Ditrysia; Noctuoidea;
OC   Noctuidae; Amphipyrinae; Spodoptera.
OX   NCBI_TaxID=7108;
RN   [1]
RP   SEQUENCE FROM N.A.
RA   Landais I., Ogliastro M., Mita K., Nohata J., Lopez-Ferber M.,
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RA   Duonor-Cerutti M., Fournier P., Devauchelle G.;
RT   "Full-length ribosomal protein sequence from an EST library of
RT   Spodoptera frugiperda cells (Sf9).";
RL   Submitted (JAN-2002) to the EMBL/GenBank/DDBJ databases.
CC   ---------------------------------------------------------------------
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CC   or send an email to license@isb-sib.ch).
CC   ---------------------------------------------------------------------
DR   EMBL; AY072289; AAL62470.1; -.
DR   InterPro; IPR002670; Ribosomal_L18ae.
DR   Pfam; PF01775; Ribosomal_L18ae; 1.
KW   Ribosomal protein.
SQ   SEQUENCE   177 AA;  20992 MW;  93D2F8517A5D0D14 CRC64;

  Query Match             2.1%;  Score 7;  DB 1;  Length 177;
  Best Local Similarity   100.0%;  Pred. No. 38;
  Matches    7;  Conservative    0;  Mismatches    0;  Indels    0;  Gaps    0;

Qy         32 SVGGAVT 38
              |||||||
Db        101 SVGGAVT 107


RESULT 9
MURB_BACLI
ID   MURB_BACLI     STANDARD;      PRT;   184 AA.
AC   Q45305;
DT   30-MAY-2000 (Rel. 39, Created)
DT   30-MAY-2000 (Rel. 39, Last sequence update)
DT   28-FEB-2003 (Rel. 41, Last annotation update)
DE   UDP-N-acetylenolpyruvoylglucosamine reductase (EC 1.1.1.158) (UDP-N-
DE   acetylmuramate dehydrogenase) (Fragment).
GN   MURB.
OS   Bacillus licheniformis.
OC   Bacteria; Firmicutes; Bacillales; Bacillaceae; Bacillus.
OX   NCBI_TaxID=1402;
RN   [1]
RP   SEQUENCE FROM N.A.
RC   STRAIN=5A2;
RX   MEDLINE=94374713; PubMed=8088553;
RA   Harry E.J., Partridge S.R., Weiss A.S., Wake R.G.;
RT   "Conservation of the 168 divIB gene in Bacillus subtilis W23 and B.
RT   licheniformis, and evidence for homology to ftsQ of Escherichia
RT   coli.";
RL   Gene 147:85-89(1994).
CC   -!- FUNCTION: Cell wall formation (By similarity).
CC   -!- CATALYTIC ACTIVITY: UDP-N-acetylmuramate + NADP(+) = UDP-N-
CC       acetyl-3-O-(1-carboxyvinyl)-D-glucosamine + NADPH.
CC   -!- COFACTOR: FAD.
CC   -!- PATHWAY: Peptidoglycan biosynthesis.
CC   -!- SUBCELLULAR LOCATION: Cytoplasmic (Probable).
CC   -!- SIMILARITY: Belongs to the murB family.
CC   ---------------------------------------------------------------------
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CC   ---------------------------------------------------------------------
DR   EMBL; U01958; AAA57244.1; -.
DR   PIR; I40220; I40220.
DR   HSSP; P08373; 2MBR.
DR   HAMAP; MF_00037; -; 1.
DR   InterPro; IPR003170; MurB.
DR   InterPro; IPR006094; Oxid_FAD_bind.
DR   Pfam; PF01565; FAD_binding_4; 1.
DR   Pfam; PF02873; MurB_C; 1.
KW   Peptidoglycan synthesis; Cell wall; Cell division; Oxidoreductase;
KW   NADP; Flavoprotein; FAD.
FT   NON_TER       1       1
SQ   SEQUENCE   184 AA;  20166 MW;  4114D8B29AE21EFD CRC64;

  Query Match             2.1%;  Score 7;  DB 1;  Length 184;
  Best Local Similarity   100.0%;  Pred. No. 39;
  Matches    7;  Conservative    0;  Mismatches    0;  Indels    0;  Gaps    0;

Qy         31 GSVGGAV 37
              |||||||
Db          9 GSVGGAV 15


RESULT 10
YD48_AQUAE
ID   YD48_AQUAE     STANDARD;      PRT;   189 AA.
AC   O67363;
DT   16-OCT-2001 (Rel. 40, Created)
DT   16-OCT-2001 (Rel. 40, Last sequence update)
DT   16-OCT-2001 (Rel. 40, Last annotation update)
DE   Hypothetical protein AQ_1348.
GN   AQ_1348.
OS   Aquifex aeolicus.
OC   Bacteria; Aquificae; Aquificales; Aquificaceae; Aquifex.
OX   NCBI_TaxID=63363;
RN   [1]
RP   SEQUENCE FROM N.A.
RC   STRAIN=VF5;
RX   MEDLINE=98196666; PubMed=9537320;
RA   Deckert G., Warren P.V., Gaasterland T., Young W.G., Lenox A.L.,
RA   Graham D.E., Overbeek R., Snead M.A., Keller M., Aujay M., Huber R.,
RA   Feldman R.A., Short J.M., Olson G.J., Swanson R.V.;
RT   "The complete genome of the hyperthermophilic bacterium Aquifex
RT   aeolicus.";
RL   Nature 392:353-358(1998).
CC   ---------------------------------------------------------------------
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CC   or send an email to license@isb-sib.ch).
CC   ---------------------------------------------------------------------
DR   EMBL; AE000736; AAC07334.1; -.
DR   PIR; H70416; H70416.
KW   Hypothetical protein; Complete proteome.
SQ   SEQUENCE   189 AA;  21788 MW;  A70F714263221FFE CRC64;

  Query Match             2.1%;  Score 7;  DB 1;  Length 189;
  Best Local Similarity   100.0%;  Pred. No. 40;
  Matches    7;  Conservative    0;  Mismatches    0;  Indels    0;  Gaps    0;

Qy        244 GLFLWFL 250
              |||||||
Db        142 GLFLWFL 148


RESULT 11
UT11_ARATH
ID   UT11_ARATH     STANDARD;      PRT;   228 AA.
AC   Q9M223;
DT   10-OCT-2003 (Rel. 42, Created)
DT   10-OCT-2003 (Rel. 42, Last sequence update)
DT   15-MAR-2004 (Rel. 43, Last annotation update)
DE   Probable U3 small nucleolar RNA-associated protein 11 (U3 snoRNA-
DE   associated protein 11).
GN   AT3G60360 OR T8B10_20.
OS   Arabidopsis thaliana (Mouse-ear cress).
OC   Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta;
OC   Spermatophyta; Magnoliophyta; eudicotyledons; core eudicots; rosids;
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OC   eurosids II; Brassicales; Brassicaceae; Arabidopsis.
OX   NCBI_TaxID=3702;
RN   [1]
RP   SEQUENCE FROM N.A.
RC   STRAIN=cv. Columbia;
RX   MEDLINE=21016720; PubMed=11130713;
RA   Salanoubat M., Lemcke K., Rieger M., Ansorge W., Unseld M.,
RA   Fartmann B., Valle G., Bloecker H., Perez-Alonso M., Obermaier B.,
RA   Delseny M., Boutry M., Grivell L.A., Mache R., Puigdomenech P.,
RA   De Simone V., Choisne N., Artiguenave F., Robert C., Brottier P.,
RA   Wincker P., Cattolico L., Weissenbach J., Saurin W., Quetier F.,
RA   Schaefer M., Mueller-Auer S., Gabel C., Fuchs M., Benes V.,
RA   Wurmbach E., Drzonek H., Erfle H., Jordan N., Bangert S.,
RA   Wiedelmann R., Kranz H., Voss H., Holland R., Brandt P., Nyakatura G.,
RA   Vezzi A., D'Angelo M., Pallavicini A., Toppo S., Simionati B.,
RA   Conrad A., Hornischer K., Kauer G., Loehnert T.-H., Nordsiek G.,
RA   Reichelt J., Scharfe M., Schoen O., Bargues M., Terol J., Climent J.,
RA   Navarro P., Collado C., Perez-Perez A., Ottenwaelder B., Duchemin D.,
RA   Cooke R., Laudie M., Berger-Llauro C., Purnelle B., Masuy D.,
RA   de Haan M., Maarse A.C., Alcaraz J.-P., Cottet A., Casacuberta E.,
RA   Monfort A., Argiriou A., Flores M., Liguori R., Vitale D.,
RA   Mannhaupt G., Haase D., Schoof H., Rudd S., Zaccaria P., Mewes H.-W.,
RA   Mayer K.F.X., Kaul S., Town C.D., Koo H.L., Tallon L.J., Jenkins J.,
RA   Rooney T., Rizzo M., Walts A., Utterback T., Fujii C.Y., Shea T.P.,
RA   Creasy T.H., Haas B., Maiti R., Wu D., Peterson J., Van Aken S.,
RA   Pai G., Militscher J., Sellers P., Gill J.E., Feldblyum T.V.,
RA   Preuss D., Lin X., Nierman W.C., Salzberg S.L., White O., Venter J.C.,
RA   Fraser C.M., Kaneko T., Nakamura Y., Sato S., Kato T., Asamizu E.,
RA   Sasamoto S., Kimura T., Idesawa K., Kawashima K., Kishida Y.,
RA   Kiyokawa C., Kohara M., Matsumoto M., Matsuno A., Muraki A.,
RA   Nakayama S., Nakazaki N., Shinpo S., Takeuchi C., Wada T.,
RA   Watanabe A., Yamada M., Yasuda M., Tabata S.;
RT   "Sequence and analysis of chromosome 3 of the plant Arabidopsis
RT   thaliana.";
RL   Nature 408:820-822(2000).
RN   [2]
RP   SEQUENCE FROM N.A.
RC   STRAIN=cv. Columbia;
RX   MEDLINE=22954850; PubMed=14593172;
RA   Yamada K., Lim J., Dale J.M., Chen H., Shinn P., Palm C.J.,
RA   Southwick A.M., Wu H.C., Kim C.J., Nguyen M., Pham P.K., Cheuk R.F.,
RA   Karlin-Newmann G., Liu S.X., Lam B., Sakano H., Wu T., Yu G.,
RA   Miranda M., Quach H.L., Tripp M., Chang C.H., Lee J.M., Toriumi M.J.,
RA   Chan M.M., Tang C.C., Onodera C.S., Deng J.M., Akiyama K., Ansari Y.,
RA   Arakawa T., Banh J., Banno F., Bowser L., Brooks S.Y., Carninci P.,
RA   Chao Q., Choy N., Enju A., Goldsmith A.D., Gurjal M., Hansen N.F.,
RA   Hayashizaki Y., Johnson-Hopson C., Hsuan V.W., Iida K., Karnes M.,
RA   Khan S., Koesema E., Ishida J., Jiang P.X., Jones T., Kawai J.,
RA   Kamiya A., Meyers C., Nakajima M., Narusaka M., Seki M., Sakurai T.,
RA   Satou M., Tamse R., Vaysberg M., Wallender E.K., Wong C., Yamamura Y.,
RA   Yuan S., Shinozaki K., Davis R.W., Theologis A., Ecker J.R.;
RT   "Empirical analysis of transcriptional activity in the Arabidopsis
RT   genome.";
RL   Science 302:842-846(2003).
RN   [3]
RP   SEQUENCE FROM N.A.
RA   Brover V., Troukhan M., Alexandrov N., Lu Y.-P., Flavell R.,
RA   Feldmann K.A.;
RT   "Full-length cDNA from Arabidopsis thaliana.";
RL   Submitted (MAR-2002) to the EMBL/GenBank/DDBJ databases.
CC   -!- FUNCTION: Involved in nucleolar processing of pre-18S ribosomal
CC       RNA (By similarity).
CC   -!- SUBUNIT: Component of the ribosomal small subunit (SSU)
CC       processome (By similarity).
CC   -!- SUBCELLULAR LOCATION: Nuclear; nucleolar (By similarity).
CC   -!- SIMILARITY: Belongs to the UTP11 family.
CC   ---------------------------------------------------------------------------
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CC   or send an email to license@isb-sib.ch).
CC   ---------------------------------------------------------------------------
DR   EMBL; AL138646; CAB81822.1; -.
DR   EMBL; AY039876; AAK63980.1; -.
DR   EMBL; AY101514; AAM26635.1; -.
DR   EMBL; BT000725; AAN31867.1; -.
DR   EMBL; AY085156; AAM61709.1; -.
DR   PIR; T47847; T47847.
DR   InterPro; IPR007144; Utp11.
DR   Pfam; PF03998; Utp11; 1.
KW   rRNA processing; Nuclear protein.
SQ   SEQUENCE   228 AA;  27149 MW;  DF6DB3112383CB5A CRC64;

  Query Match             2.1%;  Score 7;  DB 1;  Length 228;
  Best Local Similarity   100.0%;  Pred. No. 46;
  Matches    7;  Conservative    0;  Mismatches    0;  Indels    0;  Gaps    0;

Qy        305 STVEIPK 311
              |||||||
Db        155 STVEIPK 161


RESULT 12
YTML_BACSU
ID   YTML_BACSU     STANDARD;      PRT;   239 AA.
AC   O34315;
DT   30-MAY-2000 (Rel. 39, Created)
DT   30-MAY-2000 (Rel. 39, Last sequence update)
DT   10-OCT-2003 (Rel. 42, Last annotation update)
DE   Probable amino-acid ABC transporter permease protein ytmL.
GN   YTML OR BSU29360.
OS   Bacillus subtilis.
OC   Bacteria; Firmicutes; Bacillales; Bacillaceae; Bacillus.
OX   NCBI_TaxID=1423;
RN   [1]
RP   SEQUENCE FROM N.A.
RC   STRAIN=168;
RX   MEDLINE=98048467; PubMed=9387221;
RA   Lapidus A., Galleron N., Sorokin A., Ehrlich S.D.;
RT   "Sequencing and functional annotation of the Bacillus subtilis genes
RT   in the 200 kb rrnB-dnaB region.";
RL   Microbiology 143:3431-3441(1997).
RN   [2]
RP   SEQUENCE FROM N.A.
RC   STRAIN=168;
RX   MEDLINE=98044033; PubMed=9384377;
RA   Kunst F., Ogasawara N., Moszer I., Albertini A.M., Alloni G.,
RA   Azevedo V., Bertero M.G., Bessieres P., Bolotin A., Borchert S.,
RA   Borriss R., Boursier L., Brans A., Braun M., Brignell S.C., Bron S.,
RA   Brouillet S., Bruschi C.V., Caldwell B., Capuano V., Carter N.M.,
RA   Choi S.K., Codani J.J., Connerton I.F., Cummings N.J., Daniel R.A.,
RA   Denizot F., Devine K.M., Dusterhoft A., Ehrlich S.D., Emmerson P.T.,
RA   Entian K.D., Errington J., Fabret C., Ferrari E., Foulger D.,
RA   Fritz C., Fujita M., Fujita Y., Fuma S., Galizzi A., Galleron N.,
RA   Ghim S.Y., Glaser P., Goffeau A., Golightly E.J., Grandi G.,
RA   Guiseppi G., Guy B.J., Haga K., Haiech J., Harwood C.R., Henaut A.,
RA   Hilbert H., Holsappel S., Hosono S., Hullo M.F., Itaya M., Jones L.,
RA   Joris B., Karamata D., Kasahara Y., Klaerr-Blanchard M., Klein C.,
RA   Kobayashi Y., Koetter P., Koningstein G., Krogh S., Kumano M.,
RA   Kurita K., Lapidus A., Lardinois S., Lauber J., Lazarevic V.,
RA   Lee S.M., Levine A., Liu H., Masuda S., Mauel C., Medigue C.,
RA   Medina N., Mellado R.P., Mizuno M., Moestl D., Nakai S., Noback M.,
RA   Noone D., O'Reilly M., Ogawa K., Ogiwara A., Oudega B., Park S.H.,
RA   Parro V., Pohl T.M., Portetelle D., Porwollik S., Prescott A.M.,
RA   Presecan E., Pujic P., Purnelle B., Rapoport G., Rey M., Reynolds S.,
RA   Rieger M., Rivolta C., Rocha E., Roche B., Rose M., Sadaie Y.,
RA   Sato T., Scanlan E., Schleich S., Schroeter R., Scoffone F.,
RA   Sekiguchi J., Sekowska A., Seror S.J., Serror P., Shin B.S., Soldo B.,
RA   Sorokin A., Tacconi E., Takagi T., Takahashi H., Takemaru K.,
RA   Takeuchi M., Tamakoshi A., Tanaka T., Terpstra P., Tognoni A.,
RA   Tosato V., Uchiyama S., Vandenbol M., Vannier F., Vassarotti A.,
RA   Viari A., Wambutt R., Wedler E., Wedler H., Weitzenegger T.,
RA   Winters P., Wipat A., Yamamoto H., Yamane K., Yasumoto K., Yata K.,
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RA   Yoshida K., Yoshikawa H.F., Zumstein E., Yoshikawa H., Danchin A.;
RT   "The complete genome sequence of the Gram-positive bacterium Bacillus
RT   subtilis.";
RL   Nature 390:249-256(1997).
CC   -!- FUNCTION: PROBABLY PART OF A BINDING-PROTEIN-DEPENDENT TRANSPORT
CC       SYSTEM YTMKLMN FOR AN AMINO ACID. PROBABLY RESPONSIBLE FOR THE
CC       TRANSLOCATION OF THE SUBSTRATE ACROSS THE MEMBRANE.
CC   -!- SUBCELLULAR LOCATION: Integral membrane protein (Potential).
CC   -!- SIMILARITY: Belongs to the binding-protein-dependent transport
CC       system permease family. HisMQ subfamily.
CC   ---------------------------------------------------------------------
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CC   or send an email to license@isb-sib.ch).
CC   ---------------------------------------------------------------------
DR   EMBL; AF008220; AAC00327.1; -.
DR   EMBL; Z99118; CAB14896.1; -.
DR   PIR; F69996; F69996.
DR   SubtiList; BG13886; ytmL.
DR   InterPro; IPR000515; BPD_transp.
DR   Pfam; PF00528; BPD_transp; 1.
DR   PROSITE; PS50928; ABC_TM1; 1.
KW   Hypothetical protein; Transport; Amino-acid transport; Transmembrane;
KW   Complete proteome.
FT   TRANSMEM     25     45       POTENTIAL.
FT   TRANSMEM     69     89       POTENTIAL.
FT   TRANSMEM     96    116       POTENTIAL.
FT   TRANSMEM    196    216       POTENTIAL.
SQ   SEQUENCE   239 AA;  26239 MW;  AE0D17AC254D6239 CRC64;

  Query Match             2.1%;  Score 7;  DB 1;  Length 239;
  Best Local Similarity   100.0%;  Pred. No. 48;
  Matches    7;  Conservative    0;  Mismatches    0;  Indels    0;  Gaps    0;

Qy        241 FVLGLFL 247
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Db         36 FVLGLFL 42


RESULT 13
FLIP_CAUCR
ID   FLIP_CAUCR     STANDARD;      PRT;   266 AA.
AC   Q45980;
DT   01-NOV-1997 (Rel. 35, Created)
DT   01-NOV-1997 (Rel. 35, Last sequence update)
DT   10-OCT-2003 (Rel. 42, Last annotation update)
DE   Flagellar biosynthetic protein fliP.
GN   FLIP OR CC0951.
OS   Caulobacter crescentus.
OC   Bacteria; Proteobacteria; Alphaproteobacteria; Caulobacterales;
OC   Caulobacteraceae; Caulobacter.
OX   NCBI_TaxID=155892;
RN   [1]
RP   SEQUENCE FROM N.A.
RC   STRAIN=ATCC 19089 / CB15;
RX   MEDLINE=95325304; PubMed=7601828;
RA   Gober J.W., Boyd C.H., Jarvis M., Mangan E.K., Rizzo M.F.,
RA   Wingrove J.A.;
RT   "Temporal and spatial regulation of fliP, an early flagellar gene of
RT   Caulobacter crescentus that is required for motility and normal cell
RT   division.";
RL   J. Bacteriol. 177:3656-3667(1995).
RN   [2]
RP   SEQUENCE FROM N.A.
RC   STRAIN=ATCC 19089 / CB15;
RX   MEDLINE=21173698; PubMed=11259647;
RA   Nierman W.C., Feldblyum T.V., Laub M.T., Paulsen I.T., Nelson K.E.,
RA   Eisen J.A., Heidelberg J.F., Alley M.R.K., Ohta N., Maddock J.R.,
RA   Potocka I., Nelson W.C., Newton A., Stephens C., Phadke N.D., Ely B.,
RA   DeBoy R.T., Dodson R.J., Durkin A.S., Gwinn M.L., Haft D.H.,
RA   Kolonay J.F., Smit J., Craven M.B., Khouri H., Shetty J., Berry K.,
RA   Utterback T., Tran K., Wolf A., Vamathevan J., Ermolaeva M., White O.,
RA   Salzberg S.L., Venter J.C., Shapiro L., Fraser C.M.;
RT   "Complete genome sequence of Caulobacter crescentus.";
RL   Proc. Natl. Acad. Sci. U.S.A. 98:4136-4141(2001).
CC   -!- FUNCTION: MAY BE A COMPONENT OF THE FLAGELLUM. IT IS REQUIRED FOR
CC       NORMAL CELL DIVISION. MAY BE IMPLICATED IN THE SECRETION OF
CC       VIRULENCE FACTORS.
CC   -!- SUBCELLULAR LOCATION: Integral membrane protein (Potential).
CC   -!- SIMILARITY: BELONGS TO THE FLIP/MOPC/SPAP FAMILY.
CC   ---------------------------------------------------------------------
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CC   ---------------------------------------------------------------------
DR   EMBL; U20387; AAA86882.1; -.
DR   EMBL; AE005772; AAK22935.1; -.
DR   PIR; C87367; C87367.
DR   TIGR; CC0951; -.
DR   InterPro; IPR005837; FliP.
DR   InterPro; IPR005838; TypeIII_P.
DR   Pfam; PF00813; FliP; 1.
DR   PRINTS; PR01302; TYPE3IMPPROT.
DR   ProDom; PD002586; TypeIII_P; 1.
DR   TIGRFAMs; TIGR01103; fliP; 1.
DR   PROSITE; PS01060; FLIP_1; 1.
DR   PROSITE; PS01061; FLIP_2; 1.
KW   Flagellum; Transmembrane; Complete proteome.
FT   TRANSMEM     20     40       POTENTIAL.
FT   TRANSMEM     58     78       POTENTIAL.
FT   TRANSMEM    102    122       POTENTIAL.
FT   TRANSMEM    202    222       POTENTIAL.
FT   TRANSMEM    226    246       POTENTIAL.
SQ   SEQUENCE   266 AA;  28527 MW;  A84F17CB1C65A947 CRC64;

  Query Match             2.1%;  Score 7;  DB 1;  Length 266;
  Best Local Similarity   100.0%;  Pred. No. 52;
  Matches    7;  Conservative    0;  Mismatches    0;  Indels    0;  Gaps    0;

Qy         21 AASGPVK 27
              |||||||
Db        146 AASGPVK 152


RESULT 14
CFXQ_GUITH
ID   CFXQ_GUITH     STANDARD;      PRT;   293 AA.
AC   O78450;
DT   15-DEC-1998 (Rel. 37, Created)
DT   15-DEC-1998 (Rel. 37, Last sequence update)
DT   15-JUL-1999 (Rel. 38, Last annotation update)
DE   CfxQ protein homolog.
GN   CFXQ.
OS   Guillardia theta (Cryptomonas phi).
OG   Chloroplast.
OC   Eukaryota; Cryptophyta; Cryptomonadaceae; Guillardia.
OX   NCBI_TaxID=55529;
RN   [1]
RP   SEQUENCE FROM N.A.
RX   MEDLINE=99128221; PubMed=9929392;
RA   Douglas S.E., Penny S.L.;
RT   "The plastid genome of the cryptophyte alga, Guillardia theta:
RT   complete sequence and conserved synteny groups confirm its common
RT   ancestry with red algae.";
RL   J. Mol. Evol. 48:236-244(1999).
CC   -!- FUNCTION: Necessary for the expression of RuBisCO (By similarity).
CC   -!- SUBCELLULAR LOCATION: Chloroplast.
CC   -!- SIMILARITY: BELONGS TO THE CBXX/CFQX FAMILY.
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CC   ----------------------------------------------------------------------
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CC   ----------------------------------------------------------------------
DR   EMBL; AF041468; AAC35641.1; -.
DR   InterPro; IPR003593; AAA_ATPase.
DR   InterPro; IPR003959; AAA_ATPase_centr.
DR   InterPro; IPR000641; CbxX_CfqX.
DR   Pfam; PF00004; AAA; 1.
DR   PRINTS; PR00819; CBXCFQXSUPER.
DR   SMART; SM00382; AAA; 1.
KW   ATP-binding; Chloroplast.
FT   NP_BIND      72     79       ATP (POTENTIAL).
SQ   SEQUENCE   293 AA;  33560 MW;  7F7476B77EC34915 CRC64;

  Query Match             2.1%;  Score 7;  DB 1;  Length 293;
  Best Local Similarity   100.0%;  Pred. No. 57;
  Matches    7;  Conservative    0;  Mismatches    0;  Indels    0;  Gaps    0;

Qy         60 LVTIQPE 66
              |||||||
Db        277 LVTIQPE 283


RESULT 15
MURB_STRA3
ID   MURB_STRA3     STANDARD;      PRT;   300 AA.
AC   Q8E553; Q8DZI9;
DT   10-OCT-2003 (Rel. 42, Created)
DT   10-OCT-2003 (Rel. 42, Last sequence update)
DT   10-OCT-2003 (Rel. 42, Last annotation update)
DE   UDP-N-acetylenolpyruvoylglucosamine reductase (EC 1.1.1.158) (UDP-N-
DE   acetylmuramate dehydrogenase).
GN   MURB OR GBS1179 OR SAG1112.
OS   Streptococcus agalactiae (serotype III), and
OS   Streptococcus agalactiae (serotype V).
OC   Bacteria; Firmicutes; Lactobacillales; Streptococcaceae;
OC   Streptococcus.
OX   NCBI_TaxID=216495, 216466;
RN   [1]
RP   SEQUENCE FROM N.A.
RC   STRAIN=NEM316 / Serotype III;
RX   MEDLINE=22242508; PubMed=12354221;
RA   Glaser P., Rusniok C., Buchrieser C., Chevalier F., Frangeul L.,
RA   Msadek T., Zouine M., Couve E., Lalioui L., Poyart C., Trieu-Cuot P.,
RA   Kunst F.;
RT   "Genome sequence of Streptococcus agalactiae, a pathogen causing
RT   invasive neonatal disease.";
RL   Mol. Microbiol. 45:1499-1513(2002).
RN   [2]
RP   SEQUENCE FROM N.A.
RC   STRAIN=2603 V/R / Serotype V;
RX   MEDLINE=22222988; PubMed=12200547;
RA   Tettelin H., Masignani V., Cieslewicz M.J., Eisen J.A., Peterson S.,
RA   Wessels M.R., Paulsen I.T., Nelson K.E., Margarit I., Read T.D.,
RA   Madoff L.C., Wolf A.M., Beanan M.J., Brinkac L.M., Daugherty S.C.,
RA   DeBoy R.T., Durkin A.S., Kolonay J.F., Madupu R., Lewis M.R.,
RA   Radune D., Fedorova N.B., Scanlan D., Khouri H., Mulligan S.,
RA   Carty H.A., Cline R.T., Van Aken S.E., Gill J., Scarselli M., Mora M.,
RA   Iacobini E.T., Brettoni C., Galli G., Mariani M., Vegni F. Maione D.,
RA   Rinaudo D., Rappuoli R., Telford J.L., Kasper D.L., Grandi G.,
RA   Fraser C.M.;
RT   "Complete genome sequence and comparative genomic analysis of an
RT   emerging human pathogen, serotype V Streptococcus agalactiae.";
RL   Proc. Natl. Acad. Sci. U.S.A. 99:12391-12396(2002).
CC   -!- FUNCTION: Cell wall formation (By similarity).
CC   -!- CATALYTIC ACTIVITY: UDP-N-acetylmuramate + NADP(+) = UDP-N-
CC       acetyl-3-O-(1-carboxyvinyl)-D-glucosamine + NADPH.
CC   -!- COFACTOR: FAD (By similarity).
CC   -!- PATHWAY: Peptidoglycan biosynthesis.
CC   -!- SUBCELLULAR LOCATION: Cytoplasmic (Probable).
CC   -!- SIMILARITY: Belongs to the murB family.
CC   ----------------------------------------------------------------------
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CC   ----------------------------------------------------------------------
DR   EMBL; AL766849; CAD46838.1; -.
DR   EMBL; AE014242; AAM99993.1; -.
DR   SagaList; gbs1179; -.
DR   TIGR; SAG1112; -.
DR   HAMAP; MF_00037; -; 1.
DR   InterPro; IPR003170; MurB.
DR   InterPro; IPR006094; Oxid_FAD_bind.
DR   Pfam; PF01565; FAD_binding_4; 1.
DR   Pfam; PF02873; MurB_C; 1.
KW   Oxidoreductase; NADP; Flavoprotein; FAD; Cell wall; Cell division;
KW   Peptidoglycan synthesis; Complete proteome.
SQ   SEQUENCE   300 AA;  32978 MW;  3FCC5590FBF2ED97 CRC64;

  Query Match             2.1%;  Score 7;  DB 1;  Length 300;
  Best Local Similarity   100.0%;  Pred. No. 58;
  Matches    7;  Conservative    0;  Mismatches    0;  Indels    0;  Gaps    0;

Qy         31 GSVGGAV 37
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Db        125 GSVGGAV 131


Search completed: August 18, 2004, 15:59:39
Job time : 16 secs
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GenCore version 5.1.6

OM protein - protein search, using sw model

Run on: August 18, 2004, 15:42:01 ; Search time 19 Seconds
(without alignments)
910.247 Million cell updates/sec

Title: US-10-063-549-46
Perfect score: 1772
Sequence: 1 MAGSPTCLTLIYILWQLTGS.....PHSLLTMPDTPRLFAYENVI 335

Scoring table: BLOSUM62
Gapop 10.0 , Gapext 0.5

Searched: 389414 seqs, 51625971 residues

Total number of hits satisfying chosen parameters: 389414

Minimum DB seq length: 0
Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%
Maximum Match 100%
Listing first 700 summaries

Database : Issued_Patents_AA:*
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2: /cgn2_6/ptodata/2/iaa/5B_COMB.pep:*
3: /cgn2_6/ptodata/2/iaa/6A_COMB.pep:*
4: /cgn2_6/ptodata/2/iaa/6B_COMB.pep:*
5: /cgn2_6/ptodata/2/iaa/PCTUS_COMB.pep:*
6: /cgn2_6/ptodata/2/iaa/backfiles1.pep:*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	% Query Match	Length	DB	ID	Description
1	362.5	20.5	329	4	US-09-149-476-483	Sequence 483, App
2	186	10.5	343	1	US-08-348-792-10	Sequence 10, Appl
3	186	10.5	343	2	US-08-462-738-10	Sequence 10, Appl
4	186	10.5	343	4	US-09-199-955-10	Sequence 10, Appl
5	186	10.5	343	4	US-08-880-875-10	Sequence 10, Appl
6	182.5	10.3	335	1	US-08-348-792-2	Sequence 2, Appli
7	182.5	10.3	335	2	US-08-462-738-2	Sequence 2, Appli
8	182.5	10.3	335	4	US-09-199-955-2	Sequence 2, Appli
9	182.5	10.3	335	4	US-08-880-875-2	Sequence 2, Appli
10	182.5	10.3	335	4	US-09-369-248A-3	Sequence 3, Appli
11	180	10.2	307	1	US-08-348-792-8	Sequence 8, Appli
12	180	10.2	307	2	US-08-462-738-8	Sequence 8, Appli
13	180	10.2	307	4	US-09-199-955-8	Sequence 8, Appli
14	180	10.2	307	4	US-08-880-875-8	Sequence 8, Appli
15	164.5	9.3	305	1	US-08-348-792-6	Sequence 6, Appli
16	164.5	9.3	305	2	US-08-462-738-6	Sequence 6, Appli
17	164.5	9.3	305	4	US-09-199-955-6	Sequence 6, Appli
18	164.5	9.3	305	4	US-08-880-875-6	Sequence 6, Appli
19	158.5	8.9	329	1	US-08-348-792-12	Sequence 12, Appl
20	158.5	8.9	329	2	US-08-462-738-12	Sequence 12, Appl
21	158.5	8.9	329	4	US-09-199-955-12	Sequence 12, Appl
22	158.5	8.9	329	4	US-08-880-875-12	Sequence 12, Appl
23	152	8.6	298	1	US-08-348-792-4	Sequence 4, Appli
24	152	8.6	298	2	US-08-462-738-4	Sequence 4, Appli
25	152	8.6	298	4	US-09-199-955-4	Sequence 4, Appli
26	152	8.6	298	4	US-08-880-875-4	Sequence 4, Appli
27	150.5	8.5	285	4	US-09-369-248A-2	Sequence 2, Appli
28	141	8.0	149	4	US-09-227-357-443	Sequence 443, App
29	140.5	7.9	143	4	US-09-227-357-192	Sequence 192, App
30	136.5	7.7	351	3	US-08-466-465-6	Sequence 6, Appli
31	128	7.2	225	1	US-08-328-152A-31	Sequence 31, Appl
32	128	7.2	321	6	5169835-17	Patent No. 5169835
33	125.5	7.1	464	2	US-08-602-725-32	Sequence 32, Appl
34	123	6.9	199	1	US-08-328-152A-36	Sequence 36, Appl
35	119.5	6.7	365	2	US-08-979-424-3	Sequence 3, Appli
36	119.5	6.7	365	3	US-09-272-496-2	Sequence 2, Appli
37	119.5	6.7	418	3	US-08-630-172-18	Sequence 18, Appl
38	119.5	6.7	418	3	US-09-375-419-18	Sequence 18, Appl
39	117.5	6.6	344	2	US-08-602-725-34	Sequence 34, Appl
40	117.5	6.6	365	3	US-08-928-383B-2	Sequence 2, Appli
41	116.5	6.6	319	1	US-08-597-495B-22	Sequence 22, Appl
42	116.5	6.6	319	3	US-09-068-051A-22	Sequence 22, Appl
43	116.5	6.6	319	4	US-09-336-536-67	Sequence 67, Appl
44	116.5	6.6	319	4	US-09-254-465A-6	Sequence 6, Appli
45	115.5	6.5	184	3	US-08-630-172-2	Sequence 2, Appli
46	115.5	6.5	184	3	US-09-375-419-2	Sequence 2, Appli
47	114.5	6.5	642	1	US-08-217-299-1	Sequence 1, Appli
48	114.5	6.5	698	2	US-08-602-725-36	Sequence 36, Appl
49	114.5	6.5	734	2	US-08-389-459A-17	Sequence 17, Appl
50	114.5	6.5	734	3	US-08-987-867A-17	Sequence 17, Appl
51	111.5	6.3	174	2	US-08-765-536-2	Sequence 2, Appli
52	111.5	6.3	174	5	PCT-US95-08401-2	Sequence 2, Appli
53	109.5	6.2	315	4	US-09-910-174B-28	Sequence 28, Appl
54	109.5	6.2	315	4	US-09-620-461-28	Sequence 28, Appl
55	109	6.2	324	4	US-09-910-174B-6	Sequence 6, Appli
56	109	6.2	324	4	US-09-620-461-6	Sequence 6, Appli
57	105.5	6.0	323	4	US-09-651-200-21	Sequence 21, Appl
58	105.5	6.0	323	5	PCT-US94-09642-2	Sequence 2, Appli
59	105.5	6.0	329	2	US-08-456-104-2	Sequence 2, Appli
60	105.5	6.0	329	2	US-08-101-624-2	Sequence 2, Appli
61	105.5	6.0	329	3	US-08-479-744A-2	Sequence 2, Appli
62	105.5	6.0	329	3	US-08-280-757B-2	Sequence 2, Appli
63	105.5	6.0	329	3	US-08-205-697A-23	Sequence 23, Appl
64	105.5	6.0	329	3	US-08-702-525-23	Sequence 23, Appl
65	105.5	6.0	329	4	US-08-403-253A-4	Sequence 4, Appli
66	105.5	6.0	329	4	US-08-435-816A-4	Sequence 4, Appli
67	105.5	6.0	329	4	US-09-425-762-2	Sequence 2, Appli
68	105.5	6.0	329	4	US-09-837-867A-23	Sequence 23, Appl
69	105.5	6.0	329	5	PCT-US95-02576-23	Sequence 23, Appl
70	104.5	5.9	329	4	US-09-667-135-32	Sequence 32, Appl
71	101.5	5.7	270	4	US-09-254-465A-24	Sequence 24, Appl
72	101.5	5.7	273	4	US-09-254-465A-26	Sequence 26, Appl
73	100.5	5.7	638	4	US-09-228-986-74	Sequence 74, Appl
74	100	5.6	365	3	US-08-928-383B-24	Sequence 24, Appl
75	98.5	5.6	365	3	US-08-928-383B-23	Sequence 23, Appl
76	98	5.5	503	4	US-08-999-689A-6	Sequence 6, Appli
77	97	5.5	773	3	US-08-434-000A-2	Sequence 2, Appli
78	97	5.5	773	4	US-09-312-157-2	Sequence 2, Appli
79	96.5	5.4	534	4	US-09-651-200-6	Sequence 6, Appli
80	96.5	5.4	534	4	US-09-651-200-24	Sequence 24, Appl
81	96	5.4	340	4	US-09-651-200-2	Sequence 2, Appli
82	96	5.4	441	4	US-09-651-200-4	Sequence 4, Appli
83	96	5.4	526	4	US-09-910-174B-9	Sequence 9, Appli
84	96	5.4	526	4	US-09-620-461-9	Sequence 9, Appli
85	95.5	5.4	365	3	US-08-928-383B-26	Sequence 26, Appl
86	95.5	5.4	771	3	US-08-434-000A-8	Sequence 8, Appli
87	95.5	5.4	771	4	US-09-312-157-8	Sequence 8, Appli
88	93.5	5.3	299	3	US-09-188-930-189	Sequence 189, App
89	93.5	5.3	2409	6	5180808-2	Patent No. 5180808
90	93	5.2	316	4	US-09-910-174B-24	Sequence 24, Appl
91	93	5.2	316	4	US-09-620-461-24	Sequence 24, Appl
92	93	5.2	561	3	US-09-192-545-2	Sequence 2, Appli
93	92.5	5.2	299	3	US-09-188-930-331	Sequence 331, App
94	92.5	5.2	299	4	US-09-462-270-2	Sequence 2, Appli
95	92.5	5.2	299	4	US-09-254-465A-1	Sequence 1, Appli
96	92.5	5.2	299	4	US-09-312-283C-189	Sequence 189, App
97	92.5	5.2	299	4	US-09-312-283C-331	Sequence 331, App
98	92.5	5.2	299	4	US-09-907-794A-119	Sequence 119, App
99	92.5	5.2	299	4	US-09-905-125A-119	Sequence 119, App
100	92.5	5.2	299	4	US-09-902-775A-119	Sequence 119, App

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102	91	5.1	251	6	5185441-38	Patent No. 5185441
103	90.5	5.1	521	3	US-08-996-338-20	Sequence 20, Appl
104	90.5	5.1	521	4	US-09-556-972-20	Sequence 20, Appl
105	90	5.1	156	4	US-09-370-838-210	Sequence 210, App
106	90	5.1	222	1	US-08-328-152A-8	Sequence 8, Appli
107	90	5.1	240	1	US-07-940-861-12	Sequence 12, Appl
108	90	5.1	240	1	US-08-459-512-12	Sequence 12, Appl
109	90	5.1	240	2	US-08-459-657-12	Sequence 12, Appl
110	90	5.1	240	2	US-08-460-132-12	Sequence 12, Appl
111	90	5.1	240	3	US-08-466-465-4	Sequence 4, Appli
112	90	5.1	240	5	PCT-US92-02050-12	Sequence 12, Appl
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118	90	5.1	250	2	US-08-459-657-10	Sequence 10, Appl
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120	90	5.1	250	3	US-08-466-465-2	Sequence 2, Appli
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125	90	5.1	541	3	US-09-110-618-2	Sequence 2, Appli
126	90	5.1	541	4	US-09-173-151A-28	Sequence 28, Appl
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128	90	5.1	541	4	US-09-577-806-2	Sequence 2, Appli
129	90	5.1	541	4	US-09-621-502-4	Sequence 4, Appli
130	89.5	5.1	423	4	US-09-181-339-9	Sequence 9, Appli
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133	89	5.0	309	3	US-08-479-744A-23	Sequence 23, Appl
134	89	5.0	309	3	US-08-280-757B-23	Sequence 23, Appl
135	89	5.0	309	3	US-08-205-697A-21	Sequence 21, Appl
136	89	5.0	309	3	US-08-702-525-21	Sequence 21, Appl
137	89	5.0	309	4	US-09-651-200-22	Sequence 22, Appl
138	89	5.0	309	4	US-09-667-135-33	Sequence 33, Appl
139	89	5.0	309	4	US-09-425-762-23	Sequence 23, Appl
140	89	5.0	309	4	US-09-837-867A-21	Sequence 21, Appl
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144	89	5.0	314	4	US-09-837-867A-13	Sequence 13, Appl
145	89	5.0	314	5	PCT-US95-02576-13	Sequence 13, Appl
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149	88.5	5.0	611	4	US-09-991-326-10	Sequence 10, Appl
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152	88	5.0	699	2	US-08-800-825A-7	Sequence 7, Appli
153	88	5.0	699	3	US-09-158-657-7	Sequence 7, Appli
154	87.5	4.9	325	4	US-09-651-200-20	Sequence 20, Appl
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156	87.5	4.9	769	4	US-09-312-157-10	Sequence 10, Appl
157	87	4.9	490	4	US-09-336-643A-6	Sequence 6, Appli
158	87	4.9	491	4	US-09-181-339-7	Sequence 7, Appli
159	87	4.9	582	4	US-09-702-705-334	Sequence 334, App
160	87	4.9	582	4	US-09-736-457-334	Sequence 334, App
161	87	4.9	582	4	US-09-614-124B-334	Sequence 334, App
162	87	4.9	582	4	US-09-671-325-334	Sequence 334, App
163	87	4.9	582	4	US-09-589-184-334	Sequence 334, App
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165	87	4.9	583	2	US-08-684-594-2	Sequence 2, Appli
166	86.5	4.9	790	3	US-08-960-780-4	Sequence 4, Appli
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168	86.5	4.9	790	4	US-09-850-351A-4	Sequence 4, Appli
169	86	4.9	302	4	US-09-877-730-14	Sequence 14, Appl
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171	86	4.9	826	4	US-09-877-730-16	Sequence 16, Appl
172	86	4.9	904	4	US-09-877-730-6	Sequence 6, Appli
173	86	4.9	907	4	US-09-877-730-20	Sequence 20, Appl
174	86	4.9	985	4	US-09-877-730-10	Sequence 10, Appl
175	86	4.9	991	4	US-09-877-730-12	Sequence 12, Appl
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177	86	4.9	1072	4	US-09-877-730-18	Sequence 18, Appl
178	86	4.9	1150	4	US-09-877-730-8	Sequence 8, Appli
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181	85.5	4.8	746	3	US-09-233-752A-6	Sequence 6, Appli
182	85.5	4.8	746	3	US-09-402-036-6	Sequence 6, Appli
183	85.5	4.8	746	4	US-09-904-226-6	Sequence 6, Appli
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189	85.5	4.8	789	2	US-08-463-483A-32	Sequence 32, Appl
190	85.5	4.8	789	2	US-08-471-046A-29	Sequence 29, Appl
191	85.5	4.8	789	2	US-08-471-046A-32	Sequence 32, Appl
192	85.5	4.8	789	2	US-08-470-566B-29	Sequence 29, Appl
193	85.5	4.8	789	2	US-08-470-566B-32	Sequence 32, Appl
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203	85.5	4.8	789	3	US-09-233-752A-4	Sequence 4, Appli
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205	85.5	4.8	789	3	US-09-402-036-4	Sequence 4, Appli
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211	85.5	4.8	789	4	US-09-904-226-4	Sequence 4, Appli
212	85.5	4.8	789	4	US-09-589-477-78	Sequence 78, Appl
213	85.5	4.8	789	4	US-09-589-477-80	Sequence 80, Appl
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216	85.5	4.8	790	3	US-08-960-780-8	Sequence 8, Appli
217	85.5	4.8	790	3	US-09-073-898-8	Sequence 8, Appli
218	85.5	4.8	790	4	US-09-307-106-2	Sequence 2, Appli
219	85.5	4.8	790	4	US-09-850-351A-8	Sequence 8, Appli
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222	85	4.8	757	3	US-08-434-000A-6	Sequence 6, Appli
223	85	4.8	757	4	US-09-312-157-6	Sequence 6, Appli
224	85	4.8	821	4	US-09-622-880B-15	Sequence 15, Appl
225	84.5	4.8	303	3	US-08-985-950-2	Sequence 2, Appli
226	84.5	4.8	303	4	US-09-546-049-2	Sequence 2, Appli
227	84	4.7	339	4	US-09-719-243-2	Sequence 2, Appli
228	84	4.7	358	4	US-09-719-243-3	Sequence 3, Appli
229	84	4.7	668	1	US-08-530-950-13	Sequence 13, Appl
230	84	4.7	668	3	US-09-149-879-13	Sequence 13, Appl
231	84	4.7	668	4	US-09-057-009-13	Sequence 13, Appl
232	83.5	4.7	260	4	US-09-254-465A-23	Sequence 23, Appl
233	83.5	4.7	263	4	US-09-254-465A-25	Sequence 25, Appl
234	83.5	4.7	298	4	US-09-152-060-76	Sequence 76, Appl
235	83.5	4.7	312	4	US-09-254-465A-9	Sequence 9, Appli
236	83.5	4.7	312	4	US-09-907-794A-64	Sequence 64, Appl
237	83.5	4.7	312	4	US-09-905-125A-64	Sequence 64, Appl
238	83.5	4.7	312	4	US-09-902-775A-64	Sequence 64, Appl
239	83.5	4.7	318	3	US-09-068-051A-32	Sequence 32, Appl
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241	83.5	4.7	408	4	US-09-724-864-62	Sequence 62, Appl
242	83.5	4.7	450	4	US-09-907-794A-320	Sequence 320, App
243	83.5	4.7	450	4	US-09-905-125A-320	Sequence 320, App
244	83.5	4.7	450	4	US-09-902-775A-320	Sequence 320, App
245	83.5	4.7	789	4	US-09-002-285-96	Sequence 96, Appl
246	83.5	4.7	789	4	US-09-589-477-96	Sequence 96, Appl

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248	83.5	4.7	1501	2	US-08-716-679-3	Sequence 3, Appli
249	83	4.7	464	4	US-09-297-468-2	Sequence 2, Appli
250	83	4.7	846	1	US-08-149-103-3	Sequence 3, Appli
251	83	4.7	846	1	US-08-451-883-3	Sequence 3, Appli
252	83	4.7	873	1	US-08-393-734-2	Sequence 2, Appli
253	83	4.7	873	3	US-08-894-489-2	Sequence 2, Appli
254	82.5	4.7	194	3	US-08-630-172-14	Sequence 14, Appl
255	82.5	4.7	194	3	US-09-375-419-14	Sequence 14, Appl
256	82.5	4.7	238	4	US-09-149-476-485	Sequence 485, App
257	82.5	4.7	486	4	US-09-134-000C-5552	Sequence 5552, Ap
258	82.5	4.7	511	4	US-09-002-285-88	Sequence 88, Appl
259	82.5	4.7	511	4	US-09-589-477-88	Sequence 88, Appl
260	82.5	4.7	789	4	US-09-002-285-82	Sequence 82, Appl
261	82.5	4.7	789	4	US-09-002-285-84	Sequence 84, Appl
262	82.5	4.7	789	4	US-09-002-285-92	Sequence 92, Appl
263	82.5	4.7	789	4	US-09-589-477-82	Sequence 82, Appl
264	82.5	4.7	789	4	US-09-589-477-84	Sequence 84, Appl
265	82.5	4.7	789	4	US-09-589-477-92	Sequence 92, Appl
266	82.5	4.7	790	4	US-09-002-285-102	Sequence 102, App
267	82.5	4.7	790	4	US-09-589-477-102	Sequence 102, App
268	82	4.6	314	4	US-09-107-532A-4919	Sequence 4919, Ap
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270	82	4.6	449	3	US-09-286-691-4	Sequence 4, Appli
271	82	4.6	449	3	US-09-687-147-4	Sequence 4, Appli
272	82	4.6	757	4	US-09-622-880B-1	Sequence 1, Appli
273	82	4.6	874	2	US-08-456-647B-6	Sequence 6, Appli
274	82	4.6	874	2	US-08-237-401A-6	Sequence 6, Appli
275	82	4.6	880	1	US-08-445-640-10	Sequence 10, Appl
276	82	4.6	880	3	US-08-170-558-10	Sequence 10, Appl
277	82	4.6	880	3	US-08-447-314-10	Sequence 10, Appl
278	82	4.6	880	3	US-08-445-461-10	Sequence 10, Appl
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280	81.5	4.6	309	4	US-09-910-174B-7	Sequence 7, Appli
281	81.5	4.6	309	4	US-09-620-461-7	Sequence 7, Appli
282	81.5	4.6	558	4	US-09-667-135-31	Sequence 31, Appl
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284	81.5	4.6	846	1	US-08-451-883-4	Sequence 4, Appli
285	81	4.6	144	6	5169835-8	Patent No. 5169835
286	81	4.6	252	2	US-08-414-657D-56	Sequence 56, Appl
287	81	4.6	287	2	US-08-414-657D-48	Sequence 48, Appl
288	81	4.6	304	2	US-08-414-657D-44	Sequence 44, Appl
289	81	4.6	308	2	US-08-414-657D-46	Sequence 46, Appl
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291	81	4.6	325	2	US-08-414-657D-41	Sequence 41, Appl
292	81	4.6	325	4	US-09-135-080-2	Sequence 2, Appli
293	81	4.6	338	2	US-08-414-657D-60	Sequence 60, Appl
294	81	4.6	338	4	US-09-135-080-8	Sequence 8, Appli
295	81	4.6	338	4	US-09-976-594-404	Sequence 404, App
296	80.5	4.5	205	4	US-09-134-001C-4766	Sequence 4766, Ap
297	80.5	4.5	346	1	US-08-213-403-2	Sequence 2, Appli
298	80.5	4.5	346	1	US-08-458-077-2	Sequence 2, Appli
299	80.5	4.5	346	1	US-08-460-741-2	Sequence 2, Appli
300	80.5	4.5	346	1	US-08-747-240-2	Sequence 2, Appli
301	80.5	4.5	346	1	US-08-299-567-6	Sequence 6, Appli
302	80.5	4.5	346	4	US-09-039-642B-2	Sequence 2, Appli
303	80.5	4.5	650	1	US-08-121-713D-60	Sequence 60, Appl
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305	80.5	4.5	650	2	US-09-060-692-60	Sequence 60, Appl
306	80.5	4.5	650	3	US-08-833-391-60	Sequence 60, Appl
307	80.5	4.5	650	4	US-09-060-610-60	Sequence 60, Appl
308	80.5	4.5	650	5	PCT-US94-10151A-60	Sequence 60, Appl
309	80.5	4.5	721	4	US-09-390-234-20	Sequence 20, Appl
310	80.5	4.5	721	4	US-09-603-311-20	Sequence 20, Appl
311	80.5	4.5	789	3	US-08-960-780-6	Sequence 6, Appli
312	80.5	4.5	789	3	US-09-073-898-6	Sequence 6, Appli
313	80.5	4.5	789	4	US-09-850-351A-6	Sequence 6, Appli
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315	80	4.5	252	2	US-08-414-657D-57	Sequence 57, Appl
316	80	4.5	287	2	US-08-414-657D-49	Sequence 49, Appl
317	80	4.5	310	2	US-08-414-657D-45	Sequence 45, Appl
318	80	4.5	315	2	US-08-414-657D-47	Sequence 47, Appl
319	80	4.5	338	2	US-08-414-657D-42	Sequence 42, Appl
320	80	4.5	338	2	US-08-414-657D-43	Sequence 43, Appl
321	80	4.5	338	4	US-09-135-080-4	Sequence 4, Appli
322	80	4.5	499	4	US-09-252-991A-23328	Sequence 23328, A
323	80	4.5	528	4	US-09-010-147B-20	Sequence 20, Appl
324	80	4.5	529	3	US-09-383-586-31	Sequence 31, Appl
325	80	4.5	607	2	US-08-752-307B-12	Sequence 12, Appl
326	80	4.5	607	4	US-09-707-802-12	Sequence 12, Appl
327	80	4.5	607	4	US-09-991-326-12	Sequence 12, Appl
328	80	4.5	1233	3	US-09-194-613-5	Sequence 5, Appli
329	79.5	4.5	202	6	5189147-6	Patent No. 5189147
330	79.5	4.5	278	4	US-09-570-367C-21	Sequence 21, Appl
331	79.5	4.5	278	4	US-09-915-524-21	Sequence 21, Appl
332	79.5	4.5	328	3	US-08-821-994-84	Sequence 84, Appl
333	79.5	4.5	335	4	US-09-489-039A-11298	Sequence 11298, A
334	79.5	4.5	374	3	US-08-821-994-68	Sequence 68, Appl
335	79.5	4.5	402	4	US-09-292-097-16	Sequence 16, Appl
336	79.5	4.5	643	1	US-08-471-570-6	Sequence 6, Appli
337	79.5	4.5	769	1	US-08-471-570-8	Sequence 8, Appli
338	79.5	4.5	859	4	US-09-708-200-7	Sequence 7, Appli
339	79.5	4.5	859	4	US-09-788-657-16	Sequence 16, Appl
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341	78.5	4.4	439	3	US-09-383-586-32	Sequence 32, Appl
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343	78	4.4	341	1	US-08-248-628A-2	Sequence 2, Appli
344	78	4.4	345	4	US-09-214-631-5	Sequence 5, Appli
345	78	4.4	624	2	US-08-642-406A-22	Sequence 22, Appl
346	78	4.4	624	4	US-09-199-534-22	Sequence 22, Appl
347	78	4.4	624	4	US-09-199-534-22	Sequence 22, Appl
348	77.5	4.4	321	4	US-09-254-465A-2	Sequence 2, Appli
349	77.5	4.4	477	2	US-08-432-016-3	Sequence 3, Appli
350	77.5	4.4	477	2	US-08-684-594-3	Sequence 3, Appli
351	77.5	4.4	650	4	US-09-310-463-2	Sequence 2, Appli
352	77.5	4.4	650	4	US-08-842-248A-2	Sequence 2, Appli
353	77.5	4.4	662	1	US-08-261-304-7	Sequence 7, Appli
354	77.5	4.4	735	5	PCT-US93-00031-13	Sequence 13, Appl
355	77.5	4.4	736	5	PCT-US93-00031-15	Sequence 15, Appl
356	77.5	4.4	739	4	US-08-482-073-6	Sequence 6, Appli
357	77.5	4.4	739	5	PCT-US93-00031-9	Sequence 9, Appli
358	77.5	4.4	1312	4	US-09-554-572-26	Sequence 26, Appl
359	77	4.3	278	4	US-09-570-367C-2	Sequence 2, Appli
360	77	4.3	278	4	US-09-915-524-2	Sequence 2, Appli
361	77	4.3	458	4	US-09-435-956A-1	Sequence 1, Appli
362	77	4.3	523	3	US-08-948-564-8	Sequence 8, Appli
363	77	4.3	1021	1	US-08-497-025-3	Sequence 3, Appli
364	77	4.3	1033	4	US-09-252-991A-20611	Sequence 20611, A
365	76.5	4.3	292	4	US-09-800-729-175	Sequence 175, App
366	76.5	4.3	364	4	US-08-896-537A-3	Sequence 3, Appli
367	76.5	4.3	490	4	US-09-667-135-28	Sequence 28, Appl
368	76.5	4.3	589	4	US-09-866-510-12	Sequence 12, Appl
369	76.5	4.3	1089	1	US-08-180-195-36	Sequence 36, Appl
370	76.5	4.3	1089	1	US-08-168-917-4	Sequence 4, Appli
371	76.5	4.3	1089	1	US-08-477-329-36	Sequence 36, Appl
372	76.5	4.3	1089	2	US-08-475-458-36	Sequence 36, Appl
373	76.5	4.3	1089	2	US-08-460-510-4	Sequence 4, Appli
374	76.5	4.3	1089	2	US-08-460-490-4	Sequence 4, Appli
375	76.5	4.3	1089	3	US-08-980-400-36	Sequence 36, Appl
376	76.5	4.3	1089	3	US-08-462-728-2	Sequence 2, Appli
377	76.5	4.3	1089	3	US-09-583-459A-36	Sequence 36, Appl
378	76.5	4.3	1089	3	US-09-583-210-36	Sequence 36, Appl
379	76.5	4.3	1089	4	US-09-583-449A-36	Sequence 36, Appl
380	76.5	4.3	1089	4	US-09-435-059-36	Sequence 36, Appl
381	76.5	4.3	1089	4	US-08-461-917-2	Sequence 2, Appli
382	76.5	4.3	1089	4	US-08-464-436-2	Sequence 2, Appli
383	76.5	4.3	1089	4	US-08-464-436-2	Sequence 2, Appli
384	76.5	4.3	1089	4	US-09-769-987-2	Sequence 2, Appli
385	76.5	4.3	1089	4	US-09-866-510-2	Sequence 2, Appli
386	76.5	4.3	1089	4	US-09-866-510-4	Sequence 4, Appli
387	76.5	4.3	1089	4	US-09-866-510-6	Sequence 6, Appli
388	76.5	4.3	1089	4	US-09-866-510-8	Sequence 8, Appli
389	76.5	4.3	1089	4	US-09-866-510-10	Sequence 10, Appl
390	76.5	4.3	1089	5	PCT-US92-00730-4	Sequence 4, Appli
391	76.5	4.3	1089	5	PCT-US92-00862-4	Sequence 4, Appli
392	76.5	4.3	1328	3	US-08-781-891-76	Sequence 76, Appl

393	76.5	4.3	1328	4	US-09-618-166-76	Sequence 76, Appl
394	76.5	4.3	1723	4	US-09-194-612A-31	Sequence 31, Appl
395	76.5	4.3	1745	4	US-09-800-729-89	Sequence 89, Appl
396	76	4.3	277	4	US-09-543-681A-4527	Sequence 4527, Ap
397	76	4.3	378	1	US-08-225-477B-9	Sequence 9, Appli
398	76	4.3	378	5	PCT-US95-04353-9	Sequence 9, Appli
399	76	4.3	390	3	US-08-961-564A-2	Sequence 2, Appli
400	76	4.3	390	4	US-09-050-861B-2	Sequence 2, Appli
401	76	4.3	463	3	US-09-082-310-1	Sequence 1, Appli
402	76	4.3	463	4	US-09-575-205-1	Sequence 1, Appli
403	76	4.3	463	4	US-09-976-594-721	Sequence 721, App
404	76	4.3	599	1	US-08-442-542-18	Sequence 18, Appl
405	76	4.3	599	3	US-08-765-469-18	Sequence 18, Appl
406	75.5	4.3	648	2	US-08-817-436A-2	Sequence 2, Appli
407	75	4.2	303	4	US-09-509-347-7	Sequence 7, Appli
408	75	4.2	512	3	US-09-356-818A-2	Sequence 2, Appli
409	75	4.2	527	4	US-09-910-174B-10	Sequence 10, Appl
410	75	4.2	527	4	US-09-620-461-10	Sequence 10, Appl
411	75	4.2	641	3	US-09-422-869-26	Sequence 26, Appl
412	75	4.2	855	4	US-09-328-352-6216	Sequence 6216, Ap
413	75	4.2	1729	4	US-09-696-115B-2	Sequence 2, Appli
414	75	4.2	2137	4	US-09-134-001C-4463	Sequence 4463, Ap
415	74.5	4.2	218	3	US-09-068-655-7	Sequence 7, Appli
416	74.5	4.2	230	6	5169835-13	Patent No. 5169835
417	74.5	4.2	338	4	US-09-688-188B-152	Sequence 152, App
418	74.5	4.2	338	4	US-09-291-417D-152	Sequence 152, App
419	74.5	4.2	373	4	US-09-688-188B-97	Sequence 97, Appl
420	74.5	4.2	373	4	US-09-291-417D-97	Sequence 97, Appl
421	74.5	4.2	374	3	US-08-821-994-67	Sequence 67, Appl
422	74.5	4.2	374	3	US-08-821-994-69	Sequence 69, Appl
423	74.5	4.2	463	2	US-08-853-659A-52	Sequence 52, Appl
424	74.5	4.2	789	4	US-09-002-285-98	Sequence 98, Appl
425	74.5	4.2	789	4	US-09-589-477-98	Sequence 98, Appl
426	74.5	4.2	1018	1	US-08-452-052-2	Sequence 2, Appli
427	74.5	4.2	1148	2	US-08-313-185-58	Sequence 58, Appl
428	74.5	4.2	1148	3	US-09-082-614A-58	Sequence 58, Appl
429	74.5	4.2	1788	2	US-08-962-284-2	Sequence 2, Appli
430	74.5	4.2	1911	1	US-08-348-006B-5	Sequence 5, Appli
431	74.5	4.2	1911	2	US-08-800-825A-5	Sequence 5, Appli
432	74.5	4.2	1911	3	US-09-158-657-5	Sequence 5, Appli
433	74.5	4.2	1911	5	PCT-US94-10166-5	Sequence 5, Appli
434	74.5	4.2	4654	3	US-08-476-515A-84	Sequence 84, Appl
435	74.5	4.2	4655	3	US-08-652-877-84	Sequence 84, Appl
436	74.5	4.2	4655	3	US-08-652-877-86	Sequence 86, Appl
437	74.5	4.2	4655	3	US-08-652-877-88	Sequence 88, Appl
438	74.5	4.2	4655	3	US-08-652-877-90	Sequence 90, Appl
439	74	4.2	343	4	US-09-454-034-8	Sequence 8, Appli
440	74	4.2	387	4	US-09-175-928-2	Sequence 2, Appli
441	74	4.2	451	4	US-09-107-532A-6652	Sequence 6652, Ap
442	74	4.2	543	4	US-09-042-709A-18	Sequence 18, Appl
443	74	4.2	548	1	US-08-247-902A-2	Sequence 2, Appli
444	74	4.2	548	5	PCT-US93-10541-2	Sequence 2, Appli
445	74	4.2	862	4	US-08-556-422A-2	Sequence 2, Appli
446	74	4.2	1027	4	US-09-162-021B-2	Sequence 2, Appli
447	74	4.2	1333	1	US-08-447-411-76	Sequence 76, Appl
448	74	4.2	1333	2	US-08-662-227-34	Sequence 34, Appl
449	74	4.2	1333	4	US-09-017-947-34	Sequence 34, Appl
450	74	4.2	1333	4	US-09-925-442-34	Sequence 34, Appl
451	73.5	4.1	217	4	US-09-134-001C-5638	Sequence 5638, Ap
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453	73.5	4.1	321	4	US-09-171-461-22	Sequence 22, Appl
454	73.5	4.1	344	4	US-09-700-397-3	Sequence 3, Appli
455	73.5	4.1	513	4	US-09-910-174B-18	Sequence 18, Appl
456	73.5	4.1	513	4	US-09-620-461-18	Sequence 18, Appl
457	73.5	4.1	699	4	US-09-134-001C-4054	Sequence 4054, Ap
458	73.5	4.1	716	3	US-09-171-945-125	Sequence 125, App
459	73.5	4.1	913	1	US-08-445-640-4	Sequence 4, Appli
460	73.5	4.1	913	3	US-08-170-558-4	Sequence 4, Appli
461	73.5	4.1	913	3	US-08-447-314-4	Sequence 4, Appli
462	73.5	4.1	913	3	US-08-445-461-4	Sequence 4, Appli
463	73.5	4.1	1000	4	US-09-193-562D-30	Sequence 30, Appl
464	73.5	4.1	4544	1	US-08-469-486-52	Sequence 52, Appl
465	73.5	4.1	4544	2	US-08-469-658-52	Sequence 52, Appl
466	73	4.1	112	3	US-08-545-809A-136	Sequence 136, App
467	73	4.1	389	4	US-08-724-378D-3	Sequence 3, Appli
468	73	4.1	459	1	US-08-157-101A-7	Sequence 7, Appli
469	73	4.1	501	2	US-08-408-095-31	Sequence 31, Appl
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471	73	4.1	548	4	US-09-398-395A-12	Sequence 12, Appl
472	73	4.1	548	4	US-09-887-586A-12	Sequence 12, Appl
473	73	4.1	548	4	US-09-895-752-12	Sequence 12, Appl
474	73	4.1	548	4	US-09-903-012B-12	Sequence 12, Appl
475	73	4.1	548	4	US-09-900-797-12	Sequence 12, Appl
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477	73	4.1	651	4	US-09-546-049-22	Sequence 22, Appl
478	72.5	4.1	293	6	5189147-3	Patent No. 5189147
479	72.5	4.1	331	1	US-08-364-081-3	Sequence 3, Appli
480	72.5	4.1	331	1	US-08-630-552-3	Sequence 3, Appli
481	72.5	4.1	331	5	PCT-US95-16558-3	Sequence 3, Appli
482	72.5	4.1	347	4	US-09-667-135-4	Sequence 4, Appli
483	72.5	4.1	354	6	5169835-4	Patent No. 5169835
484	72.5	4.1	374	3	US-08-821-994-70	Sequence 70, Appl
485	72.5	4.1	390	2	US-08-979-424-1	Sequence 1, Appli
486	72.5	4.1	390	4	US-09-907-794A-39	Sequence 39, Appl
487	72.5	4.1	390	4	US-09-905-125A-39	Sequence 39, Appl
488	72.5	4.1	390	4	US-09-902-775A-39	Sequence 39, Appl
489	72.5	4.1	424	6	5169835-6	Patent No. 5169835
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491	72.5	4.1	521	2	US-08-504-048-9	Sequence 9, Appli
492	72.5	4.1	526	1	US-08-471-570-4	Sequence 4, Appli
493	72.5	4.1	560	4	US-09-071-035-220	Sequence 220, App
494	72.5	4.1	605	2	US-08-752-307B-8	Sequence 8, Appli
495	72.5	4.1	605	4	US-09-707-802-8	Sequence 8, Appli
496	72.5	4.1	605	4	US-09-991-326-8	Sequence 8, Appli
497	72.5	4.1	627	4	US-09-071-035-218	Sequence 218, App
498	72.5	4.1	652	1	US-08-471-570-10	Sequence 10, Appl
499	72.5	4.1	659	4	US-09-134-000C-6124	Sequence 6124, Ap
500	72.5	4.1	759	4	US-09-002-285-86	Sequence 86, Appl
501	72.5	4.1	759	4	US-09-589-477-86	Sequence 86, Appl
502	72.5	4.1	768	4	US-09-489-039A-12897	Sequence 12897, A
503	72.5	4.1	790	4	US-09-543-681A-5459	Sequence 5459, Ap
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510	72.5	4.1	1434	4	US-09-724-631-10	Sequence 10, Appl
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512	72.5	4.1	1434	5	PCT-US95-13233-10	Sequence 10, Appl
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514	72	4.1	328	4	US-09-489-039A-13216	Sequence 13216, A
515	72	4.1	348	2	US-09-031-485-28	Sequence 28, Appl
516	72	4.1	348	2	US-08-847-429A-28	Sequence 28, Appl
517	72	4.1	348	3	US-09-065-474-28	Sequence 28, Appl
518	72	4.1	348	4	US-09-557-034-28	Sequence 28, Appl
519	72	4.1	379	4	US-09-186-276B-46	Sequence 46, Appl
520	72	4.1	379	4	US-08-842-445-46	Sequence 46, Appl
521	72	4.1	379	4	US-09-186-188B-46	Sequence 46, Appl
522	72	4.1	456	1	US-08-435-933-6	Sequence 6, Appli
523	72	4.1	456	5	PCT-US96-06035-6	Sequence 6, Appli
524	72	4.1	497	4	US-08-709-731A-29	Sequence 29, Appl
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526	72	4.1	548	4	US-09-398-395A-2	Sequence 2, Appli
527	72	4.1	548	4	US-09-887-586A-2	Sequence 2, Appli
528	72	4.1	548	4	US-09-895-752-2	Sequence 2, Appli
529	72	4.1	548	4	US-09-903-012B-2	Sequence 2, Appli
530	72	4.1	548	4	US-09-900-797-2	Sequence 2, Appli
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532	72	4.1	852	4	US-09-319-588C-18	Sequence 18, Appl
533	72	4.1	1297	3	US-09-540-245A-17	Sequence 17, Appl
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535	72	4.1	1456	1	US-08-803-972-2	Sequence 2, Appli
536	72	4.1	1745	2	US-09-031-485-33	Sequence 33, Appl
537	72	4.1	1745	2	US-08-847-429A-33	Sequence 33, Appl
538	72	4.1	1745	3	US-09-065-474-33	Sequence 33, Appl

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540	71.5	4.0	206	3	US-08-821-994-77	Sequence 77, Appl
541	71.5	4.0	248	6	5169835-15	Patent No. 5169835
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543	71.5	4.0	327	3	US-09-420-915-5	Sequence 5, Appli
544	71.5	4.0	384	4	US-09-552-322-2	Sequence 2, Appli
545	71.5	4.0	403	4	US-09-638-649-5	Sequence 5, Appli
546	71.5	4.0	462	4	US-09-166-350-18	Sequence 18, Appl
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548	71.5	4.0	523	4	US-09-620-461-11	Sequence 11, Appl
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550	71.5	4.0	746	3	US-08-434-000A-4	Sequence 4, Appli
551	71.5	4.0	746	4	US-09-312-157-4	Sequence 4, Appli
552	71.5	4.0	919	2	US-08-788-674-4	Sequence 4, Appli
553	71.5	4.0	2468	4	US-09-976-594-726	Sequence 726, App
554	71	4.0	107	1	US-08-425-336-125	Sequence 125, App
555	71	4.0	107	1	US-08-488-113B-125	Sequence 125, App
556	71	4.0	107	1	US-08-477-484B-125	Sequence 125, App
557	71	4.0	107	1	US-08-107-669D-65	Sequence 65, Appl
558	71	4.0	107	1	US-08-472-788A-87	Sequence 87, Appl
559	71	4.0	107	2	US-08-477-531B-65	Sequence 65, Appl
560	71	4.0	107	2	US-08-646-360-125	Sequence 125, App
561	71	4.0	107	2	US-08-082-842A-87	Sequence 87, Appl
562	71	4.0	107	3	US-08-839-765-125	Sequence 125, App
563	71	4.0	107	3	US-09-136-389-125	Sequence 125, App
564	71	4.0	107	4	US-09-610-838-125	Sequence 125, App
565	71	4.0	107	4	US-09-711-485-125	Sequence 125, App
566	71	4.0	233	4	US-09-198-452A-244	Sequence 244, App
567	71	4.0	236	3	US-09-049-672A-7	Sequence 7, Appli
568	71	4.0	240	1	US-08-488-113B-147	Sequence 147, App
569	71	4.0	240	1	US-08-488-113B-148	Sequence 148, App
570	71	4.0	240	1	US-08-477-484B-147	Sequence 147, App
571	71	4.0	240	1	US-08-477-484B-148	Sequence 148, App
572	71	4.0	240	2	US-08-646-360-147	Sequence 147, App
573	71	4.0	240	2	US-08-646-360-148	Sequence 148, App
574	71	4.0	240	3	US-08-839-765-147	Sequence 147, App
575	71	4.0	240	3	US-08-839-765-148	Sequence 148, App
576	71	4.0	240	3	US-09-136-389-147	Sequence 147, App
577	71	4.0	240	3	US-09-136-389-148	Sequence 148, App
578	71	4.0	240	4	US-09-610-838-147	Sequence 147, App
579	71	4.0	240	4	US-09-610-838-148	Sequence 148, App
580	71	4.0	240	4	US-09-711-485-147	Sequence 147, App
581	71	4.0	240	4	US-09-711-485-148	Sequence 148, App
582	71	4.0	379	4	US-09-543-681A-7089	Sequence 7089, Ap
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584	71	4.0	615	4	US-09-297-937C-9	Sequence 9, Appli
585	71	4.0	647	3	US-08-753-007A-32	Sequence 32, Appl
586	71	4.0	647	3	US-09-398-496-32	Sequence 32, Appl
587	71	4.0	661	1	US-08-232-538-12	Sequence 12, Appl
588	71	4.0	661	2	US-08-786-164-12	Sequence 12, Appl
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590	71	4.0	687	2	US-08-786-164-6	Sequence 6, Appli
591	71	4.0	687	4	US-09-427-353-2	Sequence 2, Appli
592	71	4.0	731	4	US-09-107-532A-6999	Sequence 6999, Ap
593	71	4.0	758	2	US-08-874-678-1	Sequence 1, Appli
594	71	4.0	758	3	US-08-643-839-1	Sequence 1, Appli
595	71	4.0	758	3	US-09-051-363-24	Sequence 24, Appl
596	71	4.0	758	4	US-09-348-886-1	Sequence 1, Appli
597	71	4.0	780	1	US-08-232-538-14	Sequence 14, Appl
598	71	4.0	780	2	US-08-786-164-14	Sequence 14, Appl
599	71	4.0	821	2	US-08-451-822A-13	Sequence 13, Appl
600	71	4.0	821	4	US-08-323-430-13	Sequence 13, Appl
601	71	4.0	906	4	US-09-651-656-13	Sequence 13, Appl
602	71	4.0	906	4	US-09-650-855-13	Sequence 13, Appl
603	71	4.0	930	4	US-09-134-001C-5314	Sequence 5314, Ap
604	71	4.0	930	4	US-09-386-962C-10	Sequence 10, Appl
605	71	4.0	975	4	US-09-695-481-4	Sequence 4, Appli
606	71	4.0	1018	1	US-08-408-093-6	Sequence 6, Appli
607	71	4.0	1018	1	US-08-408-420A-6	Sequence 6, Appli
608	71	4.0	1018	1	US-08-714-901-6	Sequence 6, Appli
609	71	4.0	1018	3	US-08-040-741-6	Sequence 6, Appli
610	71	4.0	1276	4	US-09-297-937C-13	Sequence 13, Appl
611	71	4.0	1338	3	US-08-750-141A-3	Sequence 3, Appli
612	71	4.0	1338	4	US-09-119-014D-6	Sequence 6, Appli
613	71	4.0	1362	2	US-08-874-678-33	Sequence 33, Appl
614	71	4.0	1362	3	US-08-643-839-33	Sequence 33, Appl
615	71	4.0	1362	4	US-09-348-886-33	Sequence 33, Appl
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617	71	4.0	1481	2	US-08-599-654-40	Sequence 40, Appl
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619	71	4.0	1481	3	US-08-944-423A-40	Sequence 40, Appl
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634	70.5	4.0	617	3	US-09-188-930-303	Sequence 303, App
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ALIGNMENTS

RESULT 1
US-09-149-476-483
; Sequence 483, Application US/09149476
; Patent No. 6420526
; GENERAL INFORMATION:
; APPLICANT: Rosen et al.
; TITLE OF INVENTION: 186 Human Secreted proteins
; FILE REFERENCE: PZ002P1
; CURRENT APPLICATION NUMBER: US/09/149,476
; CURRENT FILING DATE: 1998-09-08
; EARLIER APPLICATION NUMBER: PCT/US98/04493
; EARLIER FILING DATE: 1998-03-06
; EARLIER APPLICATION NUMBER: 60/040,162
; EARLIER FILING DATE: 1997-03-07
; EARLIER APPLICATION NUMBER: 60/040,333
; EARLIER FILING DATE: 1997-03-07
; EARLIER APPLICATION NUMBER: 60/038,621
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; EARLIER APPLICATION NUMBER: 60/057,650
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; EARLIER APPLICATION NUMBER: 60/057,669
; EARLIER FILING DATE: 1997-09-05

; EARLIER APPLICATION NUMBER: 60/049,610
; EARLIER FILING DATE: 1997-06-13
; EARLIER APPLICATION NUMBER: 60/061,060
; EARLIER FILING DATE: 1997-10-02

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Best Local Similarity 31.5%; Pred. No. 1.6e-30;
Matches 107; Conservative 55; Mismatches 143; Indels 35; Gaps 10;

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RESULT 2
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; Sequence 10, Application US/08348792
; Patent No. 5576423
; GENERAL INFORMATION:
; APPLICANT: Aversa, Gregorio
; APPLICANT: Chang, Chia-Chun J.
; APPLICANT: Cocks, Benjamin G.
; APPLICANT: de Vries, Jan E.
; TITLE OF INVENTION: PURIFIED GENES ENCODING MAMMALIAN CELL
; TITLE OF INVENTION: SURFACE ANTIGENS; PROTEINS AND ANTIBODIES
; NUMBER OF SEQUENCES: 12
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: DNAX Research Institute
; STREET: 901 California Avenue
; CITY: Palo Alto
; STATE: California
; COUNTRY: USA
; ZIP: 94304-1104
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Floppy disk
; COMPUTER: IBM PC compatible
; OPERATING SYSTEM: PC-DOS/MS-DOS
; SOFTWARE: PatentIn Release #1.0, Version #1.25
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/08/348,792
; FILING DATE: 02-DEC-1994
; CLASSIFICATION: 530
; ATTORNEY/AGENT INFORMATION:
; NAME: Ching, Edwin P.
; REGISTRATION NUMBER: 34,090
; REFERENCE/DOCKET NUMBER: DX0436
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: 415-852-9196
; TELEFAX: 415-496-1200
; INFORMATION FOR SEQ ID NO: 10:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 343 amino acids
; TYPE: amino acid

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;      TOPOLOGY:  linear
;    MOLECULE TYPE:  protein
US-08-348-792-10

  Query Match             10.5%;  Score 186;  DB 1;  Length 343;
  Best Local Similarity   24.3%;  Pred. No. 2.1e-11;
  Matches   89;  Conservative   64;  Mismatches  130;  Indels   84;  Gaps   21;

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RESULT 3
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; Patent No. 5977303
;  GENERAL INFORMATION:
;    APPLICANT:  Aversa, Gregorio
;    APPLICANT:  Chang, Chia-Chun J.
;    APPLICANT:  Cocks, Benjamin G.
;    APPLICANT:  de Vries, Jan E.
;    TITLE OF INVENTION:  PURIFIED GENES ENCODING MAMMALIAN CELL
;    TITLE OF INVENTION:  SURFACE ANTIGENS; PROTEINS AND ANTIBODIES
;    NUMBER OF SEQUENCES:  12
;    CORRESPONDENCE ADDRESS:
;      ADDRESSEE:  DNAX Research Institute
;      STREET:  901 California Avenue
;      CITY:  Palo Alto
;      STATE:  California
;      COUNTRY:  USA
;      ZIP:  94304-1104
;    COMPUTER READABLE FORM:
;      MEDIUM TYPE:  Floppy disk
;      COMPUTER:  IBM PC compatible
;      OPERATING SYSTEM:  PC-DOS/MS-DOS
;      SOFTWARE:  PatentIn Release #1.0, Version #1.25
;    CURRENT APPLICATION DATA:
;      APPLICATION NUMBER:  US/08/462,738
;      FILING DATE:  05-JUN-1995
;      CLASSIFICATION:  435
;    PRIOR APPLICATION DATA:
;      APPLICATION NUMBER:  US 08/348,792
;      FILING DATE:  02-DEC-1994
;    ATTORNEY/AGENT INFORMATION:
;      NAME:  Ching, Edwin P.
;      REGISTRATION NUMBER:  34,090
;      REFERENCE/DOCKET NUMBER:  DX0436GB
;    TELECOMMUNICATION INFORMATION:
;      TELEPHONE:  415-852-9196
;      TELEFAX:  415-496-1200
;  INFORMATION FOR SEQ ID NO:  10:
;    SEQUENCE CHARACTERISTICS:
;      LENGTH:  343 amino acids
;      TYPE:  amino acid
;      TOPOLOGY:  linear
;    MOLECULE TYPE:  protein
US-08-462-738-10

  Query Match             10.5%;  Score 186;  DB 2;  Length 343;
  Best Local Similarity   24.3%;  Pred. No. 2.1e-11;
  Matches   89;  Conservative   64;  Mismatches  130;  Indels   84;  Gaps   21;

Qy          8 LTLIYILWQLTGSAASG----PVKELVGSVGGAVTFPL-------KSKVKQVDSIVWTFN 56
              |  : : ::|:     |    ||  ::  :|     ||       ||  | |  :| |
Db         12 LLFLSLAFELSYGTGGGVMDCPV--ILQKLGQDTWLPLTNEHQINKSVNKSVRILV-TMA 68

Qy         57 TTPLVTIQPEGGTIIVTQNRNRERVDF-------PD---GGY-------SLKLSKLKKND 99
              |:|                  |:: | |       ||    ||       |||:   ::
Db         69 TSP-------------GSKSNKKIVSFDLSKGSYPDHLEDGYHFQSKNLSLKILGNRRES 115

Qy        100 SGIYYVGIYSS-SLQQPSTQEYVLHVYEHLSKP--KVTMGLQSNKNGTCVTNLTCCMEHG 156
              | | | :  : |:||   |   | :|| :| |  ||    | |:|||   | | :: |
Db        116 EGWYLVSVEENVSVQQFCKQ---LKLYEQVSPPEIKVLNKTQENENGTCSLLLACTVKKG 172

Qy        157 EEDVIYTWK-----ALGQAANESHNGSILPISWRWGESDMTFICVARNPV---SRNFSSP 208
              :  | |:|       |   || ||   :| |:      |  : | | |||   || |:
Db        173 DH-VTYSWSDEAGTHLLSRANRSH---LLHITLSNQHQDSIYNCTASNPVSSISRTFN-- 226

Qy        209 ILARKLCEGAADDPDSSMVLLCLLLVPLLLSLFVLGLFLWFLKRERQEEYIE---EKKRV 265
              |: : |:  :    |  :   |: : :::   ::   :  :||: :  : :   |:| :
Db        227 -LSSQACKQESSSESSPWMQYTLVPLGVVIIFILVFTAIIMMKRQGKSNHCQPPVEEKSL 285

Qy        266 DICRETPNICPHSGENTEYDTIPHTNRTILKEDPANTVY--STVEIPKKMENP-----HS 318
              | :     |   |   :|        :  :||  |:|  :|   |: :: |     ::
Db        286 TIYAQVQKSGPQ--EKKLHD-------ALTDQDPCTTIYVAATEPAPESVQEPNPTTVYA 336

Qy        319 LLTMPDT 325
              :|:|::
Db        337 SVTLPES 343


RESULT 4
US-09-199-955-10
; Sequence 10, Application US/09199955
; Patent No. 6372899
;  GENERAL INFORMATION:
;    APPLICANT:  Aversa, Gregorio
;    APPLICANT:  Chang, Chia-Chun J.
;    APPLICANT:  Cocks, Benjamin G.
;    APPLICANT:  de Vries, Jan E.
;    TITLE OF INVENTION:  PURIFIED GENES ENCODING MAMMALIAN CELL
;    TITLE OF INVENTION:  SURFACE ANTIGENS: PROTEINS AND ANTIBODIES
;    NUMBER OF SEQUENCES:  12
;    CORRESPONDENCE ADDRESS:
;      ADDRESSEE:  DNAX Research Institute
;      STREET:  901 California Avenue
;      CITY:  Palo Alto
;      STATE:  California
;      COUNTRY:  USA
;      ZIP:  94304-1104
;    COMPUTER READABLE FORM:
;      MEDIUM TYPE:  Floppy disk
;      COMPUTER:  IBM PC compatible
;      OPERATING SYSTEM:  PC-DOS/MS-DOS
;      SOFTWARE:  PatentIn Release #1.0, Version #1.25
;    CURRENT APPLICATION DATA:
;      APPLICATION NUMBER:  US/09/199,955
;      FILING DATE:
;      CLASSIFICATION:
;    PRIOR APPLICATION DATA:
;      APPLICATION NUMBER:  US 08/461,473
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;      FILING DATE:  05-JUN-1995
;      APPLICATION NUMBER:  US 08/348,792
;      FILING DATE:  02-DEC-1994
;    ATTORNEY/AGENT INFORMATION:
;      NAME:  Ching, Edwin P.
;      REGISTRATION NUMBER:  34,090
;      REFERENCE/DOCKET NUMBER:  DX0436GC
;    TELECOMMUNICATION INFORMATION:
;      TELEPHONE:  415-852-9196
;      TELEFAX:  415-496-1200
;  INFORMATION FOR SEQ ID NO:  10:
;    SEQUENCE CHARACTERISTICS:
;      LENGTH:  343 amino acids
;      TYPE:  amino acid
;      TOPOLOGY:  linear
;    MOLECULE TYPE:  protein
US-09-199-955-10

  Query Match             10.5%;  Score 186;  DB 4;  Length 343;
  Best Local Similarity   24.3%;  Pred. No. 2.1e-11;
  Matches   89;  Conservative   64;  Mismatches  130;  Indels   84;  Gaps   21;

Qy          8 LTLIYILWQLTGSAASG----PVKELVGSVGGAVTFPL-------KSKVKQVDSIVWTFN 56
              |  : : ::|:     |    ||  ::  :|     ||       ||  | |  :| |
Db         12 LLFLSLAFELSYGTGGGVMDCPV--ILQKLGQDTWLPLTNEHQINKSVNKSVRILV-TMA 68

Qy         57 TTPLVTIQPEGGTIIVTQNRNRERVDF-------PD---GGY-------SLKLSKLKKND 99
              |:|                  |:: | |       ||    ||       |||:   ::
Db         69 TSP------------GSKSNKKIVSFDLSKGSYPDHLEDGYHFQSKNLSLKILGNRRES 115

Qy        100 SGIYYVGIYSS-SLQQPSTQEYVLHVYEHLSKP--KVTMGLQSNKNGTCVTNLTCCMEHG 156
              | | | :  : |:||   |   | :|| :| |  ||    | |:|||   | | :: |
Db        116 EGWYLVSVEENVSVQQFCKQ---LKLYEQVSPPEIKVLNKTQENENGTCSLLLACTVKKG 172

Qy        157 EEDVIYTWK-----ALGQAANESHNGSILPISWRWGESDMTFICVARNPV---SRNFSSP 208
              :  | |:|       |   || ||   :| |:      | : | | |||   || |:
Db        173 DH-VTYSWSDEAGTHLLSRANRSH---LLHITLSNQHQDSIYNCTASNPVSSISRTFN-- 226

Qy        209 ILARKLCEGAADDPDSSMVLLCLLLVPLLLSLFVLGLFLWFLKRERQEEYIE---EKKRV 265
              |: : |:  :    |  :   |: : :::   ::   :  :||: :  : :   |:| :
Db        227 -LSSQACKQESSSESSPWMQYTLVPLGVVIIFILVFTAIIMMKRQGKSNHCQPPVEEKSL 285

Qy        266 DICRETPNICPHSGENTEYDTIPHTNRTILKEDPANTVY--STVEIPKKMENP-----HS 318
              |  :     |   |   :|       :  :||  :|  :|  :|   |: : : |     ::
Db        286 TIYAQVQKSGPQ--EKKLHD-------ALTDQDPCTTIYVAATEPAPESVQEPNPTTVYA 336

Qy        319 LLTMPDT 325
               :|:|::
Db        337 SVTLPES 343


RESULT 5
US-08-880-875-10
; Sequence 10, Application US/08880875
; Patent No. 6399065
;  GENERAL INFORMATION:
;    APPLICANT:  Aversa, Gregorio
;    APPLICANT:  Chang, Chia-Chun J.
;    APPLICANT:  Cocks, Benjamin G.
;    APPLICANT:  de Vries, Jan E.
;    TITLE OF INVENTION:  PURIFIED GENES ENCODING MAMMALIAN CELL
;    TITLE OF INVENTION:  SURFACE ANTIGENS; PROTEINS AND ANTIBODIES
;    NUMBER OF SEQUENCES:  12
;    CORRESPONDENCE ADDRESS:
;      ADDRESSEE:  DNAX Research Institute
;      STREET:  901 California Avenue
;      CITY:  Palo Alto
;      STATE:  California
;      COUNTRY:  USA
;      ZIP:  94304-1104
;    COMPUTER READABLE FORM:
;      MEDIUM TYPE:  Floppy disk
;      COMPUTER:  IBM PC compatible
;      OPERATING SYSTEM:  PC-DOS/MS-DOS
;      SOFTWARE:  PatentIn Release #1.0, Version #1.25
;    CURRENT APPLICATION DATA:
;      APPLICATION NUMBER:  US/08/880,875
;      FILING DATE:
;      CLASSIFICATION:  435
;    PRIOR APPLICATION DATA:
;      APPLICATION NUMBER:  US 08/481,777
;      FILING DATE:  07-JUN-1995
;      APPLICATION NUMBER:  US 08/348,792
;      FILING DATE:  02-DEC-1994
;    ATTORNEY/AGENT INFORMATION:
;      NAME:  Ching, Edwin P.
;      REGISTRATION NUMBER:  34,090
;      REFERENCE/DOCKET NUMBER:  DX0436K
;    TELECOMMUNICATION INFORMATION:
;      TELEPHONE:  415-852-9196
;      TELEFAX:  415-496-1200
;  INFORMATION FOR SEQ ID NO:  10:
;    SEQUENCE CHARACTERISTICS:
;      LENGTH:  343 amino acids
;      TYPE:  amino acid
;      TOPOLOGY:  linear
;    MOLECULE TYPE:  protein
US-08-880-875-10

  Query Match             10.5%;  Score 186;  DB 4;  Length 343;
  Best Local Similarity   24.3%;  Pred. No. 2.1e-11;
  Matches   89;  Conservative   64;  Mismatches  130;  Indels   84;  Gaps   21;

Qy          8 LTLIYILWQLTGSAASG----PVKELVGSVGGAVTFPL-------KSKVKQVDSIVWTFN 56
              |  : : ::|:     |    ||  ::  :|     ||       ||  | |  :| |
Db         12 LLFLSLAFELSYGTGGGVMDCPV--ILQKLGQDTWLPLTNEHQINKSVNKSVRILV-TMA 68

Qy         57 TTPLVTIQPEGGTIIVTQNRNRERVDF-------PD---GGY-------SLKLSKLKKND 99
              |:|                  |:: | |       ||    ||       |||:   ::
Db         69 TSP------------GSKSNKKIVSFDLSKGSYPDHLEDGYHFQSKNLSLKILGNRRES 115

Qy        100 SGIYYVGIYSS-SLQQPSTQEYVLHVYEHLSKP--KVTMGLQSNKNGTCVTNLTCCMEHG 156
              | | | :  : |:||   |   | :|| :| |  ||    | |:|||   | | :: |
Db        116 EGWYLVSVEENVSVQQFCKQ---LKLYEQVSPPEIKVLNKTQENENGTCSLLLACTVKKG 172

Qy        157 EEDVIYTWK-----ALGQAANESHNGSILPISWRWGESDMTFICVARNPV---SRNFSSP 208
              :  | |:|       |   || ||   :| |:      | : | | |||   || |:
Db        173 DH-VTYSWSDEAGTHLLSRANRSH---LLHITLSNQHQDSIYNCTASNPVSSISRTFN-- 226

Qy        209 ILARKLCEGAADDPDSSMVLLCLLLVPLLLSLFVLGLFLWFLKRERQEEYIE---EKKRV 265
              |: : |:  :    |  :   |: : :::   ::   :  :||: :  : :   |:| :
Db        227 -LSSQACKQESSSESSPWMQYTLVPLGVVIIFILVFTAIIMMKRQGKSNHCQPPVEEKSL 285

Qy        266 DICRETPNICPHSGENTEYDTIPHTNRTILKEDPANTVY--STVEIPKKMENP-----HS 318
              |  :     |   |   :|       :  :||  :|  :|  :|   |: : : |     ::
Db        286 TIYAQVQKSGPQ--EKKLHD-------ALTDQDPCTTIYVAATEPAPESVQEPNPTTVYA 336

Qy        319 LLTMPDT 325
               :|:|::
Db        337 SVTLPES 343


RESULT 6
US-08-348-792-2
; Sequence 2, Application US/08348792
; Patent No. 5576423
;  GENERAL INFORMATION:
;    APPLICANT:  Aversa, Gregorio
;    APPLICANT:  Chang, Chia-Chun J.
;    APPLICANT:  Cocks, Benjamin G.
;    APPLICANT:  de Vries, Jan E.
;    TITLE OF INVENTION:  PURIFIED GENES ENCODING MAMMALIAN CELL
;    TITLE OF INVENTION:  SURFACE ANTIGENS; PROTEINS AND ANTIBODIES
;    NUMBER OF SEQUENCES:  12
;    CORRESPONDENCE ADDRESS:
;      ADDRESSEE:  DNAX Research Institute
```

```
;      STREET:  901 California Avenue
;      CITY:  Palo Alto
;      STATE:  California
;      COUNTRY:  USA
;      ZIP:  94304-1104
;    COMPUTER READABLE FORM:
;      MEDIUM TYPE:  Floppy disk
;      COMPUTER:  IBM PC compatible
;      OPERATING SYSTEM:  PC-DOS/MS-DOS
;      SOFTWARE:  PatentIn Release #1.0, Version #1.25
;    CURRENT APPLICATION DATA:
;      APPLICATION NUMBER:  US/08/348,792
;      FILING DATE:  02-DEC-1994
;      CLASSIFICATION:  530
;    ATTORNEY/AGENT INFORMATION:
;      NAME:  Ching, Edwin P.
;      REGISTRATION NUMBER:  34,090
;      REFERENCE/DOCKET NUMBER:  DX0436
;    TELECOMMUNICATION INFORMATION:
;      TELEPHONE:  415-852-9196
;      TELEFAX:  415-496-1200
;  INFORMATION FOR SEQ ID NO:  2:
;    SEQUENCE CHARACTERISTICS:
;      LENGTH:  335 amino acids
;      TYPE:  amino acid
;      TOPOLOGY:  linear
;    MOLECULE TYPE:  protein
US-08-348-792-2

  Query Match           10.3%;  Score 182.5;  DB 1;  Length 335;
  Best Local Similarity   22.5%;  Pred. No. 4.8e-11;
  Matches   82;  Conservative   72;  Mismatches  129;  Indels   81;  Gaps   19;

Qy          8 LTLIYILW-QLTGSAASGP------VKELVGSVGGAVTFPL------KSKVKQVDSIVWT 54
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Db          7 LSLTFVLFLSLAFGASYGTGGRMMNCPKILRQLGSKVLLPLTYERINKSMNKSIHIVVTM 66

Qy         55 FNT------TPLVTIQP-EGGTIIVTQNRNRERVDFPDGGYSLKLSKLKKNDSGIYYVGI 107
                :       :|:: | | |          :|  |      :| : : :| | | | : :
Db         67 AKSLENSVENKIVSLDPSEAG----PPRYLGDRYKFYLENLTLGIRESRKEDEGWYLMTL 122

Qy        108 YSS-SLQQPSTQEYVLHVYEHLSKPKVTMGLQSNKNGTCVTNLTCCMEHGEEDVIYTW-- 164
                : |:|:    |    | :|| :| |:: :  :: :|||    | | :| |:  | |:|
Db        123 EKNVSVQRFCLQ---LRLYEQVSTPEIKVLNKTQENGTCTLILGCTVEKGDH-VAYSWSE 178

Qy        165 KALGQAANESHNGSILPISWRWGESDMTFICVARNPVSRNFS--SPILARKLCEGAADDP 222
              ||     | :::  :| ::     :|  :||   ||:| |    ||          |  ||
Db        179 KAGTHPLNPANSSHLLSLTLGPQHADNIYICTVSNPISNNSQTFSP------WPGCRTDP 232

Qy        223 DSSM-----------VLLCLLLVPLLLSLFVLGLFLWFLKRERQEEYIE---EKKRVDIC 268
                :            |:: |::| :|          |:|  :  : :   ||| : |
Db        233 SETKPWAVYAGLLGGVIMILIMVVILQ-----------LRRRGKTNHYQTTVEKKSLTIY 281

Qy        269 RETPNICPHSGENTEYDTIPHTNRTILKEDPANTVY--STVEIPKKMENPHSL-----LT 321
              :     |     : |: |        :||  |:|  :|  :|: ::  :|:     :|
Db        282 AQVQKPGP---LQKKLDSFP-------AQDPCTTIYVAATEPVPESVQETNSITVYASVT 331

Qy        322 MPDT 325
              :|::
Db        332 LPES 335


RESULT 7
US-08-462-738-2
; Sequence 2, Application US/08462738
; Patent No. 5977303
;  GENERAL INFORMATION:
;    APPLICANT:  Aversa, Gregorio
;    APPLICANT:  Chang, Chia-Chun J.
;    APPLICANT:  Cocks, Benjamin G.
;    APPLICANT:  de Vries, Jan E.
;    TITLE OF INVENTION:  PURIFIED GENES ENCODING MAMMALIAN CELL
;    TITLE OF INVENTION:  SURFACE ANTIGENS; PROTEINS AND ANTIBODIES
;    NUMBER OF SEQUENCES:  12
;    CORRESPONDENCE ADDRESS:
;      ADDRESSEE:  DNAX Research Institute
;      STREET:  901 California Avenue
;      CITY:  Palo Alto
;      STATE:  California
;      COUNTRY:  USA
;      ZIP:  94304-1104
;    COMPUTER READABLE FORM:
;      MEDIUM TYPE:  Floppy disk
;      COMPUTER:  IBM PC compatible
;      OPERATING SYSTEM:  PC-DOS/MS-DOS
;      SOFTWARE:  PatentIn Release #1.0, Version #1.25
;    CURRENT APPLICATION DATA:
;      APPLICATION NUMBER:  US/08/462,738
;      FILING DATE:  05-JUN-1995
;      CLASSIFICATION:  435
;    PRIOR APPLICATION DATA:
;      APPLICATION NUMBER:  US 08/348,792
;      FILING DATE:  02-DEC-1994
;    ATTORNEY/AGENT INFORMATION:
;      NAME:  Ching, Edwin P.
;      REGISTRATION NUMBER:  34,090
;      REFERENCE/DOCKET NUMBER:  DX0436GB
;    TELECOMMUNICATION INFORMATION:
;      TELEPHONE:  415-852-9196
;      TELEFAX:  415-496-1200
;  INFORMATION FOR SEQ ID NO:  2:
;    SEQUENCE CHARACTERISTICS:
;      LENGTH:  335 amino acids
;      TYPE:  amino acid
;      TOPOLOGY:  linear
;    MOLECULE TYPE:  protein
US-08-462-738-2

  Query Match           10.3%;  Score 182.5;  DB 2;  Length 335;
  Best Local Similarity   22.5%;  Pred. No. 4.8e-11;
  Matches   82;  Conservative   72;  Mismatches  129;  Indels   81;  Gaps   19;

Qy          8 LTLIYILW-QLTGSAASGP------VKELVGSVGGAVTFPL------KSKVKQVDSIVWT 54
              |:| ::|:  |   |: |          :::  :|  |  ||      ||  | :  :| -
Db          7 LSLTFVLFLSLAFGASYGTGGRMMNCPKILRQLGSKVLLPLTYERINKSMNKSIHIVVTM 66

Qy         55 FNT------TPLVTIQP-EGGTIIVTQNRNRERVDFPDGGYSLKLSKLKKNDSGIYYVGI 107
                :       :|:: | | |          :|  |      :| : : :| | | | : :
Db         67 AKSLENSVENKIVSLDPSEAG----PPRYLGDRYKFYLENLTLGIRESRKEDEGWYLMTL 122

Qy        108 YSS-SLQQPSTQEYVLHVYEHLSKPKVTMGLQSNKNGTCVTNLTCCMEHGEEDVIYTW-- 164
                : |:|:    |    | :|| :| |:: :  :: :|||    | | :| |:  | |:|
Db        123 EKNVSVQRFCLQ---LRLYEQVSTPEIKVLNKTQENGTCTLILGCTVEKGDH-VAYSWSE 178

Qy        165 KALGQAANESHNGSILPISWRWGESDMTFICVARNPVSRNFS--SPILARKLCEGAADDP 222
              ||     | :::  :| ::     :|  :||   ||:| |    ||          |  ||
Db        179 KAGTHPLNPANSSHLLSLTLGPQHADNIYICTVSNPISNNSQTFSP------WPGCRTDP 232

Qy        223 DSSM-----------VLLCLLLVPLLLSLFVLGLFLWFLKRERQEEYIE---EKKRVDIC 268
                :            |:: |::| :|          |:|  :  : :   ||| : |
Db        233 SETKPWAVYAGLLGGVIMILIMVVILQ-----------LRRRGKTNHYQTTVEKKSLTIY 281

Qy        269 RETPNICPHSGENTEYDTIPHTNRTILKEDPANTVY--STVEIPKKMENPHSL-----LT 321
              :     |     : |: |        :||  |:|  :|  :|: ::  :|:     :|
Db        282 AQVQKPGP---LQKKLDSFP-------AQDPCTTIYVAATEPVPESVQETNSITVYASVT 331

Qy        322 MPDT 325
              :|::
Db        332 LPES 335


RESULT 8
US-09-199-955-2
; Sequence 2, Application US/09199955
; Patent No. 6372899
;  GENERAL INFORMATION:
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;    APPLICANT:  Aversa, Gregorio
;    APPLICANT:  Chang, Chia-Chun J.
;    APPLICANT:  Cocks, Benjamin G.
;    APPLICANT:  de Vries, Jan E.
;    TITLE OF INVENTION:  PURIFIED GENES ENCODING MAMMALIAN CELL
;    TITLE OF INVENTION:  SURFACE ANTIGENS: PROTEINS AND ANTIBODIES
;    NUMBER OF SEQUENCES:  12
;    CORRESPONDENCE ADDRESS:
;      ADDRESSEE:  DNAX Research Institute
;      STREET:  901 California Avenue
;      CITY:  Palo Alto
;      STATE:  California
;      COUNTRY:  USA
;      ZIP:  94304-1104
;    COMPUTER READABLE FORM:
;      MEDIUM TYPE:  Floppy disk
;      COMPUTER:  IBM PC compatible
;      OPERATING SYSTEM:  PC-DOS/MS-DOS
;      SOFTWARE:  PatentIn Release #1.0, Version #1.25
;    CURRENT APPLICATION DATA:
;      APPLICATION NUMBER:  US/09/199,955
;      FILING DATE:
;      CLASSIFICATION:
;    PRIOR APPLICATION DATA:
;      APPLICATION NUMBER:  US 08/461,473
;      FILING DATE:  05-JUN-1995
;      APPLICATION NUMBER:  US 08/348,792
;      FILING DATE:  02-DEC-1994
;    ATTORNEY/AGENT INFORMATION:
;      NAME:  Ching, Edwin P.
;      REGISTRATION NUMBER:  34,090
;      REFERENCE/DOCKET NUMBER:  DX0436GC
;    TELECOMMUNICATION INFORMATION:
;      TELEPHONE:  415-852-9196
;      TELEFAX:  415-496-1200
;  INFORMATION FOR SEQ ID NO:  2:
;    SEQUENCE CHARACTERISTICS:
;      LENGTH:  335 amino acids
;      TYPE:  amino acid
;      TOPOLOGY:  linear
;    MOLECULE TYPE:  protein
US-09-199-955-2

  Query Match           10.3%;  Score 182.5;  DB 4;  Length 335;
  Best Local Similarity   22.5%;  Pred. No. 4.8e-11;
  Matches   82;  Conservative   72;  Mismatches  129;  Indels   81;  Gaps   19;

Qy          8 LTLIYILW-QLTGSAASGP------VKELVGSVGGAVTFPL------KSKVKQVDSIVWT 54
              |:| ::|:  |   |: |          :::  :|  |  ||      ||  | :  :|
Db          7 LSLTFVLFLSLAFGASYGTGGRMMNCPKILRQLGSKVLLPLTYERINKSMNKSIHIVVTM 66

Qy         55 FNT------TPLVTIQP-EGGTIIVTQNRNRERVDFPDGGYSLKLSKLKKNDSGIYYVGI 107
               :         :|:: | | |          :|  |      :| : : :| | | | : :
Db         67 AKSLENSVENKIVSLDPSEAG----PPRYLGDRYKFYLENLTLGIRESRKEDEGWYLMTL 122

Qy        108 YSS-SLQQPSTQEYVLHVYEHLSKPKVTMGLQSNKNGTCVTNLTCCMEHGEEDVIYTW-- 164
               : |:|:   |   | :|| :| |:: :  :: :||||   | | :| |:  | |:|
Db        123 EKNVSVQRFCLQ---LRLYEQVSTPEIKVLNKTQENGTCTLILGCTVEKGDH-VAYSWSE 178

Qy        165 KALGQAANESHNGSILPISWRWGESDMTFICVARNPVSRNFS--SPILARKLCEGAADDP 222
              ||      | :::  :| ::      :|  :||   ||:| |    ||         |   ||
Db        179 KAGTHPLNPANSSHLLSLTLGPQHADNIYICTVSNPISNNSQTFSP------WPGCRTDP 232

Qy        223 DSSM----------VLLCLLLVPLLLSLFVLGLFLWFLKRERQEEYIE---EKKRVDIC 268
               :           |:: |::| :|           |:|  :  : :   ||| : |
Db        233 SETKPWAVYAGLLGGVIMILIMVVILQ----------LRRRGKTNHYQTTVEKKSLTIY 281

Qy        269 RETPNICPHSGENTEYDTIPHTNRTILKEDPANTVY--STVEIPKKMENPHSL-----LT 321
               :     |      : |: |         :||  |:|  :|  :|: ::  :|:     :|
Db        282 AQVQKPGP---LQKKLDSFP-------AQDPCTTIYVAATEPVPESVQETNSITVYASVT 331

Qy        322 MPDT 325
              :|::
Db        332 LPES 335


RESULT 9
US-08-880-875-2
; Sequence 2, Application US/08880875
; Patent No. 6399065
;  GENERAL INFORMATION:
;    APPLICANT:  Aversa, Gregorio
;    APPLICANT:  Chang, Chia-Chun J.
;    APPLICANT:  Cocks, Benjamin G.
;    APPLICANT:  de Vries, Jan E.
;    TITLE OF INVENTION:  PURIFIED GENES ENCODING MAMMALIAN CELL
;    TITLE OF INVENTION:  SURFACE ANTIGENS; PROTEINS AND ANTIBODIES
;    NUMBER OF SEQUENCES:  12
;    CORRESPONDENCE ADDRESS:
;      ADDRESSEE:  DNAX Research Institute
;      STREET:  901 California Avenue
;      CITY:  Palo Alto
;      STATE:  California
;      COUNTRY:  USA
;      ZIP:  94304-1104
;    COMPUTER READABLE FORM:
;      MEDIUM TYPE:  Floppy disk
;      COMPUTER:  IBM PC compatible
;      OPERATING SYSTEM:  PC-DOS/MS-DOS
;      SOFTWARE:  PatentIn Release #1.0, Version #1.25
;    CURRENT APPLICATION DATA:
;      APPLICATION NUMBER:  US/08/880,875
;      FILING DATE:
;      CLASSIFICATION:  435
;    PRIOR APPLICATION DATA:
;      APPLICATION NUMBER:  US 08/481,777
;      FILING DATE:  07-JUN-1995
;      APPLICATION NUMBER:  US 08/348,792
;      FILING DATE:  02-DEC-1994
;    ATTORNEY/AGENT INFORMATION:
;      NAME:  Ching, Edwin P.
;      REGISTRATION NUMBER:  34,090
;      REFERENCE/DOCKET NUMBER:  DX0436K
;    TELECOMMUNICATION INFORMATION:
;      TELEPHONE:  415-852-9196
;      TELEFAX:  415-496-1200
;  INFORMATION FOR SEQ ID NO:  2:
;    SEQUENCE CHARACTERISTICS:
;      LENGTH:  335 amino acids
;      TYPE:  amino acid
;      TOPOLOGY:  linear
;    MOLECULE TYPE:  protein
US-08-880-875-2

  Query Match           10.3%;  Score 182.5;  DB 4;  Length 335;
  Best Local Similarity   22.5%;  Pred. No. 4.8e-11;
  Matches   82;  Conservative   72;  Mismatches  129;  Indels   81;  Gaps   19;

Qy          8 LTLIYILW-QLTGSAASGP------VKELVGSVGGAVTFPL------KSKVKQVDSIVWT 54
              |:| ::|:  |   |: |          :::  :|  |  ||      ||  | :  :|
Db          7 LSLTFVLFLSLAFGASYGTGGRMMNCPKILRQLGSKVLLPLTYERINKSMNKSIHIVVTM 66

Qy         55 FNT------TPLVTIQP-EGGTIIVTQNRNRERVDFPDGGYSLKLSKLKKNDSGIYYVGI 107
               :         :|:: | | |          :|  |      :| : : :| | | | : :
Db         67 AKSLENSVENKIVSLDPSEAG----PPRYLGDRYKFYLENLTLGIRESRKEDEGWYLMTL 122

Qy        108 YSS-SLQQPSTQEYVLHVYEHLSKPKVTMGLQSNKNGTCVTNLTCCMEHGEEDVIYTW-- 164
               : |:|:   |   | :|| :| |:: :  :: :||||   | | :| |:  | |:|
Db        123 EKNVSVQRFCLQ---LRLYEQVSTPEIKVLNKTQENGTCTLILGCTVEKGDH-VAYSWSE 178

Qy        165 KALGQAANESHNGSILPISWRWGESDMTFICVARNPVSRNFS--SPILARKLCEGAADDP 222
              ||      | :::  :| ::      :|  :||   ||:| |    ||         |   ||
Db        179 KAGTHPLNPANSSHLLSLTLGPQHADNIYICTVSNPISNNSQTFSP------WPGCRTDP 232

Qy        223 DSSM----------VLLCLLLVPLLLSLFVLGLFLWFLKRERQEEYIE---EKKRVDIC 268
               :           |:: |::| :|           |:|  :  : :   ||| : |
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Db        233 SETKPWAVYAGLLGGVIMILIMVVILQ----------LRRRGKTNHYQTTVEKKSLTIY 281

Qy        269 RETPNICPHSGENTEYDTIPHTNRTILKEDPANTVY--STVEIPKKMENPHSL-----LT 321
              :      |      : |: |        :||  |:|  :|  :|: ::  :|:     :|
Db        282 AQVQKPGP---LQKKLDSFP-------AQDPCTTIYVAATEPVPESVQETNSITVYASVT 331

Qy        322 MPDT 325
              :|::
Db        332 LPES 335


RESULT 10
US-09-369-248A-3
; Sequence 3, Application US/09369248A
; Patent No. 6620912
; GENERAL INFORMATION:
;  APPLICANT:  Young, Paul
;  APPLICANT:  Ruben, Steven M.
;  TITLE OF INVENTION:  Dendritic Enriched Secreted Lymphocyte Activation
;  TITLE OF INVENTION:  Molecule
;  FILE REFERENCE:  PF448P1
;  CURRENT APPLICATION NUMBER: US/09/369,248A
;  CURRENT FILING DATE:  1999-08-05
;  PRIOR APPLICATION NUMBER:  60/073,962
;  PRIOR FILING DATE:  1998-02-06
;  PRIOR APPLICATION NUMBER:  60/078,572
;  PRIOR FILING DATE:  1998-03-19
;  NUMBER OF SEQ ID NOS:  13
;  SOFTWARE:  PatentIn Ver. 2.1
; SEQ ID NO 3
;   LENGTH: 335
;   TYPE: PRT
;   ORGANISM: Homo sapiens
US-09-369-248A-3

  Query Match           10.3%;  Score 182.5;  DB 4;  Length 335;
  Best Local Similarity   22.5%;  Pred. No. 4.8e-11;
  Matches   82;  Conservative   72;  Mismatches  129;  Indels   81;  Gaps   19;

Qy          8 LTLIYILW-QLTGSAASGP------VKELVGSVGGAVTFPL------KSKVKQVDSIVWT 54
              |:| ::|:  |   |:  |          :::  :|  |  ||      ||  | :  :|
Db          7 LSLTFVLFLSLAFGASYGTGGRMMNCPKILRQLGSKVLLPLTYERINKSMNKSIHIVVTM 66

Qy         55 FNT------TPLVTIQP-EGGTIIVTQNRNRERVDFPDGGYSLKLSKLKKNDSGIYYVGI 107
                :        :|:: | | |          :|  |      :| : : :| | | | : :
Db         67 AKSLENSVENKIVSLDPSEAG----PPRYLGDRYKFYLENLTLGIRESRKEDEGWYLMTL 122

Qy        108 YSS-SLQQPSTQEYVLHVYEHLSKPKVTMGLQSNKNGTCVTNLTCCMEHGEEDVIYTW-- 164
                : |:|:   |   | :|| :| |::  :  :: :|||   | | :| |:  | |:|
Db        123 EKNVSVQRFCLQ---LRLYEQVSTPEIKVLNKTQENGTCTLILGCTVEKGDH-VAYSWSE 178

Qy        165 KALGQAANESHNGSILPISWRWGESDMTFICVARNPVSRNFS--SPILARKLCEGAADDP 222
              ||      | :::  :| ::      :|  :||   ||:| |   ||        |   ||
Db        179 KAGTHPLNPANSSHLLSLTLGPQHADNIYICTVSNPISNNSQTFSP------WPGCRTDP 232

Qy        223 DSSM----------VLLCLLLVPLLLSLFVLGLFLWFLKRERQEEYIE---EKKRVDIC 268
                :           |:: |:: | :|            |:|  :  : :   ||| : |
Db        233 SETKPWAVYAGLLGGVIMILIMVVILQ----------LRRRGKTNHYQTTVEKKSLTIY 281

Qy        269 RETPNICPHSGENTEYDTIPHTNRTILKEDPANTVY--STVEIPKKMENPHSL-----LT 321
              :      |      : |: |        :||  |:|  :|  :|: ::  :|:     :|
Db        282 AQVQKPGP---LQKKLDSFP-------AQDPCTTIYVAATEPVPESVQETNSITVYASVT 331

Qy        322 MPDT 325
              :|::
Db        332 LPES 335


RESULT 11
US-08-348-792-8
; Sequence 8, Application US/08348792
; Patent No. 5576423
;  GENERAL INFORMATION:
;     APPLICANT:  Aversa, Gregorio
;     APPLICANT:  Chang, Chia-Chun J.
;     APPLICANT:  Cocks, Benjamin G.
;     APPLICANT:  de Vries, Jan E.
;     TITLE OF INVENTION:  PURIFIED GENES ENCODING MAMMALIAN CELL
;     TITLE OF INVENTION:  SURFACE ANTIGENS; PROTEINS AND ANTIBODIES
;     NUMBER OF SEQUENCES:  12
;     CORRESPONDENCE ADDRESS:
;       ADDRESSEE:  DNAX Research Institute
;       STREET:  901 California Avenue
;       CITY:  Palo Alto
;       STATE:  California
;       COUNTRY:  USA
;       ZIP:  94304-1104
;     COMPUTER READABLE FORM:
;       MEDIUM TYPE:  Floppy disk
;       COMPUTER:  IBM PC compatible
;       OPERATING SYSTEM:  PC-DOS/MS-DOS
;       SOFTWARE:  PatentIn Release #1.0, Version #1.25
;     CURRENT APPLICATION DATA:
;       APPLICATION NUMBER:  US/08/348,792
;       FILING DATE:  02-DEC-1994
;       CLASSIFICATION:  530
;     ATTORNEY/AGENT INFORMATION:
;       NAME:  Ching, Edwin P.
;       REGISTRATION NUMBER:  34,090
;       REFERENCE/DOCKET NUMBER:  DX0436
;     TELECOMMUNICATION INFORMATION:
;       TELEPHONE:  415-852-9196
;       TELEFAX:  415-496-1200
;   INFORMATION FOR SEQ ID NO:  8:
;     SEQUENCE CHARACTERISTICS:
;       LENGTH:  307 amino acids
;       TYPE:  amino acid
;       TOPOLOGY:  linear
;     MOLECULE TYPE:  protein
US-08-348-792-8

  Query Match           10.2%;  Score 180;  DB 1;  Length 307;
  Best Local Similarity   22.6%;  Pred. No. 7.8e-11;
  Matches   76;  Conservative   67;  Mismatches  120;  Indels   74;  Gaps   17;

Qy         28 ELVGSVGGAVTFPL------KSKVKQVDSIVWTFNT------TPLVTIQP-EGGTIIVTQ 74
              :::  :|  |  ||      ||  | :  :|    :       :|:: | | |
Db          6 KILRQLGSKVLLPLTYERINKSMNKSIHIVVTMAKSLENSVENKIVSLDPSEAG----PP 61

Qy         75 NRNRERVDFPDGGYSLKLSKLKKNDSGIYYVGIYSS-SLQQPSTQEYVLHVYEHLSKPKV 133
                 :|  |      :| : : :| | | | : :  : |:|:    |   | :|| :| |::
Db         62 RYLGDRYKFYLENLTLGIRESRKEDEGWYLMTLEKNVSVQRFCLQ---LRLYEQVSTPEI 118

Qy        134 TMGLQSNKNGTCVTNLTCCMEHGEEDVIYTW--KALGQAANESHNGSILPISWRWGESDM 191
                :  :: :||||   | | :| |:  | |:|  ||      | :::  :| ::     :|
Db        119 KVLNKTQENGTCTLILGCTVEKGDH-VAYSWSEKAGTHPLNPANSSHLLSLTLGPQHADN 177

Qy        192 TFICVARNPVSRNFS--SPILARKLCEGAADDPDSSM----------VLLCLLLVPLLL 238
              :||   ||:| |    ||         |   ||  :            |:: |::| :|
Db        178 IYICTVSNPISNNSQTFSP------WPGCRTDPSETKPWAVYAGLLGGVIMILIMVVILQ 231

Qy        239 SLFVLGLFLWFLKRERQEEYIE---EKKRVDICRETPNICPHSGENTEYDTIPHTNRTIL 295
                        |:|  :  : :   ||| : |  :      |       : |: |
Db        232 ----------LRRRGKTNHYQTTVEKKSLTIYAQVQKPGP---LQKKLDSFP------- 270

Qy        296 KEDPANTVY--STVEIPKKMENPHSL-----LTMPDT 325
              :||  |:|  :|  :|: ::  :|:     :|:|::
Db        271 AQDPCTTIYVAATEPVPESVQETNSITVYASVTLPES 307


RESULT 12
US-08-462-738-8
; Sequence 8, Application US/08462738
; Patent No. 5977303
;  GENERAL INFORMATION:
;     APPLICANT:  Aversa, Gregorio
```

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;    APPLICANT:  Chang, Chia-Chun J.
;    APPLICANT:  Cocks, Benjamin G.
;    APPLICANT:  de Vries, Jan E.
;    TITLE OF INVENTION:  PURIFIED GENES ENCODING MAMMALIAN CELL
;    TITLE OF INVENTION:  SURFACE ANTIGENS; PROTEINS AND ANTIBODIES
;    NUMBER OF SEQUENCES:  12
;    CORRESPONDENCE ADDRESS:
;      ADDRESSEE:  DNAX Research Institute
;      STREET:  901 California Avenue
;      CITY:  Palo Alto
;      STATE:  California
;      COUNTRY:  USA
;      ZIP:  94304-1104
;    COMPUTER READABLE FORM:
;      MEDIUM TYPE:  Floppy disk
;      COMPUTER:  IBM PC compatible
;      OPERATING SYSTEM:  PC-DOS/MS-DOS
;      SOFTWARE:  PatentIn Release #1.0, Version #1.25
;    CURRENT APPLICATION DATA:
;      APPLICATION NUMBER:  US/08/462,738
;      FILING DATE:  05-JUN-1995
;      CLASSIFICATION:  435
;    PRIOR APPLICATION DATA:
;      APPLICATION NUMBER:  US 08/348,792
;      FILING DATE:  02-DEC-1994
;    ATTORNEY/AGENT INFORMATION:
;      NAME:  Ching, Edwin P.
;      REGISTRATION NUMBER:  34,090
;      REFERENCE/DOCKET NUMBER:  DX0436GB
;    TELECOMMUNICATION INFORMATION:
;      TELEPHONE:  415-852-9196
;      TELEFAX:  415-496-1200
;  INFORMATION FOR SEQ ID NO:  8:
;    SEQUENCE CHARACTERISTICS:
;      LENGTH:  307 amino acids
;      TYPE:  amino acid
;      TOPOLOGY:  linear
;    MOLECULE TYPE:  protein
US-08-462-738-8

  Query Match             10.2%;  Score 180;  DB 2;  Length 307;
  Best Local Similarity   22.6%;  Pred. No. 7.8e-11;
  Matches   76;  Conservative   67;  Mismatches  120;  Indels   74;  Gaps   17;

Qy         28 ELVGSVGGAVTFPL------KSKVKQVDSIVWTFNT------TPLVTIQP-EGGTIIVTQ 74
              :::  :|  |  ||      ||  | :  :|    :        :|:: | | |
Db          6 KILRQLGSKVLLPLTYERINKSMNKSIHIVVTMAKSLENSVENKIVSLDPSEAG----PP 61

Qy         75 NRNRERVDFPDGGYSLKLSKLKKNDSGIYYVGIYSS-SLQQPSTQEYVLHVYEHLSKPKV 133
                :|  |      :| : : :| | | | : :  : |:|:   |   | :|| :| |::
Db         62 RYLGDRYKFYLENLTLGIRESRKEDEGWYLMTLEKNVSVQRFCLQ---LRLYEQVSTPEI 118

Qy        134 TMGLQSNKNGTCVTNLTCCMEHGEEDVIYTW--KALGQAANESHNGSILPISWRWGESDM 191
               :  :: :||||   | | :| |:  | |:|  ||     | :::  :| ::     :|
Db        119 KVLNKTQENGTCTLILGCTVEKGDH-VAYSWSEKAGTHPLNPANSSHLLSLTLGPQHADN 177

Qy        192 TFICVARNPVSRNFS--SPILARKLCEGAADDPDSSM-----------VLLCLLLVPLLL 238
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Db        178 IYICTVSNPISNNSQTFSP------WPGCRTDPSETKPWAVYAGLLGGVIMILIMVVILQ 231

Qy        239 SLFVLGLFLWFLKRERQEEYIE---EKKRVDICRETPNICPHSGENTEYDTIPHTNRTIL 295
                        |:|  :  : :   ||| : |  :      |      : |: |
Db        232 ----------LRRRGKTNHYQTTVEKKSLTIYAQVQKPGP---LQKKLDSFP------- 270

Qy        296 KEDPANTVY--STVEIPKKMENPHSL-----LTMPDT 325
               :||  |:|  :|  :|: ::  :|:     :|:|::
Db        271 AQDPCTTIYVAATEPVPESVQETNSITVYASVTLPES 307


RESULT 13
US-09-199-955-8
; Sequence 8, Application US/09199955
; Patent No. 6372899
;  GENERAL INFORMATION:
;    APPLICANT:  Aversa, Gregorio
;    APPLICANT:  Chang, Chia-Chun J.
;    APPLICANT:  Cocks, Benjamin G.
;    APPLICANT:  de Vries, Jan E.
;    TITLE OF INVENTION:  PURIFIED GENES ENCODING MAMMALIAN CELL
;    TITLE OF INVENTION:  SURFACE ANTIGENS: PROTEINS AND ANTIBODIES
;    NUMBER OF SEQUENCES:  12
;    CORRESPONDENCE ADDRESS:
;      ADDRESSEE:  DNAX Research Institute
;      STREET:  901 California Avenue
;      CITY:  Palo Alto
;      STATE:  California
;      COUNTRY:  USA
;      ZIP:  94304-1104
;    COMPUTER READABLE FORM:
;      MEDIUM TYPE:  Floppy disk
;      COMPUTER:  IBM PC compatible
;      OPERATING SYSTEM:  PC-DOS/MS-DOS
;      SOFTWARE:  PatentIn Release #1.0, Version #1.25
;    CURRENT APPLICATION DATA:
;      APPLICATION NUMBER:  US/09/199,955
;      FILING DATE:
;      CLASSIFICATION:
;    PRIOR APPLICATION DATA:
;      APPLICATION NUMBER:  US 08/461,473
;      FILING DATE:  05-JUN-1995
;      APPLICATION NUMBER:  US 08/348,792
;      FILING DATE:  02-DEC-1994
;    ATTORNEY/AGENT INFORMATION:
;      NAME:  Ching, Edwin P.
;      REGISTRATION NUMBER:  34,090
;      REFERENCE/DOCKET NUMBER:  DX0436GC
;    TELECOMMUNICATION INFORMATION:
;      TELEPHONE:  415-852-9196
;      TELEFAX:  415-496-1200
;  INFORMATION FOR SEQ ID NO:  8:
;    SEQUENCE CHARACTERISTICS:
;      LENGTH:  307 amino acids
;      TYPE:  amino acid
;      TOPOLOGY:  linear
;    MOLECULE TYPE:  protein
US-09-199-955-8

  Query Match             10.2%;  Score 180;  DB 4;  Length 307;
  Best Local Similarity   22.6%;  Pred. No. 7.8e-11;
  Matches   76;  Conservative   67;  Mismatches  120;  Indels   74;  Gaps   17;

Qy         28 ELVGSVGGAVTFPL------KSKVKQVDSIVWTFNT------TPLVTIQP-EGGTIIVTQ 74
              :::  :|  |  ||      ||  | :  :|    :        :|:: | | |
Db          6 KILRQLGSKVLLPLTYERINKSMNKSIHIVVTMAKSLENSVENKIVSLDPSEAG----PP 61

Qy         75 NRNRERVDFPDGGYSLKLSKLKKNDSGIYYVGIYSS-SLQQPSTQEYVLHVYEHLSKPKV 133
                :|  |      :| : : :| | | | : :  : |:|:   |   | :|| :| |::
Db         62 RYLGDRYKFYLENLTLGIRESRKEDEGWYLMTLEKNVSVQRFCLQ---LRLYEQVSTPEI 118

Qy        134 TMGLQSNKNGTCVTNLTCCMEHGEEDVIYTW--KALGQAANESHNGSILPISWRWGESDM 191
               :  :: :||||   | | :| |:  | |:|  ||     | :::  :| ::     :|
Db        119 KVLNKTQENGTCTLILGCTVEKGDH-VAYSWSEKAGTHPLNPANSSHLLSLTLGPQHADN 177

Qy        192 TFICVARNPVSRNFS--SPILARKLCEGAADDPDSSM-----------VLLCLLLVPLLL 238
               :||   ||:| |   ||       |   ||  :             |:: |::| :|
Db        178 IYICTVSNPISNNSQTFSP------WPGCRTDPSETKPWAVYAGLLGGVIMILIMVVILQ 231

Qy        239 SLFVLGLFLWFLKRERQEEYIE---EKKRVDICRETPNICPHSGENTEYDTIPHTNRTIL 295
                        |:|  :  : :   ||| : |  :      |      : |: |
Db        232 ----------LRRRGKTNHYQTTVEKKSLTIYAQVQKPGP---LQKKLDSFP------- 270

Qy        296 KEDPANTVY--STVEIPKKMENPHSL-----LTMPDT 325
               :||  |:|  :|  :|: ::  :|:     :|:|::
Db        271 AQDPCTTIYVAATEPVPESVQETNSITVYASVTLPES 307
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RESULT 14
US-08-880-875-8
; Sequence 8, Application US/08880875
; Patent No. 6399065
;  GENERAL INFORMATION:
;    APPLICANT:  Aversa, Gregorio
;    APPLICANT:  Chang, Chia-Chun J.
;    APPLICANT:  Cocks, Benjamin G.
;    APPLICANT:  de Vries, Jan E.
;    TITLE OF INVENTION:  PURIFIED GENES ENCODING MAMMALIAN CELL
;    TITLE OF INVENTION:  SURFACE ANTIGENS; PROTEINS AND ANTIBODIES
;    NUMBER OF SEQUENCES:  12
;    CORRESPONDENCE ADDRESS:
;      ADDRESSEE:  DNAX Research Institute
;      STREET:  901 California Avenue
;      CITY:  Palo Alto
;      STATE:  California
;      COUNTRY:  USA
;      ZIP:  94304-1104
;    COMPUTER READABLE FORM:
;      MEDIUM TYPE:  Floppy disk
;      COMPUTER:  IBM PC compatible
;      OPERATING SYSTEM:  PC-DOS/MS-DOS
;      SOFTWARE:  PatentIn Release #1.0, Version #1.25
;    CURRENT APPLICATION DATA:
;      APPLICATION NUMBER:  US/08/880,875
;      FILING DATE:
;      CLASSIFICATION:  435
;    PRIOR APPLICATION DATA:
;      APPLICATION NUMBER:  US 08/481,777
;      FILING DATE:  07-JUN-1995
;      APPLICATION NUMBER:  US 08/348,792
;      FILING DATE:  02-DEC-1994
;    ATTORNEY/AGENT INFORMATION:
;      NAME:  Ching, Edwin P.
;      REGISTRATION NUMBER:  34,090
;      REFERENCE/DOCKET NUMBER:  DX0436K
;    TELECOMMUNICATION INFORMATION:
;      TELEPHONE:  415-852-9196
;      TELEFAX:  415-496-1200
;  INFORMATION FOR SEQ ID NO:  8:
;    SEQUENCE CHARACTERISTICS:
;      LENGTH:  307 amino acids
;      TYPE:  amino acid
;      TOPOLOGY:  linear
;    MOLECULE TYPE:  protein
US-08-880-875-8

  Query Match             10.2%;  Score 180;  DB 4;  Length 307;
  Best Local Similarity   22.6%;  Pred. No. 7.8e-11;
  Matches   76;  Conservative   67;  Mismatches  120;  Indels   74;  Gaps   17;

Qy         28 ELVGSVGGAVTFPL------KSKVKQVDSIVWTFNT------TPLVTIQP-EGGTIIVTQ 74
              :::  :|  |  ||      ||  | :  :|    :        :|:: | | |
Db          6 KILRQLGSKVLLPLTYERINKSMNKSIHIVVTMAKSLENSVENKIVSLDPSEAG----PP 61

Qy         75 NRNRERVDFPDGGYSLKLSKLKKNDSGIYYVGIYSS-SLQQPSTQEYVLHVYEHLSKPKV 133
                :|  |     :| : : :| | | | : :  : |:|:   |   | :|| :| |::
Db         62 RYLGDRYKFYLENLTLGIRESRKEDEGWYLMTLEKNVSVQRFCLQ---LRLYEQVSTPEI 118

Qy        134 TMGLQSNKNGTCVTNLTCCMEHGEEDVIYTW--KALGQAANESHNGSILPISWRWGESDM 191
               :  :: :|||   | | :| |:  | |:|  ||     | :::  :| ::     :|
Db        119 KVLNKTQENGTCTLILGCTVEKGDH-VAYSWSEKAGTHPLNPANSSHLLSLTLGPQHADN 177

Qy        192 TFICVARNPVSRNFS--SPILARKLCEGAADDPDSSM----------VLLCLLLVPLLL 238
              :||   ||:| |   ||       |   ||  :           |:: |::| :|
Db        178 IYICTVSNPISNNSQTFSP------WPGCRTDPSETKPWAVYAGLLGGVIMILIMVVILQ 231

Qy        239 SLFVLGLFLWFLKRERQEEYIE---EKKRVDICRETPNICPHSGENTEYDTIPHTNRTIL 295
                          |:|  :  : :   ||| : |  :      |      : |: |
Db        232 ----------LRRRGKTNHYQTTVEKKSLTIYAQVQKPGP---LQKKLDSFP------- 270

Qy        296 KEDPANTVY--STVEIPKKMENPHSL-----LTMPDT 325
```

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                :||  |:|  :|  :|: ::  :|:     :|:|::
Db        271 AQDPCTTIYVAATEPVPESVQETNSITVYASVTLPES 307


RESULT 15
US-08-348-792-6
; Sequence 6, Application US/08348792
; Patent No. 5576423
;  GENERAL INFORMATION:
;    APPLICANT:  Aversa, Gregorio
;    APPLICANT:  Chang, Chia-Chun J.
;    APPLICANT:  Cocks, Benjamin G.
;    APPLICANT:  de Vries, Jan E.
;    TITLE OF INVENTION:  PURIFIED GENES ENCODING MAMMALIAN CELL
;    TITLE OF INVENTION:  SURFACE ANTIGENS; PROTEINS AND ANTIBODIES
;    NUMBER OF SEQUENCES:  12
;    CORRESPONDENCE ADDRESS:
;      ADDRESSEE:  DNAX Research Institute
;      STREET:  901 California Avenue
;      CITY:  Palo Alto
;      STATE:  California
;      COUNTRY:  USA
;      ZIP:  94304-1104
;    COMPUTER READABLE FORM:
;      MEDIUM TYPE:  Floppy disk
;      COMPUTER:  IBM PC compatible
;      OPERATING SYSTEM:  PC-DOS/MS-DOS
;      SOFTWARE:  PatentIn Release #1.0, Version #1.25
;    CURRENT APPLICATION DATA:
;      APPLICATION NUMBER:  US/08/348,792
;      FILING DATE:  02-DEC-1994
;      CLASSIFICATION:  530
;    ATTORNEY/AGENT INFORMATION:
;      NAME:  Ching, Edwin P.
;      REGISTRATION NUMBER:  34,090
;      REFERENCE/DOCKET NUMBER:  DX0436
;    TELECOMMUNICATION INFORMATION:
;      TELEPHONE:  415-852-9196
;      TELEFAX:  415-496-1200
;  INFORMATION FOR SEQ ID NO:  6:
;    SEQUENCE CHARACTERISTICS:
;      LENGTH:  305 amino acids
;      TYPE:  amino acid
;      TOPOLOGY:  linear
;    MOLECULE TYPE:  protein
US-08-348-792-6

  Query Match             9.3%;  Score 164.5;  DB 1;  Length 305;
  Best Local Similarity   21.7%;  Pred. No. 3.7e-09;
  Matches   76;  Conservative   64;  Mismatches  127;  Indels   83;  Gaps   17;

Qy          8 LTLIYILW-QLTGSAASGP------VKELVGSVGGAVTFPL------KSKVKQVDSIVWT 54
              |:| ::|:  |   |: |          :::  :|  |  ||      || | :  :|
Db          7 LSLTFVLFLSLAFGASYGTGGRMMNCPKILRQLGSKVLLPLTYERINKSMNKSIHIVVTM 66

Qy         55 FNT------TPLVTIQP-EGGTIIVTQNRNRERVDFPDGGYSLKLSKLKKNDSGIYYVGI 107
                :       :|:: | | |     :|  |       :| : : :| | | : :
Db         67 AKSLENSVENKIVSLDPSEAG----PPRYLGDRYKFYLENLTLGIRESRKEDEGWYLMTL 122

Qy        108 YSS-SLQQPSTQEYVLHVYEHLSKPKVTMGLQSNKNGTCVTNLTCCMEHGEEDVIYTW-- 164
               : |:|:   |   | :|| :| |:: :  :: :|||   | | :| |:  | |:|
Db        123 EKNVSVQRFCLQ---LRLYEQVSTPEIKVLNKTQENGTCTLILGCTVEKGDH-VAYSWSE 178

Qy        165 KALGQAANESHNGSILPISWRWGESDMTFICVARNPVSRNFS--SPILARKLCEGAADDP 222
              ||      | :::  :| ::      :|  :||   ||:| |    ||         |  ||
Db        179 KAGTHPLNPANSSHLLSLTLGPQHADNIYICTVSNPISNNSQTFSP------WPGCRTDP 232

Qy        223 DSSMVLLCLLLVPLLLSLFVLGLFLWFLKRERQEEYIEEKKRVDICRETPNICPHSGENT 282
                                       :    :   ||| : |  :      |
Db        233 SG-------------------------KTNHYQTTVEKKSLTIYAQVQKPGP---LQK 262

Qy        283 EYDTIPHTNRTILKEDPANTVY--STVEIPKKMENPHSL-----LTMPDT 325
              : |: |        :||  |:|  :|  :|: ::  :|:     :|:|::
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Db 263 KLDSFP-------AQDPCTTIYVAATEPVPESVQETNSITVYASVTLPES 305

Search completed: August 18, 2004, 15:45:20
Job time : 22 secs

GenCore version 5.1.6

OM protein - protein search, using sw model

Run on: August 18, 2004, 15:49:27 ; Search time 17 Seconds
(without alignments)
1895.539 Million cell updates/sec

Title: US-10-063-549-46
Perfect score: 1772
Sequence: 1 MAGSPTCLTLIYILWQLTGS.....PHSLLTMPDTPRLFAYENVI 335

Scoring table: BLOSUM62
Gapop 10.0 , Gapext 0.5

Searched: 283366 seqs, 96191526 residues

Total number of hits satisfying chosen parameters: 283366

Minimum DB seq length: 0
Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%
Maximum Match 100%
Listing first 700 summaries

Database : PIR_78:*
1: pir1:*
2: pir2:*
3: pir3:*
4: pir4:*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	% Query Match	Length	DB	ID	Description
1	343	19.4	629	2	A46500	Ly-9.2 antigen - m
2	182.5	10.3	335	2	S58892	signaling lymphocy
3	144	8.1	344	2	B28967	T-cell surface gly
4	138	7.8	344	2	I49585	CD2 antigen protei
5	136.5	7.7	351	1	RWHUC2	T-cell surface gly
6	134	7.6	240	2	S01299	OX-45 membrane gly
7	130	7.3	344	1	RWRTC2	T-cell surface gly
8	126.5	7.1	240	2	JL0143	antigen BCM1 precu
9	125.5	7.1	321	2	JH0395	biliary glycoprote
10	125.5	7.1	351	2	JH0396	biliary glycoprote
11	125.5	7.1	417	2	JH0394	biliary glycoprote
12	125.5	7.1	464	2	C30127	transmembrane carc
13	125.5	7.1	526	1	A32164	biliary glycoprote
14	124.5	7.0	344	2	A27681	nonspecific cross-
15	122.5	6.9	521	2	S34338	biliary glycoprote
16	119	6.7	458	2	JC1509	biliary glycoprote
17	114.5	6.5	702	2	A36319	carcinoembryonic a
18	113.5	6.4	458	1	WMMSR1	biliary glycoprote
19	113.5	6.4	521	2	JC1508	biliary glycoprote
20	109.5	6.2	432	2	S30193	T-cell surface gly
21	108.5	6.1	365	2	JC7780	coxsackie- and ade
22	107.5	6.1	398	2	I49443	gene 2B4 protein -
23	106	6.0	897	2	G84613	hypothetical prote
24	105.5	6.0	329	1	A48754	B7-2 antigen - hum
25	104	5.9	349	2	A34815	carcinoembryonic a
26	102.5	5.8	458	2	S23969	cell-adhesion mole
27	102.5	5.8	526	2	A37821	butyrophilin - bov
28	101.5	5.7	761	2	T00940	hypothetical prote
29	101	5.7	587	2	JH0464	DM-GRASP precursor
30	101	5.7	588	2	JH0506	adhesion molecule
31	100.5	5.7	259	2	A86822	hypothetical prote
32	100	5.6	392	2	B44194	poliovirus recepto
33	99	5.6	417	2	A44194	poliovirus recepto
34	99	5.6	588	2	A45254	surface glycoprote
35	98.5	5.6	1227	2	T23004	hypothetical prote
36	98	5.5	347	2	S41638	T-cell surface gly
37	98	5.5	503	2	JC5287	SHP substrate-1 pr
38	97	5.5	523	2	I50478	neurolin - goldfis
39	97	5.5	773	1	QRRBG	secretory componen
40	96.5	5.4	402	2	A40678	T-cell adhesion re
41	96	5.4	210	2	S36297	T-cell receptor ga
42	96	5.4	526	2	S70587	butyrophilin precu
43	96	5.4	1087	2	I51552	platelet-derived g
44	96	5.4	1451	2	S42167	190K protein - hum
45	95.5	5.4	341	2	JC1512	biliary glycoprote
46	95.5	5.4	417	1	RWHUPA	poliovirus recepto
47	95.5	5.4	458	2	S68177	C-CAM2a protein is
48	95.5	5.4	519	2	A44783	ecto-ATPase precur
49	95.5	5.4	700	1	S12053	protein-tyrosine-p
50	94.5	5.3	218	2	A36198	T-cell receptor be
51	94	5.3	233	2	JH0372	42K surface glycop
52	94	5.3	1088	1	IJXLNL	neural cell adhesi
53	93.5	5.3	2409	1	A60979	versican precursor
54	93	5.2	419	2	A36109	pregnancy-specific
55	93	5.2	419	2	B54312	pregnancy-specific
56	93	5.2	419	2	JC4123	pregnancy-specific
57	92.5	5.2	299	2	S56749	junctional adhesio
58	92.5	5.2	330	2	I46691	CD86 precursor - r
59	92.5	5.2	761	2	A96810	probable Mutator-l
60	92	5.2	822	2	T01095	hypothetical prote
61	91.5	5.2	1079	2	T28197	probable DNA-direc
62	91	5.1	417	2	A28277	pregnancy-specific
63	91	5.1	419	2	A33258	pregnancy-specific
64	91	5.1	426	2	B33258	pregnancy-specific
65	91	5.1	467	1	HLMSP3	poliovirus recepto
66	90	5.1	250	2	A28564	lymphocyte functio
67	90	5.1	395	2	D43354	pregnancy-specific
68	90	5.1	397	2	C43354	pregnancy-specific
69	90	5.1	406	2	E43354	pregnancy-specific
70	90	5.1	419	2	A31135	pregnancy-specific
71	90	5.1	426	2	A35964	pregnancy-specific
72	90	5.1	426	2	A35341	pregnancy-specific
73	90	5.1	428	2	A27658	pregnancy-specific
74	89.5	5.1	243	2	A53244	leukocyte antigen
75	89.5	5.1	349	2	E84968	outer membrane pro
76	89.5	5.1	428	2	T36565	probable penicilli
77	89	5.0	309	2	I49522	gene B7-2 protein
78	89	5.0	341	2	JC1511	biliary glycoprote
79	89	5.0	821	1	CIHUH3	calpain (EC 3.4.22
80	89	5.0	5175	2	T20992	hypothetical prote
81	89	5.0	5198	2	T43290	hemicentin precurs
82	88.5	5.0	1390	1	TVHUME	hepatocyte growth
83	88	5.0	363	2	F70195	UDP-N-acetylglucos
84	88	5.0	422	2	A71147	hypothetical prote
85	88	5.0	530	2	A53437	poliovirus recepto
86	88	5.0	668	2	S56909	polymyxin B resist
87	88	5.0	699	2	JC6132	protein-tyrosine-p
88	88	5.0	821	1	B34488	calpain (EC 3.4.22
89	88	5.0	1092	1	JN0635	neural cell adhesi
90	88	5.0	6669	2	S55024	nebulin, skeletal
91	87.5	4.9	265	2	A55811	carcinoembryonic a
92	87.5	4.9	276	2	S20690	31.6K hypothetical
93	87.5	4.9	392	1	RWHUPD	poliovirus recepto
94	87.5	4.9	769	1	QRRTGS	secretory componen
95	87.5	4.9	2340	2	I48310	kinase-related pro
96	87.5	4.9	4162	2	T42633	connectin/titin -
97	87	4.9	457	1	RWMST4	T-cell surface gly
98	87	4.9	583	2	I39428	alcam - human
99	87	4.9	1666	2	A48594	skelemin - mouse
100	87	4.9	1907	2	S50893	protein-tyrosine-p
101	87	4.9	3707	2	S18252	heparan sulfate pr
102	86.5	4.9	528	2	B75364	extracellular solu

103	86	4.9	212	2	C33258	pregnancy-specific
104	86	4.9	354	1	VGBE67	glycoprotein D pre
105	86	4.9	428	2	I57486	pregnancy-specific
106	86	4.9	885	2	B86257	NBS/LRR disease re
107	86	4.9	1327	2	T09402	immunoglobulin-lik
108	85.5	4.8	324	2	G43354	pregnancy-specific
109	85.5	4.8	326	2	F43354	pregnancy-specific
110	85.5	4.8	333	2	A43354	pregnancy-specific
111	85.5	4.8	335	2	H43354	pregnancy-specific
112	85.5	4.8	941	1	TVMVMD	protein-tyrosine k
113	85.5	4.8	2588	2	T14342	NSD1 protein - mou
114	85	4.8	428	2	JS0032	pregnancy-specific
115	85	4.8	731	2	T16524	hypothetical prote
116	85	4.8	757	1	S48841	secretory componen
117	84.5	4.8	656	2	A96724	hypothetical prote
118	84	4.7	275	2	JC7604	CD86 spliced varia
119	84	4.7	851	2	D90216	hypothetical prote
120	84	4.7	1379	1	S01254	hepatocyte growth
121	84	4.7	1499	2	I50212	protein-tyrosine-p
122	84	4.7	3034	2	T14119	seven-pass transme
123	83.5	4.7	315	2	H71009	probable prolifera
124	83.5	4.7	392	2	T33444	hypothetical prote
125	83.5	4.7	656	2	B49423	semaphorin I - fru
126	83.5	4.7	775	2	T21436	hypothetical prote
127	83.5	4.7	1501	2	I58148	protein-tyrosine-p
128	83.5	4.7	1863	2	S46217	protein-tyrosine-p
129	83	4.7	335	2	A33514	pregnancy-specific
130	83	4.7	757	2	I45956	polymeric immunogl
131	83	4.7	873	1	A49729	VLDL receptor prec
132	83	4.7	925	2	T37475	lipoprotein recept
133	83	4.7	1106	2	T29496	hypothetical prote
134	83	4.7	2489	2	S59782	probable membrane
135	82.5	4.7	393	2	B96780	hypothetical prote
136	82.5	4.7	826	2	B36203	iron-responsive el
137	82.5	4.7	1004	2	A71617	SERA antigen/papai
138	82.5	4.7	26926	1	I38344	titin, cardiac mus
139	82	4.6	386	2	B69666	Na+ ABC transporte
140	82	4.6	609	2	S43009	hemagglutinin - ri
141	82	4.6	880	2	B53743	protein-tyrosine k
142	82	4.6	3562	2	A47171	chondroitin sulfat
143	81.5	4.6	278	1	TDRTOX	OX-2 membrane glyc
144	81.5	4.6	352	2	I77374	pregnancy-specific
145	81.5	4.6	355	2	T06122	cysteine proteinas
146	81.5	4.6	378	2	S00842	leukosialin precur
147	81.5	4.6	497	2	D97264	galactose-1-phosph
148	81.5	4.6	524	2	S44982	flagellin - Shigel
149	81.5	4.6	708	2	T48022	hypothetical prote
150	81	4.6	335	2	B33251	nonspecific cross-
151	81	4.6	338	2	JC4776	limbic-system-asso
152	81	4.6	374	2	S57750	naringenin 3-dioxy
153	81	4.6	760	2	S19374	probable membrane
154	81	4.6	769	2	E97092	glycosyltransferas
155	81	4.6	829	1	IJHUCP	cadherin 3 precurs
156	81	4.6	1898	2	S46216	leukocyte antigen-
157	81	4.6	1941	2	T30554	ubiquitin-protein
158	80.5	4.5	346	2	S46993	elk ligand - human
159	80.5	4.5	376	2	E85435	cysteine proteinas
160	80.5	4.5	462	2	H97292	UDP-N-acetylmuramo
161	80.5	4.5	473	2	AG0612	probable transport
162	80.5	4.5	475	2	I76668	pregnancy-specific
163	80.5	4.5	540	2	H90751	probable transport
164	80.5	4.5	540	2	F85615	probable transport
165	80.5	4.5	540	2	B64829	membrane protein b
166	80.5	4.5	721	2	T09631	probable acylamino
167	80.5	4.5	823	2	T08092	plus fringe glycop
168	80.5	4.5	3343	2	S44887	ZK112.7 protein -
169	80.5	4.5	6642	2	T29757	protein UNC-89 - C
170	80	4.5	307	1	RWMSBC	T-cell receptor be
171	80	4.5	341	2	I61725	natural killer ass
172	80	4.5	343	2	G90680	probable periplasm
173	80	4.5	343	2	C85531	periplasmic ferric
174	80	4.5	454	2	A46532	Ig mu chain C regi
175	80	4.5	482	2	JH0110	arginine/ornithine
176	80	4.5	1040	2	A49356	transient axonal g
177	80	4.5	1170	2	A40558	thrombospondin 1 p
178	79.5	4.5	134	2	I46627	rearranged T-cell
179	79.5	4.5	249	1	A61087	myelin P0 glycopro
180	79.5	4.5	273	2	B28928	pregnancy-specific
181	79.5	4.5	275	2	A28928	pregnancy-specific
182	79.5	4.5	282	2	C28928	pregnancy-specific
183	79.5	4.5	289	2	G90314	oxidoreductase [im
184	79.5	4.5	328	2	JQ1121	cysteine proteinas
185	79.5	4.5	400	2	AI0104	probable galactosi
186	79.5	4.5	430	2	T28143	tapasin 1 homolog,
187	79.5	4.5	446	2	T34782	probable signal pe
188	79.5	4.5	490	2	I41293	EcoE type I restri
189	79.5	4.5	769	2	S16236	fibroblast growth
190	79.5	4.5	822	2	A45081	fibroblast growth
191	79.5	4.5	822	2	A41794	keratinocyte growt
192	79.5	4.5	873	1	I48952	VLDL receptor prec
193	79.5	4.5	980	1	TVCTMD	macrophage colony-
194	79.5	4.5	1465	2	S43529	165K protein, skel
195	79.5	4.5	2491	1	A28372	insulin-like growt
196	79	4.5	210	2	C87256	hypothetical prote
197	79	4.5	244	2	AC1765	B. subtilis TagA p
198	79	4.5	438	2	G64513	hypothetical prote
199	79	4.5	479	2	G84099	carboxy-terminal p
200	79	4.5	584	2	T08678	hypothetical prote
201	79	4.5	657	2	S77543	short-chain alcoho
202	79	4.5	903	2	T20804	hypothetical prote
203	79	4.5	1228	2	G96751	hypothetical prote
204	79	4.5	1361	2	T30884	neural specific DN
205	78.5	4.4	235	2	S25750	Ig lambda chain -
206	78.5	4.4	429	1	EHRT	Ig epsilon chain C
207	78.5	4.4	497	2	C91225	probable oxidoredu
208	78.5	4.4	497	2	A86072	probable oxidoredu
209	78.5	4.4	539	2	T01513	CTP synthase (EC 6
210	78.5	4.4	588	2	I37202	B-CAM protein - hu
211	78.5	4.4	628	2	I38000	Lutheran blood gro
212	78.5	4.4	638	2	T51383	receptor protein k
213	78.5	4.4	831	2	S39835	hypothetical prote
214	78.5	4.4	847	2	JH0371	B-cell adhesion pr
215	78.5	4.4	1036	2	S22383	axonin 1 precursor
216	78.5	4.4	1038	2	AG2187	hypothetical prote
217	78.5	4.4	1468	2	T05672	hypothetical prote
218	78	4.4	257	2	A97121	undecaprenyl pyrop
219	78	4.4	272	2	I48268	biliary glycoprote
220	78	4.4	286	2	A28333	carcinoembryonic a
221	78	4.4	335	2	C54312	pregnancy-specific
222	78	4.4	402	2	T09062	probable advanced
223	78	4.4	490	2	T43184	DEAD box ATP-depen
224	78	4.4	604	2	T41249	DEAD box ATP-depen
225	78	4.4	608	2	AB3562	gtp-binding protei
226	78	4.4	609	1	HMNZKA	hemagglutinin - ri
227	78	4.4	761	1	IJHUNG	neural cell adhesi
228	78	4.4	836	2	T42323	hypothetical prote
229	78	4.4	905	2	S43064	cadherin - African
230	78	4.4	905	2	T38314	probable vacuolar
231	77.5	4.4	172	2	T34227	hypothetical prote
232	77.5	4.4	214	2	C89833	hypothetical prote
233	77.5	4.4	236	2	T41012	conserved hypothet
234	77.5	4.4	239	2	I46082	CD8 alpha-chain -
235	77.5	4.4	448	2	H98007	exodeoxyribonuclea
236	77.5	4.4	509	2	JC5288	SHP substrate-1 pr
237	77.5	4.4	513	2	JC5289	SHP substrate-1 pr
238	77.5	4.4	539	2	G86465	F12G12.2 protein -
239	77.5	4.4	591	2	H83362	gluconate dehydrog
240	77.5	4.4	717	2	AD3097	ferrienterobactin-
241	77.5	4.4	717	2	E98189	ferrienterobactin-
242	77.5	4.4	739	2	A41288	vascular cell adhe
243	77.5	4.4	757	1	S64742	dynamin-related pr
244	77.5	4.4	863	2	S06017	neuraxin - rat
245	77.5	4.4	881	2	S03068	env protein - huma
246	77.5	4.4	968	2	T25667	hypothetical prote
247	77.5	4.4	991	2	T48631	polynucleotide pho
248	77.5	4.4	1015	2	T32186	hypothetical prote

249	77.5	4.4	1099	2	T18713	hypothetical prote
250	77.5	4.4	1205	2	T13959	timeless protein T
251	77.5	4.4	1262	1	B48758	protein-tyrosine-p
252	77.5	4.4	1496	1	A48758	protein-tyrosine-p
253	77.5	4.4	1894	2	C54689	protein-tyrosine-p
254	77.5	4.4	1912	2	A56178	protein-tyrosine-p
255	77.5	4.4	1950	2	S12332	ubiquitin-protein
256	77	4.3	327	2	S06611	Ig gamma-2 chain C
257	77	4.3	328	2	I47158	Ig gamma 1 chain c
258	77	4.3	338	2	JC5519	50K glycoprotein p
259	77	4.3	398	2	B86353	protein F2E2.6 [im
260	77	4.3	439	2	S51378	probable membrane
261	77	4.3	491	2	JE0276	voltage-gated pota
262	77	4.3	502	2	S61935	SKS1 protein - yea
263	77	4.3	523	2	T05946	cytochrome P450 78
264	77	4.3	796	2	JC7966	xylan 1,4-beta-xyl
265	77	4.3	873	1	QRRBVD	VLDL receptor prec
266	77	4.3	1021	2	I39207	leukocyte surface
267	77	4.3	1029	2	D83120	probable RND efflu
268	77	4.3	1041	2	S55862	probable membrane
269	77	4.3	1897	1	TDHULK	leukocyte antigen-
270	77	4.3	2167	2	AF1489	cell wall-associat
271	77	4.3	4836	2	T14346	herc2 protein - mo
272	76.5	4.3	177	1	C40428	nonspecific cross-
273	76.5	4.3	191	2	E75132	molybdopterin-guan
274	76.5	4.3	238	2	T24314	hypothetical prote
275	76.5	4.3	251	2	S75312	hypothetical prote
276	76.5	4.3	296	2	G82131	conserved hypothet
277	76.5	4.3	390	2	D86291	hypothetical prote
278	76.5	4.3	394	2	S20905	hypothetical prote
279	76.5	4.3	402	2	A54312	pregnancy-specific
280	76.5	4.3	423	2	AB1142	N-carbamyl-L-amino
281	76.5	4.3	426	2	S09016	pregnancy-specific
282	76.5	4.3	426	2	C55181	pregnancy-specific
283	76.5	4.3	426	2	B35334	pregnancy-specific
284	76.5	4.3	436	2	B55181	pregnancy-specific
285	76.5	4.3	495	2	A55181	pregnancy-specific
286	76.5	4.3	497	2	D65189	yigC protein - Esc
287	76.5	4.3	582	2	A71906	DNA polymerase III
288	76.5	4.3	727	2	T23585	hypothetical prote
289	76.5	4.3	788	2	S17906	hypothetical prote
290	76.5	4.3	839	2	B96538	hypothetical prote
291	76.5	4.3	876	2	S71277	serine/threonine-s
292	76.5	4.3	876	2	D85350	hypothetical prote
293	76.5	4.3	1005	2	T18537	Ig heavy chain - c
294	76.5	4.3	1043	2	T19734	hypothetical prote
295	76.5	4.3	1071	2	T18307	suppressor protein
296	76.5	4.3	1089	1	PFHUGA	platelet-derived g
297	76.5	4.3	1124	2	JX0293	zinc finger protei
298	76.5	4.3	1154	2	A56242	E-box-binding repr
299	76.5	4.3	1328	2	S62467	ATP-dependent DNA
300	76.5	4.3	1461	2	B70588	probable polyketid
301	76.5	4.3	1802	2	S69703	HKR1 protein precu
302	76.5	4.3	2039	2	T15347	ankyrin-related un
303	76	4.3	138	2	S16199	photosystem I prot
304	76	4.3	144	2	AH1172	mannose-specific p
305	76	4.3	230	2	S49449	Ig lambda chain -
306	76	4.3	239	2	T23147	hypothetical prote
307	76	4.3	262	2	A64882	probable carboxype
308	76	4.3	262	2	A99867	probable carboxype
309	76	4.3	262	2	H85751	probable carboxype
310	76	4.3	286	2	B97010	prephenate dehydro
311	76	4.3	305	2	H69759	conserved hypothet
312	76	4.3	333	2	A31923	amalgam protein pr
313	76	4.3	378	2	I46268	brevican precursor
314	76	4.3	487	1	S55194	DNA-directed DNA p
315	76	4.3	507	2	T47021	hypothetical prote
316	76	4.3	508	2	AD0236	L-asparagine perme
317	76	4.3	550	2	G90497	hypothetical prote
318	76	4.3	758	2	T15577	hypothetical prote
319	76	4.3	841	2	T01011	hypothetical prote
320	76	4.3	964	2	T15746	hypothetical prote
321	76	4.3	978	2	S16385	macrophage colony-
322	76	4.3	1018	2	JC4211	neural adhesion pr
323	76	4.3	1093	2	T51503	valine-tRNA ligase
324	76	4.3	2029	1	TDFFLK	protein-tyrosine-p
325	75.5	4.3	246	2	A47712	myelin/oligodendro
326	75.5	4.3	326	2	JC4124	pregnancy-specific
327	75.5	4.3	419	2	S42989	T48 protein - frui
328	75.5	4.3	421	2	T40614	G beta repeat prot
329	75.5	4.3	432	2	T30130	hypothetical prote
330	75.5	4.3	446	2	A95140	exodeoxyribonuclea
331	75.5	4.3	462	2	A84689	chloroplast membra
332	75.5	4.3	485	2	T28076	hypothetical prote
333	75.5	4.3	819	2	T05744	hypothetical prote
334	75.5	4.3	933	2	H69045	hypothetical prote
335	75.5	4.3	1020	2	S05944	neuronal cell surf
336	75.5	4.3	2109	1	I50421	aggrecan precursor
337	75	4.2	150	2	D95131	hypothetical prote
338	75	4.2	208	2	D71529	probable anthranil
339	75	4.2	466	2	D84906	probable beta-keto
340	75	4.2	491	2	AC2650	glucose-6-phosphat
341	75	4.2	503	2	B97432	glucose-6-phosphat
342	75	4.2	543	2	S26609	glutamate/aspartat
343	75	4.2	572	2	B46529	Ig Y heavy chain (
344	75	4.2	573	2	S12838	Ig mu chain precur
345	75	4.2	622	2	B96751	hypothetical prote
346	75	4.2	686	2	A55665	microtubule-associ
347	75	4.2	747	1	QRECFE	ferrichrome-iron r
348	75	4.2	747	2	B85499	outer membrane rec
349	75	4.2	747	2	B90648	outer membrane rec
350	75	4.2	821	1	TVMSBK	fibroblast growth
351	75	4.2	976	1	TVMSMD	macrophage colony-
352	75	4.2	1091	1	IJCHNL	neural cell adhesi
353	75	4.2	1256	2	T03096	CDO protein - rat
354	75	4.2	1338	2	T02206	hypothetical prote
355	75	4.2	7962	2	I38346	elastic titin - hu
356	74.5	4.2	232	1	DXCH	ovalbumin-related
357	74.5	4.2	278	2	A39037	carcinoembryonic a
358	74.5	4.2	309	2	T31908	hypothetical prote
359	74.5	4.2	321	2	S10006	hypothetical prote
360	74.5	4.2	379	2	B55522	lipoprotein D prec
361	74.5	4.2	379	2	D91078	probable lipoprote
362	74.5	4.2	379	2	E85923	lipoprotein [impor
363	74.5	4.2	463	2	T14884	hypothetical prote
364	74.5	4.2	518	2	D69539	conserved hypothet
365	74.5	4.2	544	2	I51593	protein-tyrosine k
366	74.5	4.2	688	2	A47705	triacylglycerol li
367	74.5	4.2	705	2	S51635	fibroblast growth
368	74.5	4.2	741	2	F90739	probable transport
369	74.5	4.2	741	2	H85589	probable transport
370	74.5	4.2	764	2	A49448	irregular chiasm C
371	74.5	4.2	771	2	T34376	hypothetical prote
372	74.5	4.2	786	2	H64817	probable membrane
373	74.5	4.2	795	2	T20609	hypothetical prote
374	74.5	4.2	889	1	VCLJG5	env polyprotein -
375	74.5	4.2	984	2	T00326	hypothetical prote
376	74.5	4.2	1003	2	T19638	hypothetical prote
377	74.5	4.2	1007	2	PN0156	glutamate receptor
378	74.5	4.2	1008	2	S28858	glutamate receptor
379	74.5	4.2	1021	2	A57112	contactin precurso
380	74.5	4.2	1178	2	E87145	[beta] subunit of
381	74.5	4.2	1179	2	S31145	DNA-directed RNA p
382	74.5	4.2	1522	2	T00028	brain-specific ang
383	74.5	4.2	1723	2	S58880	receptor DEC-205 -
384	74.5	4.2	1896	2	T08851	Down syndrome cell
385	74.5	4.2	2256	2	AD1018	large repetitive p
386	74.5	4.2	2364	2	A56577	microtubule-associ
387	74.5	4.2	2783	2	T34416	hypothetical prote
388	74	4.2	203	2	S36291	T-cell receptor ga
389	74	4.2	234	2	S01320	Ig kappa chain pre
390	74	4.2	278	2	JC1506	biliary glycoprote
391	74	4.2	333	2	PS0018	Ig gamma-2b chain
392	74	4.2	334	2	T19637	hypothetical prote
393	74	4.2	349	2	S68092	protein-glutamine
394	74	4.2	384	2	H64161	hypothetical prote

395	74	4.2	403	2	I52590	m33-B isoform - mo
396	74	4.2	424	2	T43498	hypothetical prote
397	74	4.2	463	2	C69997	probable proline t
398	74	4.2	468	2	S70297	SPS2 protein homol
399	74	4.2	502	2	T40792	hypothetical prote
400	74	4.2	548	2	A44302	protein-glutamine
401	74	4.2	586	2	T15259	hypothetical prote
402	74	4.2	611	2	F82442	probable peptide A
403	74	4.2	645	2	T39614	kinase-binding pro
404	74	4.2	673	2	T48701	hypothetical prote
405	74	4.2	860	2	JC5702	ErbB kinase activa
406	74	4.2	862	2	I49583	differentiation an
407	74	4.2	876	2	B96693	probable receptor
408	74	4.2	900	2	G96617	probable disease r
409	74	4.2	1063	2	A33830	cation efflux syst
410	74	4.2	1063	2	JC4700	cadmium, zinc, cob
411	74	4.2	1130	2	T23104	hypothetical prote
412	74	4.2	1133	2	T23103	hypothetical prote
413	74	4.2	1165	1	S45879	chitin synthase (E
414	74	4.2	1237	2	E86457	probable RNA helic
415	74	4.2	1367	2	T33819	hypothetical prote
416	74	4.2	1582	2	T15308	hypothetical prote
417	74	4.2	4344	1	A53489	dynein heavy chain
418	74	4.2	5232	2	A45086	HC-toxin synthetas
419	74	4.2	6658	2	T13931	projectin - fruit
420	73.5	4.1	325	2	S49451	cysteine proteinas
421	73.5	4.1	364	2	A30521	myeloid cell surfa
422	73.5	4.1	428	2	B83967	dihydroorotase pyr
423	73.5	4.1	647	2	T33773	hypothetical prote
424	73.5	4.1	740	2	AH0600	probable membrane
425	73.5	4.1	797	2	T27518	hypothetical prote
426	73.5	4.1	850	2	JC5700	ErbB kinase activa
427	73.5	4.1	880	1	VCLJS2	env polyprotein pr
428	73.5	4.1	923	2	F84732	probable ligand-ga
429	73.5	4.1	926	2	D83888	glucan 1,4-beta-gl
430	73.5	4.1	957	2	C69463	type I restriction
431	73.5	4.1	1166	2	S37692	probable tumor sup
432	73.5	4.1	1225	2	T48251	ubiquitin-protein
433	73.5	4.1	1240	2	T03097	CDO protein - huma
434	73.5	4.1	2013	2	AD1129	probable peptidogl
435	73.5	4.1	2042	2	T18399	variant-specific s
436	73.5	4.1	2301	1	GNNYTN	genome polyprotein
437	73.5	4.1	3255	2	G81702	adherence factor T
438	73.5	4.1	4544	1	S02392	alpha-2-macroglobu
439	73	4.1	147	2	T34265	hypothetical prote
440	73	4.1	220	1	G69047	conserved hypothet
441	73	4.1	235	2	S14675	Ig lambda chain -
442	73	4.1	250	2	S27544	hypothetical prote
443	73	4.1	293	2	H96906	hypothetical prote
444	73	4.1	322	2	H84095	hypothetical prote
445	73	4.1	354	2	T27712	hypothetical prote
446	73	4.1	389	2	T46722	conserved hypothet
447	73	4.1	397	2	E86304	F6I1.9 protein - A
448	73	4.1	413	2	S65948	hemolin - cecropia
449	73	4.1	413	2	A37778	hemolin precursor
450	73	4.1	432	1	RWMQT4	T-cell surface gly
451	73	4.1	476	2	H84524	probable fatty aci
452	73	4.1	519	2	S38921	hypothetical prote
453	73	4.1	590	2	I56526	interleukin 1 rece
454	73	4.1	666	1	A36026	kinesin-related pr
455	73	4.1	730	2	S64998	hypothetical prote
456	73	4.1	735	2	T00850	probable receptor-
457	73	4.1	853	1	IJBONC	neural cell adhesi
458	73	4.1	864	2	JH0438	penicillin-binding
459	73	4.1	901	1	P3XR17	core protein VP3 -
460	73	4.1	1014	2	T13476	hypothetical prote
461	73	4.1	1072	2	A38457	integrin alpha-6 c
462	73	4.1	1171	2	T31635	hypothetical prote
463	73	4.1	1179	2	T05673	hypothetical prote
464	73	4.1	1515	1	S51863	cadmium resistance
465	73	4.1	1737	2	A59235	unconventional myo
466	73	4.1	1806	2	T23298	hypothetical prote
467	73	4.1	3788	2	T30851	lysosomal traffick
468	72.5	4.1	202	2	S36293	T-cell receptor ga
469	72.5	4.1	221	2	T31620	hypothetical prote
470	72.5	4.1	334	2	G01650	malate dehydrogena
471	72.5	4.1	336	2	C27658	pregnancy-specific
472	72.5	4.1	342	2	AG1729	protein gp19 (Bact
473	72.5	4.1	351	2	B34595	pregnancy-specific
474	72.5	4.1	363	2	I39726	mannopine biosynth
475	72.5	4.1	371	2	T40287	hypothetical prote
476	72.5	4.1	377	2	B90437	hypothetical prote
477	72.5	4.1	399	2	AI1114	surface protein (p
478	72.5	4.1	424	2	A34595	pregnancy-specific
479	72.5	4.1	435	2	D33258	pregnancy-specific
480	72.5	4.1	440	2	S52895	TyA protein - yeas
481	72.5	4.1	443	2	AE3294	tolB protein [impo
482	72.5	4.1	478	2	A49228	trypsin-like prote
483	72.5	4.1	487	2	AI1146	hypothetical cell
484	72.5	4.1	491	2	T22844	hypothetical prote
485	72.5	4.1	527	2	D75127	hypothetical prote
486	72.5	4.1	666	2	A39610	SLY1 protein - yea
487	72.5	4.1	682	2	A35969	heparin-binding gr
488	72.5	4.1	687	2	T39838	hypothetical prote
489	72.5	4.1	768	2	JC7352	glucose-regulated
490	72.5	4.1	769	2	T45854	hypothetical prote
491	72.5	4.1	842	2	E96641	hypothetical prote
492	72.5	4.1	851	2	S44890	ncl-1 ZK112.2 prot
493	72.5	4.1	876	2	A49508	protein-tyrosine k
494	72.5	4.1	895	2	T11979	Preprotein translo
495	72.5	4.1	913	2	A48280	receptor tyrosine
496	72.5	4.1	1057	2	S45801	probable membrane
497	72.5	4.1	1123	2	AB0125	exodeoxyribonuclea
498	72.5	4.1	1138	2	A82939	membrane nuclease
499	72.5	4.1	1272	2	S26180	neurofascin - chic
500	72.5	4.1	1434	2	T30172	transmembrane prot
501	72.5	4.1	1575	2	T18545	lysobactin synthet
502	72.5	4.1	4367	1	B54802	dynein heavy chain
503	72.5	4.1	4924	2	T50176	probable peptide s
504	72.5	4.1	4936	2	AH2515	hypothetical prote
505	72	4.1	265	2	H72233	purine nucleoside
506	72	4.1	320	2	C89867	hypothetical prote
507	72	4.1	378	2	T51237	scarecrow-like pro
508	72	4.1	423	2	T29549	hypothetical prote
509	72	4.1	437	2	AF3613	hypothetical prote
510	72	4.1	442	2	E71523	hypothetical prote
511	72	4.1	446	2	B89922	conserved hypothet
512	72	4.1	469	2	C69628	gamma-aminobutyrat
513	72	4.1	506	2	F69867	two-component sens
514	72	4.1	510	2	A84707	probable pseudouri
515	72	4.1	521	2	E82377	ABC transporter, p
516	72	4.1	543	2	S38353	glutamate transpor
517	72	4.1	549	2	T33517	hypothetical prote
518	72	4.1	558	2	T01343	hypothetical prote
519	72	4.1	565	2	C82280	sensor kinase citA
520	72	4.1	585	2	S48929	hypothetical prote
521	72	4.1	599	2	T16774	hypothetical prote
522	72	4.1	617	2	T23197	hypothetical prote
523	72	4.1	646	2	I38049	cell surface glyco
524	72	4.1	783	2	T45899	receptor protein k
525	72	4.1	808	2	F81180	conserved hypothet
526	72	4.1	868	2	JC5701	ErbB kinase activa
527	72	4.1	873	2	H96503	protein F9C16.17 [
528	72	4.1	885	2	D86151	F22M8.8 protein -
529	72	4.1	900	2	T04839	protein kinase hom
530	72	4.1	901	2	S07419	core protein P3 -
531	72	4.1	911	2	B34721	androgen receptor
532	72	4.1	1038	2	H90053	hypothetical prote
533	72	4.1	1186	2	T19334	hypothetical prote
534	72	4.1	1214	2	JC7259	Smad interacting p
535	72	4.1	1216	2	H85023	hypothetical prote
536	72	4.1	1273	2	T42405	sax-3 protein - Ca
537	72	4.1	1348	2	S51656	vascular endotheli
538	72	4.1	1906	1	S68235	myosin-light-chain
539	72	4.1	2383	2	D64962	probable membrane
540	72	4.1	4872	2	S27272	ryanodine receptor

541	71.5	4.0	145	2	S25743	Ig lambda chain -
542	71.5	4.0	229	1	B43685	nonstructural prot
543	71.5	4.0	238	2	A49633	Ig lambda-like cha
544	71.5	4.0	299	2	S50803	hypothetical prote
545	71.5	4.0	312	2	A64461	hypothetical prote
546	71.5	4.0	338	2	A64303	conserved hypothet
547	71.5	4.0	339	2	S08981	malate dehydrogena
548	71.5	4.0	362	2	T05167	hypothetical prote
549	71.5	4.0	443	2	T14916	mitosis-specific c
550	71.5	4.0	498	2	G90067	malate quinone oxi
551	71.5	4.0	500	2	T11946	ribosomal protein
552	71.5	4.0	542	2	AF2587	MFS permease [impo
553	71.5	4.0	542	2	F97369	hypothetical prote
554	71.5	4.0	589	2	T50385	hypothetical coile
555	71.5	4.0	603	2	H84442	hypothetical prote
556	71.5	4.0	669	2	T48466	hypothetical prote
557	71.5	4.0	707	2	A54846	fibroblast growth
558	71.5	4.0	707	2	A38429	keratinocyte growt
559	71.5	4.0	764	1	QRHUGS	secretory componen
560	71.5	4.0	822	2	B54846	fibroblast growth
561	71.5	4.0	919	2	S33942	hexon protein - hu
562	71.5	4.0	921	2	F71486	probable yopC/gen
563	71.5	4.0	1032	2	H64100	acriflavine resist
564	71.5	4.0	1089	1	S33727	platelet-derived g
565	71.5	4.0	1180	2	E86719	hypothetical prote
566	71.5	4.0	1348	2	S27812	probable epidermal
567	71.5	4.0	1348	2	A43917	probable epidermal
568	71.5	4.0	1374	2	S62524	probable RNA helic
569	71.5	4.0	1377	2	C70148	DNA-directed RNA p
570	71.5	4.0	1413	2	D84481	probable retroelem
571	71.5	4.0	1462	2	T11648	probable mitotic s
572	71.5	4.0	2397	1	A55535	versican precursor
573	71	4.0	61	2	C82536	hypothetical prote
574	71	4.0	142	2	S38392	T-cell receptor be
575	71	4.0	189	2	G64496	hypothetical prote
576	71	4.0	207	2	T50206	hypothetical zinc
577	71	4.0	221	2	T21117	hypothetical prote
578	71	4.0	224	2	H81568	conserved hypothet
579	71	4.0	231	2	G72102	ct181 hypothetical
580	71	4.0	231	2	B86520	CT181 hypothetical
581	71	4.0	258	2	S73803	MG256 homolog H91_
582	71	4.0	329	1	DEDFLM	L-lactate dehydrog
583	71	4.0	333	2	AF0407	lipoprotein [impor
584	71	4.0	343	2	AI0358	probable fimbrial
585	71	4.0	344	2	I56551	neurotrimin - rat
586	71	4.0	345	2	I48780	Stra1/Eplg2 protei
587	71	4.0	346	2	AF1820	sialoglycoproteina
588	71	4.0	387	2	B71611	hypothetical prote
589	71	4.0	389	2	S68155	ubiquinol-cytochro
590	71	4.0	390	2	T27033	hypothetical prote
591	71	4.0	407	2	T34442	hypothetical prote
592	71	4.0	423	1	EHMSS	Ig epsilon chain C
593	71	4.0	455	2	S50391	hypothetical prote
594	71	4.0	462	2	JN0719	drought-inducible
595	71	4.0	463	2	AH1758	amino acid transpo
596	71	4.0	509	1	WMVZMX	M9-R protein - myx
597	71	4.0	570	2	T11647	probable pyruvate
598	71	4.0	609	2	H82039	GTP-binding protei
599	71	4.0	615	2	B38575	gluconate 2-dehydr
600	71	4.0	682	2	T22064	hypothetical prote
601	71	4.0	687	2	A49636	soluble vascular e
602	71	4.0	690	2	A24545	triacylglycerol li
603	71	4.0	691	2	B89797	glycerol ester hyd
604	71	4.0	765	2	E96558	hypothetical prote
605	71	4.0	821	1	TVHUF2	fibroblast growth
606	71	4.0	876	2	T51507	WD40-repeat protei
607	71	4.0	902	1	S54495	probable carrier p
608	71	4.0	940	2	T41992	hypothetical prote
609	71	4.0	956	2	G70327	isoleucine-tRNA li
610	71	4.0	1018	2	A54744	contactin 1 precur
611	71	4.0	1027	2	B85089	receptor protein k
612	71	4.0	1082	2	S64903	regulatory protein
613	71	4.0	1217	2	T22672	hypothetical prote
614	71	4.0	1251	2	T21389	hypothetical prote
615	71	4.0	1338	2	S09982	protein-tyrosine k
616	71	4.0	4391	2	A38096	perlecan precursor
617	71	4.0	5107	2	T29144	partial CDS - Caen
618	70.5	4.0	203	2	F69381	flagellin (flaB1-1
619	70.5	4.0	223	2	A81068	hypothetical prote
620	70.5	4.0	238	2	D86302	hypothetical prote
621	70.5	4.0	246	2	B82764	hypothetical prote
622	70.5	4.0	332	2	T45770	hypothetical prote
623	70.5	4.0	338	1	DERTMM	malate dehydrogena
624	70.5	4.0	358	2	E89588	protein R09F10.8 [
625	70.5	4.0	429	1	B41902	arsenical pump mem
626	70.5	4.0	455	2	G01923	KIR (cl-5) NK rece
627	70.5	4.0	502	2	T19108	hypothetical prote
628	70.5	4.0	505	2	T15159	hypothetical prote
629	70.5	4.0	522	2	T26319	hypothetical prote
630	70.5	4.0	526	1	TVFV60	protein-tyrosine k
631	70.5	4.0	533	1	TVCHS	protein-tyrosine k
632	70.5	4.0	537	1	A45501	protein-tyrosine k
633	70.5	4.0	545	2	S52313	protein-tyrosine k
634	70.5	4.0	546	2	S52314	protein-tyrosine k
635	70.5	4.0	557	1	TVFVS2	protein-tyrosine k
636	70.5	4.0	558	1	MWXRRT	RNA 10 protein - r
637	70.5	4.0	568	1	TVFVS1	protein-tyrosine k
638	70.5	4.0	569	2	A45624	trophozoite cystei
639	70.5	4.0	587	1	TVFVPR	protein-tyrosine k
640	70.5	4.0	627	2	S14683	Ig mu chain precur
641	70.5	4.0	627	2	A69663	DNA mismatch repai
642	70.5	4.0	630	2	A39344	tumor-associated m
643	70.5	4.0	646	2	T48644	negative regulator
644	70.5	4.0	656	2	H84206	acetyl-CoA synthet
645	70.5	4.0	663	1	TVMVRR	protein-tyrosine k
646	70.5	4.0	669	2	T13640	probable minor str
647	70.5	4.0	743	2	F71062	hypothetical prote
648	70.5	4.0	787	2	T41974	replication origin
649	70.5	4.0	793	2	T41703	dipeptidyl aminope
650	70.5	4.0	844	2	S05988	translation elonga
651	70.5	4.0	877	1	IJBOCN	N-cadherin precurs
652	70.5	4.0	878	2	S11842	hypothetical prote
653	70.5	4.0	895	2	A55413	triglyceride trans
654	70.5	4.0	906	1	IJMSCN	N-cadherin precurs
655	70.5	4.0	928	2	G86546	polymorphic outer
656	70.5	4.0	928	2	G81591	polymorphic membra
657	70.5	4.0	938	2	F86548	polymorphic outer
658	70.5	4.0	938	2	H72074	polymorphic membra
659	70.5	4.0	1088	2	B56715	calcium receptor (
660	70.5	4.0	1200	2	T17404	hyalin - sea urchi
661	70.5	4.0	1356	2	JC1402	protein-tyrosine k
662	70.5	4.0	1402	2	F84480	probable retroelem
663	70.5	4.0	1427	2	I51669	tumor suppressor -
664	70.5	4.0	1694	2	S50065	sialoadhesin - mou
665	70.5	4.0	2051	2	T30938	receptor tyrosine
666	70.5	4.0	2303	1	GNNYTP	genome polyprotein
667	70.5	4.0	2303	2	S13554	genome polyprotein
668	70.5	4.0	2464	1	QRMSP1	microtubule-associ
669	70.5	4.0	6831	2	A88852	protein unc-22 [im
670	70.5	4.0	6839	2	S57242	twitchin [similari
671	70.5	4.0	7160	2	T27935	hypothetical prote
672	70	4.0	115	1	KVMSL6	Ig kappa chain pre
673	70	4.0	203	2	S23043	T-cell receptor ga
674	70	4.0	224	2	I37243	CMRF-35 antigen -
675	70	4.0	236	2	S25746	Ig lambda chain -
676	70	4.0	283	2	AB0105	probable maltodext
677	70	4.0	292	2	T44230	hypothetical prote
678	70	4.0	299	2	D83010	probable binding p
679	70	4.0	304	2	G71624	rifin PFB0025c - m
680	70	4.0	347	2	T29415	hypothetical prote
681	70	4.0	356	2	G82938	hemin transport sy
682	70	4.0	374	2	A46352	ORF1 protein - Chl
683	70	4.0	403	2	B36151	tryptophan synthas
684	70	4.0	410	2	I50494	serine proteinase
685	70	4.0	469	2	T46929	hypothetical prote
686	70	4.0	491	2	T27661	hypothetical prote

687	70	4.0	517	2	T00980	hypothetical prote
688	70	4.0	536	2	T37544	hypothetical serin
689	70	4.0	548	2	B71549	hypothetical prote
690	70	4.0	550	2	T03714	5-epi-aristolochen
691	70	4.0	576	2	A32604	interleukin-1 rece
692	70	4.0	599	2	T48450	hypothetical prote
693	70	4.0	609	2	AE2062	gamma-glutamyltran
694	70	4.0	611	1	W1WLEP	E1 protein - Europ
695	70	4.0	611	2	H70938	probable fadE5 pro
696	70	4.0	648	2	T08856	hypothetical prote
697	70	4.0	687	1	A39045	protein-glutamine
698	70	4.0	790	2	T01537	S-receptor kinase
699	70	4.0	805	2	S68441	leptin receptor, s
700	70	4.0	810	1	S57196	calpain (EC 3.4.22

ALIGNMENTS

RESULT 1
A46500
Ly-9.2 antigen - mouse
C;Species: Mus musculus (house mouse)
C;Date: 18-Jun-1993 #sequence_revision 18-Nov-1994 #text_change 05-Nov-1999
C;Accession: A46500
R;Sandrin, M.S.; Gumley, T.P.; Henning, M.M.; Vaughan, H.A.; Gonez, L.J.; Trapani, J.A.;
J. Immunol. 149, 1636-1641, 1992
A;Title: Isolation and characterization of cDNA clones for mouse Ly-9.
A;Reference number: A46500; MUID:92373005; PMID:1506686
A;Accession: A46500
A;Status: preliminary
A;Molecule type: mRNA; protein
A;Residues: 1-629 <SAN>
A;Cross-references: GB:M84412; NID:g198931; PIDN:AAA39468.1; PID:g198932
A;Experimental source: C57BL/6
A;Note: sequence extracted from NCBI backbone (NCBIN:111651, NCBIP:111654)
C;Keywords: transmembrane protein

Query Match 19.4%; Score 343; DB 2; Length 629;
Best Local Similarity 29.3%; Pred. No. 2.2e-20;
Matches 105; Conservative 58; Mismatches 143; Indels 52; Gaps 14;

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Qy          14 LWQL-TGSA----ASGPVKELVGSVGGAVTFPLKSK-VKQVDSIVWTFNTTPLVTIQPEG 67
               :|| .||::    |:|  | :|| :|  || ||: :  :   ::||  ||:  |  |
Db         217 IWQFCTGASRRKTAAG--KTVVGILGEPVTLPLEFRATRATKNVVWVLNTS--VISQERR 272

Qy          68 GTIIVTQNR-----NRERVDFPDGGYSLKLSKLKKNDSGIYYVGIYSSSLQQPSTQEYVL 122
               |     |       ||   |   |||:|:||  |:| |:  : | : : || : : |
Db         273 GAATADSRRKPKGSEERRVRTSDQDQSLKISQLKMEDAGPYHAYVCSEASRDPSVRHFTL 332

Qy         123 HVYEHLSKPKVTMGLQSNKNGTCVTNLTCCMEHGEEDVIYTWKALGQAANESHNGSILPI 182
               ||: | || ||        || |   ||| :: |  :| |||  |   |   |   | | :
Db         333 LVYKRLEKPSVTKSPVHMMNGICEVVLTCSVDGGGNNVTYTWMPLQNKAVMSQGKSHLNV 392

Qy         183 SWRWGESDMTFICVARNPVSRNFSSPILARKLCEGAADDPDSSMVLLCLLLVPLLLSLFV 242
               ||  ||    | | | |||| | ||   :  :| |   |: :     |||: ||| : :
Db         393 SWESGEHLPNFTCTAHNPVS-NSSSQFSSGTICSG----PERNKRFWLLLLLVLLLLMLI 447

Qy         243 LGLFLWFLKRERQEEYIEEK-KRVDICRETPNICPHSG-----------------ENTE 283
               | |:  |::::|   :  : :: ::  | |   | :|                 : |
Db         448 GGYFI--LRKKKQCSSLATRYRQAEVPAEIPE--PPTGHGQFSVLSQRYEKLDMSAKTTR 503

Qy         284 Y------DTIPHTNRTILKEDPANTVYSTVEIPKKMENPHSLLTMPDTPRLFAYENVI 335
               :      ||   :: |  ::|    ::||     ::   : |:|  |     |||  :
Db         504 HQPTPTSDTSSESSATTEEDDEKTRMHSTANSRNQL---YDLVTHQDIAHALAYEGQV 558
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RESULT 2
S58892
signaling lymphocytic activation molecule - human
C;Species: Homo sapiens (man)
C;Date: 15-Feb-1996 #sequence_revision 01-Mar-1996 #text_change 05-Nov-1999
C;Accession: S58892
R;Cocks, B.G.; Chang, C.C.; Carballido, J.M.; Yssel, H.; de Vries, J.E.; Aversa, G.
Nature 376, 260-263, 1995
A;Title: A novel receptor involved in T-cell activation.
A;Reference number: S58892; MUID:95342241; PMID:7617038
A;Accession: S58892
A;Status: preliminary; nucleic acid sequence not shown
A;Molecule type: mRNA
A;Residues: 1-335 <COC>
A;Cross-references: EMBL:U33017; NID:g984968; PIDN:AAA75380.1; PID:g984969

Query Match 10.3%; Score 182.5; DB 2; Length 335;
Best Local Similarity 22.5%; Pred. No. 1.9e-07;
Matches 82; Conservative 72; Mismatches 129; Indels 81; Gaps 19;

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Qy           8 LTLIYILW-QLTGSAASGP------VKELVGSVGGAVTFPL------KSKVKQVDSIVWT 54
               |:| ::|:  |   |: |         :::  :|  |  ||      ||  | :  :|
Db           7 LSLTFVLFLSLAFGASYGTGGRMMNCPKILRQLGSKVLLPLTYERINKSMNKSIHIVVTM 66

Qy          55 FNT------TPLVTIQP-EGGTIIVTQNRNRERVDFPDGGYSLKLSKLKKNDSGIYYVGI 107
                 :      :|:: | | |           :|  |     :| : : :| | | | : :
Db          67 AKSLENSVENKIVSLDPSEAG----PPRYLGDRYKFYLENLTLGIRESRKEDEGWYLMTL 122

Qy         108 YSS-SLQQPSTQEYVLHVYEHLSKPKVTMGLQSNKNGTCVTNLTCCMEHGEEDVIYTW-- 164
                 : |:|:.   |   | :|| :| |:: :  :: :|||   | | :| |:  | |:|
Db         123 EKNVSVQRFCLQ---LRLYEQVSTPEIKVLNKTQENGTCTLILGCTVEKGDH-VAYSWSE 178

Qy         165 KALGQAANESHNGSILPISWRWGESDMTFICVARNPVSRNFS--SPILARKLCEGAADDP 222
               ||      | :::  :| ::     :|  :||   ||:| |    ||         |  ||
Db         179 KAGTHPLNPANSSHLLSLTLGPQHADNIYICTVSNPISNNSQTFSP------WPGCRTDP 232

Qy         223 DSSM----------VLLCLLLVPLLLSLFVLGLFLWFLKRERQEEYIE---EKKRVDIC 268
                 :           |:: |::| :|              |:|  :  : :   ||| : |
Db         233 SETKPWAVYAGLLGGVIMILIMVVILQ----------LRRRGKTNHYQTTVEKKSLTIY 281

Qy         269 RETPNICPHSGENTEYDTIPHTNRTILKEDPANTVY--STVEIPKKMENPHSL-----LT 321
                 :      |      : |: |        :||  |:|  :|  :|: ::  :|:     :|
Db         282 AQVQKPGP---LQKKLDSFP-------AQDPCTTIYVAATEPVPESVQETNSITVYASVT 331

Qy         322 MPDT 325
               :|::
Db         332 LPES 335
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RESULT 3
B28967
T-cell surface glycoprotein CD2 precursor - mouse
N;Alternate names: CD2 antigen; T-lymphocyte antigen CD2; T11 protein
C;Species: Mus musculus (house mouse)
C;Date: 30-Jun-1989 #sequence_revision 03-Jun-1993 #text_change 23-Jul-1999
C;Accession: B28967; S01347; S02293
R;Diamond, D.J.; Clayton, L.K.; Sayre, P.H.; Reinherz, E.L.
Proc. Natl. Acad. Sci. U.S.A. 85, 1615-1619, 1988
A;Title: Exon-intron organization and sequence comparison of human and murine T11 (CD2)
A;Reference number: A28967; MUID:88144486; PMID:2894031
A;Accession: B28967
A;Molecule type: mRNA
A;Residues: 1-344 <DIA>
A;Cross-references: GB:M19807; NID:g192479; PIDN:AAA37393.1; PID:g387122; GB:J03622; GB:
A;Note: the authors translated the codon TAT for residue 99 as Thr
R;Clayton, L.K.; Sayre, P.H.; Novotny, J.; Reinherz, E.L.
Eur. J. Immunol. 17, 1367-1370, 1987
A;Title: Murine and human T11 (CD2) cDNA sequences suggest a common signal transduction
A;Reference number: S01347; MUID:88004738; PMID:2820751
A;Accession: S01347
A;Molecule type: mRNA
A;Residues: 1-127,'M',129-174,'N',176-190,'NM',193-344 <CLA>
A;Cross-references: EMBL:X06143; NID:g54223; PIDN:CAA29500.1; PID:g54224
R;Sewell, W.A.; Brown, M.H.; Owen, M.J.; Fink, P.J.; Kozak, C.A.; Crumpton, M.J.
Eur. J. Immunol. 17, 1015-1020, 1987
A;Title: The murine homologue of the T lymphocyte CD2 antigen: molecular cloning, chromo
A;Reference number: S02293; MUID:87276135; PMID:2440689
A;Accession: S02293
A;Status: not compared with conceptual translation

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A;Molecule type: mRNA
A;Residues: 1-127,'M',129-174,'N',176-191,'M',193-344 <SEW>
A;Cross-references: EMBL:Y00023; NID:g50346; PIDN:CAA68258.1; PID:g50347
C;Genetics:
A;Map position: 3
C;Superfamily: T-cell surface glycoprotein CD2
C;Keywords: glycoprotein; surface antigen; T-cell; transmembrane protein
F;1-22/Domain: signal sequence #status predicted <SIG>
F;23-344/Product: T-cell surface glycoprotein CD2 #status predicted <MAT>
F;23-203/Domain: extracellular #status predicted <EXT>
F;204-228/Domain: transmembrane #status predicted <TMM>
F;229-344/Domain: intracellular #status predicted <INT>

  Query Match             8.1%;  Score 144;  DB 2;  Length 344;
  Best Local Similarity   21.4%;  Pred. No. 0.0003;
  Matches   72;  Conservative   56;  Mismatches  132;  Indels   76;  Gaps   16;

Qy         12 YILWQLTGSAASGPVKELV-GSVGGAVT--FPLKSKVKQVDSIVWTFNTTPLVTIQPEGG 68
              ::|: |:|  |      | : | :|  :|    |        :| : |           |
Db         10 FLLFSLSGKGADCRDNETIWGVLGHGITLNIPNFQMTDDIDEVRWV-----------RRG 58

Qy         69 TIIVTQNRNR------ERVDFPDGGYSLKLSK-LKKNDSGIYYVGIYSSSLQQPSTQEYV 121
              |::    | :      |  :    | |||: | : :|||| | | :| ::      ::
Db         59 TLVAEFKRKKPPFLISETYEVLANG-SLKIKKPMMRNDSGTYNVMVYGTNGMTRLEKDLD 117

Qy        122 LHVYEHLSKPKVTMGLQSNKNGTCV-TNLTCCMEHGEEDVIYTWKALGQAANESHNGSIL 180
              : : | :||| :        :  |  | ||| :  | :  :  ::  |:    |     |
Db        118 VRILERVSKPVI--------HWECPNTTLTCAVLQGTDFELKLYQ--GETLLNS-----L 162

Qy        181 P---ISWRWGESDMTFICVARNPVSRNFSSPILARKLCEGAADDPDSSMVLLCL------ 231
              |   :|::|       | | | ||||:   : ::        : |:  :
Db        163 PQKNMSYQWTNLSAPFKCEAINPVSKESKTEVV---------NCPEKGLSFYVTVGVGAG 213

Qy        232 -LLVPLLLSLFVLGLFLWFLKRERQEEYIEEKKRVDICRETPNICPHSGENTEYDTIPHT 290
               ||: ||::||:   |    :|:|     :|:  :   | :           |    ||:
Db        214 GLLLVLLVALFI---FCICKRRKRNRRRKDEELEIKASRTS---------TVERGPKPHS 261

Qy        291 NRTILKEDPANTVYSTVEIPKKMENPHSLLTMPDTP 326
                      ||    ::| :       | | |    |
Db        262 T-------PAAAAQNSVALQAPPPPGHHLQTPGHRP 290


RESULT 4
I49585
CD2 antigen protein precursor - mouse
C;Species: Mus musculus (house mouse)
C;Date: 02-Jul-1996 #sequence_revision 02-Jul-1996 #text_change 23-Jul-1999
C;Accession: I49585
R;Yagita, H.; Okumura, K.; Nakauchi, H.
J. Immunol. 140, 1321-1326, 1988
A;Title: Molecular cloning of the murine homologue of CD2: Homology of the molecule to i
A;Reference number: I49585; MUID:88140313; PMID:3257775
A;Accession: I49585
A;Status: preliminary; translated from GB/EMBL/DDBJ
A;Molecule type: mRNA
A;Residues: 1-344 <RES>
A;Cross-references: GB:M18934; NID:g192486; PIDN:AAA37397.1; PID:g309158
C;Superfamily: T-cell surface glycoprotein CD2

  Query Match             7.8%;  Score 138;  DB 2;  Length 344;
  Best Local Similarity   21.1%;  Pred. No. 0.00095;
  Matches   71;  Conservative   56;  Mismatches  133;  Indels   76;  Gaps   16;

Qy         12 YILWQLTGSAASGPVKELV-GSVGGAVT--FPLKSKVKQVDSIVWTFNTTPLVTIQPEGG 68
              ::|: |:|  |      | : | :|  :|    |        :| : |           |
Db         10 FLLFSLSGKGADCRDNETIWGVLGHGITLNIPNFQMTDDIDEVRWV-----------RRG 58

Qy         69 TIIVTQNRNR------ERVDFPDGGYSLKLSK-LKKNDSGIYYVGIYSSSLQQPSTQEYV 121
              |::    | :      |  :    | |||: | : :|||| | | :| ::      ::
Db         59 TLVAEFKRKKPPFLISETYEVLANG-SLKIKKPMMRNDSGTYNVMVYGTNGMTRLEKDLD 117

Qy        122 LHVYEHLSKPKVTMGLQSNKNGTCV-TNLTCCMEHGEEDVIYTWKALGQAANESHNGSIL 180
              : : | :||| :        :  |  | | | :  | :  :  ::  |:    |     |
Db        118 VRILERVSKPVI--------HWECPNTTLTCAVLQGTDFELKLYQ--GETLLNS-----L 162

Qy        181 P---ISWRWGESDMTFICVARNPVSRNFSSPILARKLCEGAADDPDSSMVLLCL------ 231
              |   :|::|       | | | ||||:   : ::        : |:  :
Db        163 PQKNMSYQWTNLSAPFKCEAINPVSKESKTEVV---------NCPEKGLSFYVTVGVGAG 213

Qy        232 -LLVPLLLSLFVLGLFLWFLKRERQEEYIEEKKRVDICRETPNICPHSGENTEYDTIPHT 290
               ||: ||::||:   |    :|:|     :|:  :   | :           |    ||:
Db        214 GLLLVLLVALFI---FCICKRRKRNRRRKDEELEIKASRTS---------TVERGPKPHS 261

Qy        291 NRTILKEDPANTVYSTVEIPKKMENPHSLLTMPDTP 326
                      ||    ::| :       | | |    |
Db        262 T-------PAAAAQNSVALQAPPPPGHHLQTPGHRP 290


RESULT 5
RWHUC2
T-cell surface glycoprotein CD2 precursor - human
N;Alternate names: E rosette receptor; erythrocyte receptor; erythrocyte-binding protei
C;Species: Homo sapiens (man)
C;Date: 31-Mar-1989 #sequence_revision 31-Mar-1989 #text_change 22-Jun-1999
C;Accession: A28967; A26486; B26486; A28416; A28023; S02292; A30430; S00829; A29874
R;Diamond, D.J.; Clayton, L.K.; Sayre, P.H.; Reinherz, E.L.
Proc. Natl. Acad. Sci. U.S.A. 85, 1615-1619, 1988
A;Title: Exon-intron organization and sequence comparison of human and murine T11 (CD2)
A;Reference number: A28967; MUID:88144486; PMID:2894031
A;Accession: A28967
A;Molecule type: DNA
A;Residues: 1-351 <DIA>
A;Cross-references: GB:M19806; GB:J03622; GB:J03623; NID:g180079; PIDN:AAA53095.1; PID:
R;Sewell, W.A.; Brown, M.H.; Dunne, J.; Owen, M.J.; Crumpton, M.J.
Proc. Natl. Acad. Sci. U.S.A. 83, 8718-8722, 1986
A;Title: Molecular cloning of the human T-lymphocyte surface CD2 (T11) antigen.
A;Reference number: A26486; MUID:87041523; PMID:3490670
A;Accession: A26486
A;Molecule type: mRNA
A;Residues: 1-338,'M',340,'QQKTHCPLPLIKKDRNCLFQ' <SE1>
A;Accession: B26486
A;Molecule type: protein
A;Residues: 25-46,'X',50 <SE2>
R;Sewell, W.A.; Brown, M.H.; Dunne, J.; Owen, M.J.; Crumpton, M.J.
Proc. Natl. Acad. Sci. U.S.A. 84, 7256, 1987
A;Reference number: A28416
A;Contents: revision
A;Accession: A28416
A;Molecule type: mRNA
A;Residues: 333-351 <SE3>
R;Seed, B.; Aruffo, A.
Proc. Natl. Acad. Sci. U.S.A. 84, 3365-3369, 1987
A;Title: Molecular cloning of the CD2 antigen, the T-cell erythrocyte receptor, by a ra
A;Reference number: A28023; MUID:87204137; PMID:2437578
A;Accession: A28023
A;Molecule type: mRNA
A;Residues: 1-265,'Q',267-351 <SEE>
A;Cross-references: GB:M16445; NID:g178668; PIDN:AAA51738.1; PID:g178669
R;Sayre, P.H.; Chang, H.C.; Hussey, R.E.; Brown, N.R.; Richardson, N.E.; Spagnoli, G.;
Proc. Natl. Acad. Sci. U.S.A. 84, 2941-2945, 1987
A;Title: Molecular cloning and expression of T11 cDNAs reveal a receptor-like structure
A;Reference number: S02292; MUID:87204243; PMID:2883656
A;Accession: S02292
A;Molecule type: mRNA
A;Residues: 1-338,'M',340,'QQKTHCPLPLIKKDRNCLFQ' <SA1>
A;Cross-references: GB:M16336; NID:g180093; PIDN:AAA51946.1; PID:g180094
A;Accession: A30430
A;Molecule type: protein
A;Residues: 25-43,152-163 <SA2>
R;Lang, G.; Wotton, D.; Owen, M.J.; Sewell, W.A.; Brown, M.H.; Mason, D.Y.; Crumpton, M
EMBO J. 7, 1675-1682, 1988
A;Title: The structure of the human CD2 gene and its expression in transgenic mice.
A;Reference number: S00829; MUID:89005055; PMID:2901953
A;Accession: S00829
A;Molecule type: DNA
A;Residues: 1-351 <LAN>
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A;Cross-references: EMBL:X07871
C;Comment: CD2 is a surface antigen expressed on all peripheral blood T-cells. It appear
or is closely associated with, the erythrocyte receptor.
C;Genetics:
A;Gene: GDB:CD2
A;Cross-references: GDB:118735; OMIM:186990
A;Map position: 1p13.1-1p13.1
A;Introns: 21/1; 128/1; 205/1; 246/1
C;Superfamily: T-cell surface glycoprotein CD2
C;Keywords: glycoprotein; T-cell; transmembrane protein
F;1-24/Domain: signal sequence #status predicted <SIG>
F;25-351/Product: T-cell surface glycoprotein CD2 #status predicted <MAT>
F;25-206/Domain: extracellular #status predicted <EXT>
F;210-234/Domain: transmembrane #status predicted <TMM>
F;237-351/Domain: intracellular #status predicted <INT>
F;89,141,150/Binding site: carbohydrate (Asn) (covalent) #status predicted

  Query Match             7.7%;  Score 136.5;  DB 1;  Length 351;
  Best Local Similarity   23.9%;  Pred. No. 0.0013;
  Matches   71;  Conservative   44;  Mismatches  111;  Indels   71;  Gaps   15;

Qy         28 ELVGSVGGAVTFPLKS--KVKQVDSIVW--TFNTTPLVTIQPEGGTIIVTQNRNRERVDF 83
              |  |::|  :  : |         :| | |  | :  :   : |  |    : ::  :: |
Db         32 ETWGALGQDINLDIPSFQMSDDIDDIKWEKTSDKKKIAQFRKEKETF---KEKDTYKL-F 87

Qy         84 PDGGYSLKLSKLKKNDSGIYYVGIYSSSLQQPSTQEYVLHVYEHLSKPKVTMGLQSNKNG 143
              :|  :||:  || :|  || | ||  :  :    : : | : | :||||::
Db         88 KNG--TLKIKHLKTDDQDIYKVSIYDTKGKNVLEKIFDLKIQERVSKPKISW-------- 137

Qy        144 TCV-TNLTCCMEHGEEDVIYTWKALGQAANESHNGSILPISWR-----WGES-DMTFICV 196
             ||: | ||| : :| :  :              |   :|  | :| |      |  |   | |
Db        138 TCINTTLTCEVMNGTDPEL----------NLYQDGKHLKLSQRVITHKWTTSLSAKFKCT 187

Qy        197 ARNPVSRNFS-SPI----------LARKLCEGAADDPDSSMVLLCLLLVPLLLSLFVLGL 245
              | | ||:  |  |:          |   :| | :                || :||  |
Db        188 AGNKVSKESSVEPVSCPEKGLDIYLIIGICGGGS----------------LLMVFVALL 230

Qy        246 FLWFLKRERQEEYIEEKKRVDICRETPNICPHSGENTEYDTIPHTNRTILKEDPANT 302
                :  ||::|      :| |   ||     |      |    ||       ::|| :
Db        231 VFYITKRKKQ-----RSRRNDEELETR---AHRVATEERGRKPHQIPASTPQNPATS 279


RESULT 6
S01299
OX-45 membrane glycoprotein precursor - rat
N;Alternate names: MRC OX-45 antigen
C;Species: Rattus norvegicus (Norway rat)
C;Date: 30-Sep-1989 #sequence_revision 30-Sep-1989 #text_change 23-Jul-1999
C;Accession: S01299
R;Killeen, N.; Moessner, R.; Arvieux, J.; Willis, A.; Williams, A.F.
EMBO J. 7, 3087-3091, 1988
A;Title: The MRC OX-45 antigen of rat leukocytes and endothelium is in a subset of the i
A;Reference number: S01299; MUID:89030603; PMID:3181129
A;Accession: S01299
A;Molecule type: mRNA
A;Residues: 1-240 <KIL>
A;Cross-references: EMBL:X13016; NID:g56804; PIDN:CAA31438.1; PID:g56805
C;Superfamily: B-cell surface glycoprotein blast-1
C;Keywords: glycoprotein; membrane protein; surface antigen
F;1-22/Domain: signal sequence #status predicted <SIG>
F;23-240/Product: OX-45 membrane glycoprotein #status predicted <MAT>
F;38,97,140,186,203/Binding site: carbohydrate (Asn) (covalent) #status predicted

  Query Match             7.6%;  Score 134;  DB 2;  Length 240;
  Best Local Similarity   24.6%;  Pred. No. 0.0013;
  Matches   48;  Conservative   33;  Mismatches  104;  Indels   10;  Gaps    4;

Qy         13 ILWQLTGSAASGPVKELVGSV----GGAVTFP-LKSKVKQVDSIVWTFNTTPLVTIQPEG 67
              ||  |  |  :|   : | :|     |  ||   ||  :     : |   |   :
Db         11 ILESLLLSLVTGFQDQSVPNVNAITGSNVTLTILKHPLASYQRLTWLHTTNQKILEYFPN 70

Qy         68 GTIIVTQNRNRERVDFPDGGYSLKLSKLKKNDSGIYYVGIYSSSLQQPSTQEYVLHVYEH 127
              |   | ::  ::|||      :|::  : | | | ||: :   :  |    :  : ||:
Db         71 GKKTVPESVFKDRVDLDKTNGALRIYNVSKEDRGDYYMRMLHETEDQ---WKITMEVYDL 127

Qy        128 LSKPKVTMGLQSNKNGTCVTNLTCCMEHGEEDVIYTWKALGQAANESHNGSILPISWRWG 187
              :||| : :    |   :|   |:| :|  :: | |||         : : | :| |:
Db        128 VSKPAIKIEKTKNLTDSCHLRLSCKVE--DQGVDYTWYEDSGPFPQRNPGYVLEITITPH 185

Qy        188 ESDMTFICVARNPVS 202
                 : |   ||||
Db        186 NKSTFYTCQVSNPVS 200


RESULT 7
RWRTC2
T-cell surface glycoprotein CD2 precursor - rat
N;Alternate names: CD2 antigen; OX-34 antigen
C;Species: Rattus norvegicus (Norway rat)
C;Date: 30-Jun-1990 #sequence_revision 30-Jun-1990 #text_change 25-Oct-1996
C;Accession: A33071; B27560; A27560; A32346
R;Barclay, A.N.; Williams, A.F.
submitted to the EMBL Data Library, May 1987
A;Reference number: A33071
A;Accession: A33071
A;Molecule type: mRNA
A;Residues: 1-344 <BAR>
R;Williams, A.F.; Barclay, A.N.; Clark, S.J.; Paterson, D.J.; Willis, A.C.
J. Exp. Med. 165, 368-380, 1987
A;Title: Similarities in sequences and cellular expression between rat CD2 and CD4 antig
A;Reference number: A27560; MUID:87139793; PMID:3102667
A;Accession: B27560
A;Molecule type: protein
A;Residues: 'X',24-52,'X',54-55,'X',57-62;93-109;119-150;238-245 <WI1>
A;Accession: A27560
A;Molecule type: mRNA
A;Residues: 44-344 <WI2>
A;Note: 112-Asn was also found
R;He, Q.; Beyers, A.D.; Barclay, A.N.; Williams, A.F.
Cell 54, 979-984, 1988
A;Title: A role in transmembrane signaling for the cytoplasmic domain of the CD2 T lymph
A;Reference number: A32346; MUID:88327862; PMID:2901293
A;Accession: A32346
A;Molecule type: mRNA
A;Residues: 1-33,'H',35-41 <HE1>
A;Cross-references: GB:X05111
C;Superfamily: T-cell surface glycoprotein CD2
C;Keywords: glycoprotein; T-cell; transmembrane protein
F;1-22/Domain: signal sequence #status predicted <SIG>
F;23-344/Product: T-cell surface glycoprotein CD2 #status predicted <MAT>
F;23-199/Domain: extracellular #status predicted <EXT>
F;200-228/Domain: transmembrane #status predicted <TMM>
F;229-344/Domain: intracellular #status predicted <INT>
F;99,106,134/Binding site: carbohydrate (Asn) (covalent) #status experimental

  Query Match             7.3%;  Score 130;  DB 1;  Length 344;
  Best Local Similarity   22.4%;  Pred. No. 0.0044;
  Matches   65;  Conservative   51;  Mismatches  112;  Indels   62;  Gaps   13;

Qy         12 YILWQLTGSAA----SGPVKELVGSVGGAVTFPLKSKVKQVDSIVWTFNTTPLVTIQPEG 67
              ::|: |:    |    || |  :|  |  :  |       :| : |           |
Db         10 FLLFSLSSKGADCRDSGTVWGALGR-GINLNIPNFQMTDDIDEVRW-----------ER 56

Qy         68 GTIIVTQNRNRERVDFPDGGY------SLKLSKLKKNDSGIYYVGIYSSSLQQPSTQEYV 121
              |: :| : : : :      | :        ||:  | ::||| | | :||::  :   :
Db         57 GSTLVAEFKRKMKPFLKSGAFEILANGDLKIKNLTRDDSGTYNVTVYSTNGTRILDKALD 116

Qy        122 LHVYEHLSKPKVTMGLQSNKNGTCV----TNLTCCMEHGEEDVIYTWKALGQAANESHNG 177
              | : | :||| :      ||   ||      |::   :  |:| :    ::| |
Db        117 LRILEMVSKPMIYWEC-SNATLTCEVLEGTDVELKLYQGKEHL----RSLRQKT------ 165

Qy        178 SILPISWRWGESDMTFICVARNPVSRNFSSPILARKLCEGAADDPDSSMVLLCLLLVPL- 236
                :|::|       | | | | ||:      ::          : |:  : |  :: |
Db        166 ----MSYQWTNLRAPFKCKAVNRVSQESEMEVV---------NCPEKGLPLYLIVGVSAG 212

Qy        237 -LLSLFVLGLFLWFL------KRERQEEYIEEK-KRVDICRETPNICPHS 278
```

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                 || :|   ||:: :       | |: | :| |  |:       |   |||
Db        213 GLLLVFFGALFIFCICKRKKRNRRRKGEELEIKASRMSTVERGPK--PHS 260
```

RESULT 8
JL0143
antigen BCM1 precursor - mouse
N;Alternate names: CD48 antigen homolog sgp-60; OX45 antigen, Blast-1 antigen
C;Species: Mus musculus (house mouse)
C;Date: 31-Dec-1991 #sequence_revision 31-Dec-1991 #text_change 31-Jan-2000
C;Accession: JL0143; S21319; A47469; B47469
R;Wong, Y.W.; Williams, A.F.; Kingsmore, S.F.; Seldin, M.F.
J. Exp. Med. 171, 2115-2130, 1990
A;Title: Structure, expression, and genetic linkage of the mouse BCM1 (OX45 or Blast-1) region on mouse chromosome 3.
A;Reference number: JL0143; MUID:90278362; PMID:1693656
A;Accession: JL0143
A;Molecule type: mRNA
A;Residues: 1-240 <WON>
A;Cross-references: EMBL:X17501; NID:g50134; PIDN:CAA35542.1; PID:g50135
R;Wong, Y.W.; Williams, A.F.; Kingsmore, S.F.; Seldin, M.F.
submitted to the EMBL Data Library, June 1990
A;Description: Structure, expression and genetic linkage of the mouse BCM1 (OX45 or Blas
3 region on mouse chromosome 3.
A;Reference number: S21319
A;Accession: S21319
A;Status: preliminary
A;Molecule type: mRNA
A;Residues: 1-240 <WON2>
A;Cross-references: EMBL:X53526; NID:g50138; PIDN:CAA37604.1; PID:g50139
R;Cabrero, J.G.; Freeman, G.J.; Lane, W.S.; Reiser, H.
Proc. Natl. Acad. Sci. U.S.A. 90, 3418-3422, 1993
A;Title: Identification, by protein sequencing and gene transfection, of sgp-60 as the m
A;Reference number: A47469; MUID:93234508; PMID:8475091
A;Accession: A47469
A;Molecule type: protein
A;Residues: 74-80 <CAB>
A;Experimental source: EL-4 lymphoma cells
A;Note: sequence extracted from NCBI backbone (NCBIP:129658)
A;Accession: B47469
A;Molecule type: protein
A;Residues: 84-98 <CA2>
A;Experimental source: EL-4 lymphoma cells
A;Note: sequence extracted from NCBI backbone (NCBIP:129660)
C;Comment: This antigen is widely expressed on leukocytes and is likely to be anchored t
C;Superfamily: B-cell surface glycoprotein blast-1
C;Keywords: blocked carboxyl end; glycoprotein; lipoprotein; phosphatidylinositol linkag
F;1-22/Domain: signal sequence #status predicted <SIG>
F;23-217/Product: antigen BCM1 #status predicted <MAT>
F;218-240/Domain: carboxyl-terminal propeptide #status predicted <CPT>
F;32,38,70,136,186,203/Binding site: carbohydrate (Asn) (covalent) #status predicted
F;217/Modified site: GPI-anchor ethanolamine amidated carboxyl end (Ser) (in mature form

  Query Match   7.1%; Score 126.5; DB 2; Length 240;
  Best Local Similarity   21.4%; Pred. No. 0.0055;
  Matches   52; Conservative   45; Mismatches 125; Indels   21; Gaps   8;

```
Qy          7 CLTLIYILWQLTGSAASGPVKELVGSVGGAVTFPL-KSKVKQVDSIVWTFNTTPLVTIQP 65
              || |  :| |         : ::  : |  ||  : |  :     | |       :
Db          9 CLVLELLLLPLGTGFQGHSIPDINATTGSNVTLKIHKDPLGPYKRITWLHTKNQKILEYN 68

Qy         66 EGGTIIVTQNRNRERVDFPDGGYSLKLSKLKKNDSGIYYVGIYSSSLQQPSTQ-EYVLHV 124
                 | : ::  : ||   :   :| :| ::| | | ||: :    |::   : :  | |
Db         69 YNSTKTIFESEFKGRVYLEENNGALHISNVRKEDKGTYYMRV----LRETENELKITLEV 124

Qy        125 YEHLSKPKVTMGLQSNKNGTCVTNLTCCMEHGEEDVIYTWKALGQAANESHNGSILPISW 184
              :: : || : :       :|   |:|  |  :: | |||         :   | :| :
Db        125 FDPVPKPSIEIINKTEASTDSCHLRLSC--EVKDQHVDYTWYESSGPFPKKSPGYVLDLIV 182

Qy        185 RWGESDMTFICVARNPVSRN-----FSSPI-LARK--LCEGAADDPDSSMVLLCLLLVPL 236
                    : |   ||||       |: |  |||   :|  |     : :|:  |::  :
Db        183 TPQNKSTFYTCQVSNPVSSKNDTVYFTLPCDLARSSGVCWTA-----TWLVVTTLIIHRI 237
```

```
Qy        237 LLS 239
              ||:
Db        238 LLT 240
```

RESULT 9
JH0395
biliary glycoprotein h precursor - human
C;Species: Homo sapiens (man)
C;Date: 30-Sep-1991 #sequence_revision 30-Sep-1991 #text_change 23-Jul-1999
C;Accession: JH0395
R;Kuroki, M.; Arakawa, F.; Matsuo, Y.; Oikawa, S.; Nakazato, H.; Matsuoka, Y.
Biochem. Biophys. Res. Commun. 176, 578-585, 1991
A;Title: Three novel molecular forms of biliary glycoprotein deduced from cDNA clones f
A;Reference number: JH0394; MUID:91222218; PMID:2025273
A;Accession: JH0395
A;Molecule type: mRNA
A;Residues: 1-321 <KUR>
A;Cross-references: GB:M69176; NID:g179434; PIDN:AAA51825.1; PID:g179435
A;Experimental source: leukocyte
C;Comment: Biliary glycoproteins belong to the carcinoembryonic antigen gene family.
C;Superfamily: carcinoembryonic antigen; carcinoembryonic antigen precursor amino-termir
C;Keywords: glycoprotein; transmembrane protein
F;1-138/Domain: carcinoembryonic antigen precursor amino-terminal homology <CEAN>
F;1-34/Domain: signal sequence #status predicted <SIG>
F;35-321/Product: biliary glycoprotein h #status predicted <MAT>
F;160-217/Domain: immunoglobulin homology <IMM1>
F;252-301/Domain: immunoglobulin homology <IMM2>

  Query Match   7.1%; Score 125.5; DB 2; Length 321;
  Best Local Similarity   25.1%; Pred. No. 0.0094;
  Matches   67; Conservative   36; Mismatches   93; Indels   71; Gaps   17;

```
Qy         68 GTIIVTQ-------NRNRERVDFPDGGYSLKLSKLKKNDSGIYYVGIYSSSL-QQPSTQE 119
              |  | ||        |  || : :|:   || :  : :||:| | : :  | |  : :| :
Db         81 GYAIGTQQATPGPANSGRETI-YPNA--SLLIQNVTQNDTGFYTLQVIKSDLVNEEATGQ 137

Qy        120 YVLHVYEHLSKPKVTMGLQSNKNGTCVTNLTCCMEHGEEDVIYTWKALGQAANESHNGSI 179
              :  |||  | || ::    :           ||  |   :|  | |          |
Db        138 F--HVYPELPKPSISSNNSNPVEDKDAVAFTC--EPETQDTTYLWWI---------NNQS 184

Qy        180 LPISWRW----GESDMTFICVAR-----------NPVSRNFSSPILARKLCEG------A 218
              ||:| |     |   :| : | |           |||| | | |:    :  |       :
Db        185 LPVSPRLQLSNGNRTLTLLSVTRNDTGPYECEIQNPVSANRSDPV-TLNVTYGPDTPTIS 243

Qy        219 ADD----PDSSMVLLCLLL--VPLLLSLFVLGLFLWFLKRERQEEYIEEKKRVDICRETP 272
                 |    | ::: | |       |   |  : | |    ::  || :|            |
Db        244 PSDTYYRPGANLSLSCYAASNPPAQYSWLINGTF----QQSTQELFI------------P 287

Qy        273 NI-CPHSGENTEY--DTIPHTNRTILK 296
              ||   :||  | :  :::   ||| :|
Db        288 NITVNNSGSYTCHANNSVTGCNRTTVK 314
```

RESULT 10
JH0396
biliary glycoprotein i precursor - human
C;Species: Homo sapiens (man)
C;Date: 30-Sep-1991 #sequence_revision 30-Sep-1991 #text_change 23-Jul-1999
C;Accession: JH0396
R;Kuroki, M.; Arakawa, F.; Matsuo, Y.; Oikawa, S.; Nakazato, H.; Matsuoka, Y.
Biochem. Biophys. Res. Commun. 176, 578-585, 1991
A;Title: Three novel molecular forms of biliary glycoprotein deduced from cDNA clones f
A;Reference number: JH0394; MUID:91222218; PMID:2025273
A;Accession: JH0396
A;Molecule type: mRNA
A;Residues: 1-351 <KUR>
A;Cross-references: GB:M72238; NID:g179436; PIDN:AAA58393.1; PID:g179437
A;Experimental source: leukocyte
C;Comment: Biliary glycoproteins belong to the carcinoembryonic antigen gene family.
C;Superfamily: carcinoembryonic antigen; carcinoembryonic antigen precursor amino-termir
C;Keywords: glycoprotein; transmembrane protein
F;1-138/Domain: carcinoembryonic antigen precursor amino-terminal homology <CEAN>

```
F;1-34/Domain: signal sequence #status predicted <SIG>
F;35-351/Product: biliary glycoprotein i #status predicted <MAT>
F;160-217/Domain: immunoglobulin homology <IMM1>
F;252-301/Domain: immunoglobulin homology <IMM2>

  Query Match             7.1%;  Score 125.5;  DB 2;  Length 351;
  Best Local Similarity   25.1%;  Pred. No. 0.011;
  Matches   67;  Conservative   36;  Mismatches   93;  Indels   71;  Gaps   17;

Qy         68 GTIIVTQ-------NRNRERVDFPDGGYSLKLSKLKKNDSGIYYVGIYSSSL-QQPSTQE 119
              |  | ||        |  || : :|:   || :  : :||:| | : :  | |  : :| :
Db         81 GYAIGTQQATPGPANSGRETI-YPNA--SLLIQNVTQNDTGFYTLQVIKSDLVNEEATGQ 137

Qy        120 YVLHVYEHLSKPKVTMGLQSNKNGTCVTNLTCCMEHGEEDVIYTWKALGQAANESHNGSI 179
              :  |||  | || ::    :           ||  |   :|  | |              |
Db        138 F--HVYPELPKPSISSNNSNPVEDKDAVAFTC--EPETQDTTYLWWI---------NNQS 184

Qy        180 LPISWRW----GESDMTFICVAR-----------NPVSRNFSSPILARKLCEG------A 218
              ||:| |     |   :| : | |           |||| | | |:    :  |      :
Db        185 LPVSPRLQLSNGNRTLTLLSVTRNDTGPYECEIQNPVSANRSDPV-TLNVTYGPDTPTIS 243

Qy        219 ADD----PDSSMVLLCLLL--VPLLLSLFVLGLFLWFLKRERQEEYIEEKKRVDICRETP 272
              |    | ::: | |      |   |  : | |    ::  || :|            |
Db        244 PSDTYYRPGANLSLSCYAASNPPAQYSWLINGTF----QQSTQELFI-----------P 287

Qy        273 NI-CPHSGENTEY--DTIPHTNRTILK 296
              ||   :||  | :  :::   ||| :|
Db        288 NITVNNSGSYTCHANNSVTGCNRTTVK 314


RESULT 11
JH0394
biliary glycoprotein g precursor - human
C;Species: Homo sapiens (man)
C;Date: 30-Sep-1991 #sequence_revision 30-Sep-1991 #text_change 23-Jul-1999
C;Accession: JH0394
R;Kuroki, M.; Arakawa, F.; Matsuo, Y.; Oikawa, S.; Nakazato, H.; Matsuoka, Y.
Biochem. Biophys. Res. Commun. 176, 578-585, 1991
A;Title: Three novel molecular forms of biliary glycoprotein deduced from cDNA clones fr
A;Reference number: JH0394; MUID:91222218; PMID:2025273
A;Accession: JH0394
A;Molecule type: mRNA
A;Residues: 1-417 <KUR>
A;Cross-references: GB:M72238; NID:g179436; PIDN:AAA58394.1; PID:g179438
A;Experimental source: leukocyte
C;Comment: Biliary glycoproteins belong to the carcinoembryonic antigen gene family.
C;Superfamily: carcinoembryonic antigen; carcinoembryonic antigen precursor amino-termin
C;Keywords: glycoprotein; transmembrane protein
F;1-138/Domain: carcinoembryonic antigen precursor amino-terminal homology <CEAN>
F;1-34/Domain: signal sequence #status predicted <SIG>
F;35-383/Product: biliary glycoprotein g #status predicted <MAT>
F;160-217/Domain: immunoglobulin homology <IMM1>
F;252-301/Domain: immunoglobulin homology <IMM2>
F;341-398/Domain: immunoglobulin homology <IMM3>

  Query Match             7.1%;  Score 125.5;  DB 2;  Length 417;
  Best Local Similarity   25.1%;  Pred. No. 0.013;
  Matches   67;  Conservative   36;  Mismatches   93;  Indels   71;  Gaps   17;

Qy         68 GTIIVTQ-------NRNRERVDFPDGGYSLKLSKLKKNDSGIYYVGIYSSSL-QQPSTQE 119
              |  | ||        |  || : :|:   || :  : :||:| | : :  | |  : :| :
Db         81 GYAIGTQQATPGPANSGRETI-YPNA--SLLIQNVTQNDTGFYTLQVIKSDLVNEEATGQ 137

Qy        120 YVLHVYEHLSKPKVTMGLQSNKNGTCVTNLTCCMEHGEEDVIYTWKALGQAANESHNGSI 179
              :  |||  | || ::    :           ||  |   :|  | |              |
Db        138 F--HVYPELPKPSISSNNSNPVEDKDAVAFTC--EPETQDTTYLWWI---------NNQS 184

Qy        180 LPISWRW----GESDMTFICVAR-----------NPVSRNFSSPILARKLCEG------A 218
              ||:| |     |   :| : | |           |||| | | |:    :  |      :
Db        185 LPVSPRLQLSNGNRTLTLLSVTRNDTGPYECEIQNPVSANRSDPV-TLNVTYGPDTPTIS 243

Qy        219 ADD----PDSSMVLLCLLL--VPLLLSLFVLGLFLWFLKRERQEEYIEEKKRVDICRETP 272
              |    | ::: | |      |   |  : | |    ::  || :|            |
Db        244 PSDTYYRPGANLSLSCYAASNPPAQYSWLINGTF----QQSTQELFI-----------P 287

Qy        273 NI-CPHSGENTEY--DTIPHTNRTILK 296
              ||   :||  | :  :::   ||| :|
Db        288 NITVNNSGSYTCHANNSVTGCNRTTVK 314


RESULT 12
C30127
transmembrane carcinoembryonic antigen 3 precursor - human
N;Alternate names: CD66 splice form BGPc
C;Species: Homo sapiens (man)
C;Date: 07-Sep-1990 #sequence_revision 07-Sep-1990 #text_change 23-Jul-1999
C;Accession: C30127; I52597
R;Barnett, T.R.; Kretschmer, A.; Austen, D.A.; Goebel, S.J.; Hart, J.T.; Elting, J.J.; K
J. Cell Biol. 108, 267-276, 1989
A;Title: Carcinoembryonic antigens: alternative splicing accounts for the multiple mRNAs
A;Reference number: A92752; MUID:89139550; PMID:2537311
A;Accession: C30127
A;Molecule type: mRNA
A;Residues: 1-464 <BAR>
A;Cross-references: EMBL:X16356; EMBL:X14784
R;Watt, S.M.; Fawcett, J.; Murdoch, S.J.; Teixeira, A.M.; Gschmeissner, S.E.; Hajibagher
Blood 84, 200-210, 1994
A;Title: CD66 identifies the biliary glycoprotein (BGP) adhesion molecule: cloning, expr
A;Reference number: I52597; MUID:94289702; PMID:8018919
A;Accession: I52597
A;Status: preliminary; translated from GB/EMBL/DDBJ
A;Molecule type: mRNA
A;Residues: 1-464 <RES>
A;Cross-references: GB:S71326; NID:g550030; PIDN:AAB31183.1; PID:g550031
C;Superfamily: carcinoembryonic antigen; carcinoembryonic antigen precursor amino-termin
C;Keywords: alternative splicing; glycoprotein; surface antigen; transmembrane protein
F;1-138/Domain: carcinoembryonic antigen precursor amino-terminal homology <CEAN>
F;1-34/Domain: signal sequence #status predicted <SIG>
F;35-464/Product: transmembrane carcinoembryonic antigen 3 #status predicted <MAT>
F;160-217/Domain: immunoglobulin homology <IMM1>
F;252-301/Domain: immunoglobulin homology <IMM2>
F;341-398/Domain: immunoglobulin homology <IMM3>
F;424-455/Domain: transmembrane #status predicted <TMM>
F;104,111,115,152,182,197,208,224,232,254,274,288,292,302,309,345,351,363,378,405/Bindin

  Query Match             7.1%;  Score 125.5;  DB 2;  Length 464;
  Best Local Similarity   25.1%;  Pred. No. 0.015;
  Matches   67;  Conservative   36;  Mismatches   93;  Indels   71;  Gaps   17;

Qy         68 GTIIVTQ-------NRNRERVDFPDGGYSLKLSKLKKNDSGIYYVGIYSSSL-QQPSTQE 119
              |  | ||        |  || : :|:   || :  : :||:| | : :  | |  : :| :
Db         81 GYAIGTQQATPGPANSGRETI-YPNA--SLLIQNVTQNDTGFYTLQVIKSDLVNEEATGQ 137

Qy        120 YVLHVYEHLSKPKVTMGLQSNKNGTCVTNLTCCMEHGEEDVIYTWKALGQAANESHNGSI 179
              :  |||  | || ::    :           ||  |   :|  | |              |
Db        138 F--HVYPELPKPSISSNNSNPVEDKDAVAFTC--EPETQDTTYLWWI---------NNQS 184

Qy        180 LPISWRW----GESDMTFICVAR-----------NPVSRNFSSPILARKLCEG------A 218
              ||:| |     |   :| : | |           |||| | | |:    :  |      :
Db        185 LPVSPRLQLSNGNRTLTLLSVTRNDTGPYECEIQNPVSANRSDPV-TLNVTYGPDTPTIS 243

Qy        219 ADD----PDSSMVLLCLLL--VPLLLSLFVLGLFLWFLKRERQEEYIEEKKRVDICRETP 272
              |    | ::: | |      |   |  : | |    ::  || :|            |
Db        244 PSDTYYRPGANLSLSCYAASNPPAQYSWLINGTF----QQSTQELFI-----------P 287

Qy        273 NI-CPHSGENTEY--DTIPHTNRTILK 296
              ||   :||  | :  :::   ||| :|
Db        288 NITVNNSGSYTCHANNSVTGCNRTTVK 314


RESULT 13
A32164
biliary glycoprotein 1 precursor, splice form a - human
N;Alternate names: transmembrane carcinoembryonic antigen 1 (TM1-CEA); transmembrane car
N;Contains: biliary glycoprotein 1, splice form b; biliary glycoprotein 1, splice form x
C;Species: Homo sapiens (man)
```

C;Date: 20-Apr-2000 #sequence_revision 20-Apr-2000 #text_change 20-Apr-2000
C;Accession: A32164; A30127; B30127; A48078; S45664; S65939; A30847; G44476
R;Hinoda, Y.; Neumaier, M.; Hefta, S.A.; Drzeniek, Z.; Wagener, C.; Shively, L.; Hefta,
Proc. Natl. Acad. Sci. U.S.A. 86, 1668, 1989
A;Reference number: A32164
A;Contents: erratum
A;Accession: A32164
A;Molecule type: mRNA
A;Residues: 1-526 <HIN>
A;Cross-references: GB:J03858; NID:g179439; PIDN:AAA51826.1; PID:g179440
R;Hinoda, Y.; Neumaier, M.; Hefta, S.A.; Drzeniek, Z.; Wagener, C.; Shively, L.; Hefta,
Proc. Natl. Acad. Sci. U.S.A. 85, 6959-6963, 1988
A;Title: Molecular cloning of a cDNA coding biliary glycoprotein I: Primary structure of
A;Reference number: A94206; MUID:88320555; PMID:2457922
A;Contents: annotation
A;Note: the sequence shown in this reference has been completely corrected in reference
R;Barnett, T.R.; Kretschmer, A.; Austen, D.A.; Goebel, S.J.; Hart, J.T.; Elting, J.J.; K
J. Cell Biol. 108, 267-276, 1989
A;Title: Carcinoembryonic antigens: alternative splicing accounts for the multiple mRNAs
A;Reference number: A92752; MUID:89139550; PMID:2537311
A;Accession: A30127
A;Molecule type: mRNA
A;Residues: 1-526 <BAR1>
A;Cross-references: EMBL:X16354; NID:g37197; PIDN:CAA34404.1; PID:g37198; EMBL:X14784
A;Experimental source: splice form a
A;Accession: B30127
A;Molecule type: mRNA
A;Residues: 1-319,'D',417-526 <BAR2>
A;Cross-references: EMBL:X14831; NID:g37199; PIDN:CAA32940.1; PID:g37200; EMBL:X14784
A;Experimental source: splice form b
R;Barnett, T.R.; Drake, L.; Pickle II, W.
Mol. Cell. Biol. 13, 1273-1282, 1993
A;Title: Human biliary glycoprotein gene: characterization of a family of novel alternat
A;Reference number: A48078; MUID:93140765; PMID:8423792
A;Accession: A48078
A;Molecule type: mRNA
A;Residues: 124-141,'H',417-526 <BAR3>
A;Cross-references: GB:M76742; NID:g179480; PIDN:AAA57142.1; PID:g179481
A;Experimental source: splice form x
A;Note: sequence extracted from NCBI backbone (NCBIN:123602, NCBIP:123606)
A;Note: neither the complete nucleic acid sequence nor the complete translation are show
R;Hauck, W.; Nedellec, P.; Turbide, C.; Stanners, C.P.; Barnett, T.R.; Beauchemin, N.
Eur. J. Biochem. 223, 529-541, 1994
A;Title: Transcriptional control of the human biliary glycoprotein gene, a CEA gene fami
A;Reference number: S45664; MUID:94333343; PMID:8055923
A;Accession: S45664
A;Status: preliminary
A;Molecule type: DNA
A;Residues: 1-21 <HAU>
A;Cross-references: EMBL:X67277; NID:g29447; PIDN:CAA47694.1; PID:g606777
R;Nedellec, P.; Turbide, C.; Beauchemin, N.
Eur. J. Biochem. 231, 104-114, 1995
A;Title: Characterization and transcriptional activity of the mouse biliary glycoprotein
A;Reference number: S65939; MUID:95354678; PMID:7628460
A;Accession: S65939
A;Status: preliminary; translation not shown
A;Molecule type: DNA
A;Residues: 1-21 <NED>
A;Cross-references: EMBL:X67277; NID:g29447; PIDN:CAA47694.1; PID:g606777
A;Note: the nucleotide sequence was submitted to the EMBL Data Library, July 1992
A;Note: only a part of the coding sequence is given
R;Khan, W.N.; Fraengsmyr, L.; Teglund, S.; Israelsson, A.; Bremer, K.; Hammarstroem, S.
Genomics 14, 384-390, 1992
A;Title: Identification of three new genes and estimation of the size of the carcinoembr
A;Reference number: A44476; MUID:93052339; PMID:1427854
A;Contents: annotation; alignment of related sequences
C;Genetics:
A;Gene: GDB:BGP
A;Cross-references: GDB:127992; OMIM:109770
A;Map position: 19q13.2-19q13.2
C;Superfamily: carcinoembryonic antigen; carcinoembryonic antigen precursor amino-termir
C;Keywords: alternative splicing; glycoprotein; surface antigen; transmembrane protein
F;1-138/Domain: carcinoembryonic antigen precursor amino-terminal homology <CEAN>
F;1-34/Domain: signal sequence #status predicted <SIG>
F;35-526/Product: biliary glycoprotein 1, splice form a #status predicted <MATA>
F;35-428/Domain: extracellular #status predicted <EXT>
F;35-319,'D',417-526/Product: biliary glycoprotein 1, splice form b #status predicted <I
F;35-141,'H',417-526/Product: biliary glycoprotein 1, splice form x #status predicted <I
F;160-217/Domain: immunoglobulin homology <IMM1>
F;252-301/Domain: immunoglobulin homology <IMM2>
F;341-398/Domain: immunoglobulin homology <IMM3>
F;425-454/Domain: transmembrane #status predicted <TMM>
F;453-526/Domain: intracellular #status predicted <INT>
F;104,111,115,152,182,197,208,224,232,254,274,288,292,302,309,345,351,363,378,405,475/Bi

Query Match 7.1%; Score 125.5; DB 1; Length 526;
Best Local Similarity 25.1%; Pred. No. 0.017;
Matches 67; Conservative 36; Mismatches 93; Indels 71; Gaps 17;

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Qy         68 GTIIVTQ-------NRNRERVDFPDGGYSLKLSKLKKNDSGIYYVGIYSSSL-QQPSTQE 119
              |  | ||       |  || : :|:   || :  : :||:| | : :  | |  : :| :
Db         81 GYAIGTQQATPGPANSGRETI-YPNA--SLLIQNVTQNDTGFYTLQVIKSDLVNEEATGQ 137

Qy        120 YVLHVYEHLSKPKVTMGLQSNKNGTCVTNLTCCMEHGEEDVIYTWKALGQAANESHNGSI 179
              :  |||  | || ::   :           || |   :|  | |           |
Db        138 F--HVYPELPKPSISSNNSNPVEDKDAVAFTC--EPETQDTTYLWWI---------NNQS 184

Qy        180 LPISWRW----GESDMTFICVAR----------NPVSRNFSSPILARKLCEG------A 218
              ||:| |     |   :| : | |          |||| | | |:    :  |      :
Db        185 LPVSPRLQLSNGNRTLTLLSVTRNDTGPYECEIQNPVSANRSDPV-TLNVTYGPDTPTIS 243

Qy        219 ADD----PDSSMVLLCLLL--VPLLLSLFVLGLFLWFLKRERQEEYIEEKKRVDICRETP 272
                 |    | ::: | |       |   |  : | |    ::  || :|            |
Db        244 PSDTYYRPGANLSLSCYAASNPPAQYSWLINGTF----QQSTQELFI----------P 287

Qy        273 NI-CPHSGENTEY--DTIPHTNRTILK 296
              ||   :||  | :  :::   ||| :|
Db        288 NITVNNSGSYTCHANNSVTGCNRTTVK 314
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RESULT 14
A27681
nonspecific cross-reacting antigen precursor - human
N;Alternate names: NCA; TEX/NCA
C;Species: Homo sapiens (man)
C;Date: 31-Mar-1989 #sequence_revision 16-Sep-1992 #text_change 31-Jan-2000
C;Accession: A26902; A29875; A27681; B31037; A29918; A27709; A36271; C26414; E44476; F44
R;Oikawa, S.; Kosaki, G.; Nakazato, H.
Biochem. Biophys. Res. Commun. 146, 464-469, 1987
A;Title: Molecular cloning of a gene for a member of carcinoembryonic antigen (CEA) gene
A;Reference number: A26902; MUID:87298464; PMID:3619891
A;Accession: A26902
A;Molecule type: DNA
A;Residues: 1-141 <OIK>
A;Cross-references: GB:M17082; NID:g180230; PIDN:AAA51971.1; PID:g553222
R;Thompson, J.A.; Pande, H.; Paxton, R.J.; Shively, L.; Padma, A.; Simmer, R.L.; Todd,
Proc. Natl. Acad. Sci. U.S.A. 84, 2965-2969, 1987
A;Title: Molecular cloning of a gene belonging to the carcinoembryonic antigen gene fam
A;Reference number: A29875; MUID:87204248; PMID:3033672
A;Accession: A29875
A;Molecule type: DNA
A;Residues: 23-141 <THO>
A;Cross-references: GB:M16337
A;Note: the authors translated the codon ACT for residue 64 as Tyr
R;Tawaragi, Y.; Oikawa, S.; Matsuoka, Y.; Kosaki, G.; Nakazato, H.
Biochem. Biophys. Res. Commun. 150, 89-96, 1988
A;Title: Primary structure of nonspecific crossreacting antigen (NCA), a member of carci
A;Reference number: A27681; MUID:88106638; PMID:3337731
A;Accession: A27681
A;Molecule type: mRNA
A;Residues: 1-238,'V',240-344 <TAW>
A;Cross-references: GB:M18728; NID:g189084; PIDN:AAA59907.1; PID:g189085
R;Barnett, T.; Goebel, S.J.; Nothdurft, M.A.; Elting, J.J.
Genomics 3, 59-66, 1988
A;Title: Carcinoembryonic antigen family: characterization of cDNAs coding for NCA and
A;Reference number: A31037; MUID:89122014; PMID:3220478

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A;Accession: B31037
A;Molecule type: mRNA
A;Residues: 1-137,'L',139-344 <BAR>
A;Cross-references: GB:M29541; NID:g189103; PIDN:AAA59915.1; PID:g189104
A;Note: the authors translated the codon TTG for residue 138 as Phe
R;Neumaier, M.; Zimmermann, W.; Shively, L.; Hinoda, Y.; Riggs, A.D.; Shively, J.E.
J. Biol. Chem. 263, 3202-3207, 1988
A;Title: Characterization of a cDNA clone for the nonspecific cross-reacting antigen (NC
A;Reference number: A29918; MUID:88139389; PMID:2830274
A;Accession: A29918
A;Molecule type: mRNA
A;Residues: 1-344 <NEU>
A;Cross-references: GB:M18216; GB:J03550; NID:g178690; PIDN:AAA51739.1; PID:g178691
R;Grunert, F.; Kolbinger, F.; Schwarz, K.; Schwaibold, H.; von Kleist, S.
Biochem. Biophys. Res. Commun. 153, 1105-1115, 1988
A;Title: Protein analysis of NCA-50 shows identity to NCA cDNA deduced sequences and ind
A;Reference number: A27709; MUID:88268882; PMID:3390172
A;Accession: A27709
A;Molecule type: protein
A;Residues: 35-95;99-120;123-138;149-151,'X',153-162;166,'X',168-172,'X',174-193;231-235
R;Hefta, S.A.; Paxton, R.J.; Shively, J.E.
J. Biol. Chem. 265, 8618-8626, 1990
A;Title: Sequence and glycosylation site identity of two distinct glycoforms of nonspeci
A;Reference number: A36271; MUID:90256782; PMID:2341397
A;Accession: A36271
A;Molecule type: protein
A;Residues: 35-42;44-53;55-80;83-134;139-160;166-172;174-180;191-194,204-224;233-308;310
R;Paxton, R.J.; Mooser, G.; Pande, H.; Lee, T.D.; Shively, J.E.
Proc. Natl. Acad. Sci. U.S.A. 84, 920-924, 1987
A;Title: Sequence analysis of carcinoembryonic antigen: identification of glycosylation
A;Reference number: A26414; MUID:87147209; PMID:3469650
A;Accession: C26414
A;Molecule type: protein
A;Residues: 35-69 <PAX>
R;Khan, W.N.; Fraengsmyr, L.; Teglund, S.; Israelsson, A.; Bremer, K.; Hammarstroem, S.
Genomics 14, 384-390, 1992
A;Title: Identification of three new genes and estimation of the size of the carcinoembr
A;Reference number: A44476; MUID:93052339; PMID:1427854
A;Accession: E44476
A;Status: preliminary; not compared with conceptual translation
A;Molecule type: DNA
A;Residues: 35-141 <KHA>
A;Accession: F44476
A;Status: preliminary; not compared with conceptual translation
A;Molecule type: DNA
A;Residues: 35-137,'L',139-141 <KH2>
C;Comment: This protein appears to be processed at the carboxyl terminus and anchored th
C;Genetics:
A;Gene: GDB:NCA
A;Cross-references: GDB:120221; OMIM:163980
A;Map position: 19q13.2-19q13.2
A;Introns: 22/1
A;Note: the list of introns may be incomplete
C;Superfamily: carcinoembryonic antigen; carcinoembryonic antigen precursor amino-termin
C;Keywords: blocked carboxyl end; glycoprotein; lipoprotein; membrane protein; phosphati
F;1-138/Domain: carcinoembryonic antigen precursor amino-terminal homology <CEAN>
F;1-34/Domain: signal sequence #status predicted <SIG>
F;35-320/Product: nonspecific cross-reacting antigen #status experimental <MAT>
F;160-217/Domain: immunoglobulin homology <IMM1>
F;252-301/Domain: immunoglobulin homology <IMM2>
F;321-344/Domain: carboxyl-terminal propeptide #status predicted <CTP>
F;104,111,115,152,173,197,224,256,274,288,292/Binding site: carbohydrate (Asn) (covalent
F;309/Binding site: carbohydrate (Asn) (covalent) #status predicted
F;320/Modified site: GPI-anchor ethanolamine amidated carboxyl end (Gly) (in mature form

  Query Match             7.0%;  Score 124.5;  DB 2;  Length 344;
  Best Local Similarity   22.4%;  Pred. No. 0.012;
  Matches   75;  Conservative   35;  Mismatches  118;  Indels  107;  Gaps   16;

Qy         53 WTFNTTPLVTIQ------PEGGTII-----VTQNR------NRERVD------------ 82
              |   ||  :||:       ||  ::     : |||       ||||
Db         28 WNPPTTAKLTIESTPFNVAEGKEVLLLAHNLPQNRIGYSWYKGERVDGNSLIVGYVIGTQ 87

Qy         83 --FPDGGY----------SLKLSKLKKNDSGIYYVGIYSSSL-QQPSTQEYVLHVYEHLS 129
                 |   |          || :  : :||:| | : :  | |  : :| ::  |||  |
Db         88 QATPGPAYSGRETIYPNASLLIQNVTQNDTGFYTLQVIKSDLVNEEATGQF--HVYPELP 145

Qy        130 KPKVTMGLQSNKNGTCVTNLTCCMEHGEEDVIYTWKALGQAANESHNGSILPISWRW--- 186
              || ::    :          ||  |   ::   | |              ||  ||:| |
Db        146 KPSISSNNSNPVEDKDAVAFTC--EPEVQNTTYLWWV---------NGQSLPVSPRLQLS 194

Qy        187 -GESDMTFI----------CVARNPVSRNFSSPILARKLC---------EGAADDPDSS 225
               |   :| :          |  :|| | | | |:    |              |   | :
Db        195 NGNMTLTLLSVKRNDAGSYECEIQNPASANRSDPVTLNVLYGPDGPTISPSKANYRPGEN 254

Qy        226 MVLLCLLL--VPLLLSLFVLGLFLWFLKRERQEEYIEEKKRVDICRETPNI--------- 274
              : | |      |   | |: | |    ::  || :|            |||
Db        255 LNLSCHAASNPPAQYSWFINGTF----QQSTQELFI-----------PNITVNNSGSYM 298

Qy        275 CPHSGENTEYDTIPHTNRTILKEDPANTVYSTVEI 309
              |      |  :   |  |:    |  :  :|| |
Db        299 CQAHNSATGLNRTTVTMITVSGSAPVLSAVATVGI 333


RESULT 15
S34338
biliary glycoprotein F - mouse
N;Alternate names: mouse hepatitis virus (MHV) receptor glycoprotein
C;Species: Mus musculus (house mouse)
C;Date: 20-Feb-1995 #sequence_revision 20-Feb-1995 #text_change 23-Jul-1999
C;Accession: S34338; JC1510; A41093
R;Huang, D.C.; Huang, X.F.; Novel, M.; Novel, G.
submitted to the EMBL Data Library, July 1992
A;Description: A Clp-family gene present on the lactose-protease plasmid of lactococcus
A;Reference number: S34338
A;Accession: S34338
A;Status: preliminary
A;Molecule type: mRNA
A;Residues: 1-521 <HUA>
A;Cross-references: EMBL:X67281; NID:g312585; PIDN:CAA47698.1; PID:g312586
R;McCuaig, K.; Rosenberg, M.; Nedellec, P.; Turbide, C.; Beauchemin, N.
Gene 127, 173-183, 1993
A;Title: Expression of the Bgp gene and characterization of mouse colon biliary glycopro
A;Reference number: JC1505; MUID:93273228; PMID:8500759
A;Accession: JC1510
A;Molecule type: mRNA
A;Residues: 1-81,'Q',83-141,'P',143-521 <MCC>
A;Cross-references: GB:X67281
R;Williams, R.K.; Jiang, G.S.; Holmes, K.V.
Proc. Natl. Acad. Sci. U.S.A. 88, 5533-5536, 1991
A;Title: Receptor for mouse hepatitis virus is a member of the carcinoembryonic antigen
A;Reference number: A41093; MUID:91288498; PMID:1648219
A;Accession: A41093
A;Status: preliminary
A;Molecule type: protein
A;Residues: 35-59 <WIL>
C;Comment: This protein is expressed at the cell surface and plays a determinant role in
C;Genetics:
A;Gene: BgpF
C;Superfamily: carcinoembryonic antigen; carcinoembryonic antigen precursor amino-termin
C;Keywords: glycoprotein; receptor
F;1-138/Domain: carcinoembryonic antigen precursor amino-terminal homology <CEAN>
F;160-219/Domain: immunoglobulin homology <IMM1>
F;254-303/Domain: immunoglobulin homology <IMM2>
F;339-396/Domain: immunoglobulin homology <IMM3>
F;87,104,148,199,206,210,226,258,290,294,304,333,375/Binding site: carbohydrate (Asn) (c

  Query Match             6.9%;  Score 122.5;  DB 2;  Length 521;
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  Matches   47;  Conservative   32;  Mismatches   70;  Indels   61;  Gaps    8;

Qy         53 WTFNTTPLVTIQ-------PEGGTIIVTQN----------------RNRERVDFPDG-- 86
                |:  ||  |||:        :   :::  |                | | | |  |
Db         28 WSPPTTAEVTIEAVPPQVAEDNNVLLLVHNLPLALGAFAWYKGNPVSTNAEIVHFVTGTN 87

Qy         87 ----------------GYSLKLSKLKKNDSGIYYVGIYSSSLQQPSTQEYV-LHVYEHLS 129
```

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                           || : ::   |:|:| : :   : ::  |:  |  ||:: |
Db         88 KTTTGPAHSGRETVYSNGSLLIQRVTVKDTGVYTIEMTDENFRR--TEATVQFHVHQLLL 145

Qy        130 KPKVTMGLQSNKNGTCVTNLTCCMEHGEEDVIYTWKALGQAANESHNGSILPISWRWGES 189
              || :|    :   |    :|||      ::: | |   |:: :|   |  | :|   |
Db        146 KPNITSNNSNPVEGDDSVSLTCDSYTDPDNITYLWSRNGESLSE---GDRLKLS--EGNR 200

Qy        190 DMT-----------FICVARNPVSRNFSSP 208
               :|           ::|  ||||| | | |
Db        201 TLTLLNVTRNDTGPYVCETRNPVSVNRSDP 230
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Search completed: August 18, 2004, 15:52:53
Job time : 21 secs

OM protein - protein search, using sw model

Run on: August 18, 2004, 15:45:27 ; Search time 14 Seconds
(without alignments)
1245.964 Million cell updates/sec

Title: US-10-063-549-46
Perfect score: 1772
Sequence: 1 MAGSPTCLTLIYILWQLTGS.....PHSLLTMPDTPRLFAYENVI 335

Scoring table: BLOSUM62
Gapop 10.0 , Gapext 0.5

Searched: 141681 seqs, 52070155 residues

Total number of hits satisfying chosen parameters: 141681

Minimum DB seq length: 0
Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%
Maximum Match 100%
Listing first 700 summaries

Database : SwissProt_42:*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	% Query Match	Length	DB	ID	Description
1	354.5	20.0	654	1	LY9_MOUSE	Q01965 mus musculu
2	318	17.9	655	1	LY9_HUMAN	Q9hbg7 homo sapien
3	186	10.5	343	1	SLAM_MOUSE	Q9qum4 mus musculu
4	182.5	10.3	335	1	SLAM_HUMAN	Q13291 homo sapien
5	144	8.1	344	1	CD2_MOUSE	P08920 mus musculu
6	134	7.6	240	1	CD48_RAT	P10252 rattus norv
7	133.5	7.5	351	1	CD2_HUMAN	P06729 homo sapien
8	130	7.3	344	1	CD2_RAT	P08921 rattus norv
9	126.5	7.1	240	1	CD48_MOUSE	P18181 mus musculu
10	125.5	7.1	526	1	CEA1_HUMAN	P13688 homo sapien
11	124.5	7.0	344	1	CEA6_HUMAN	P40199 homo sapien
12	119.5	6.7	365	1	CXAR_HUMAN	P78310 homo sapien
13	116.5	6.6	319	1	A33_HUMAN	Q99795 homo sapien
14	114.5	6.5	702	1	CEA5_HUMAN	P06731 homo sapien
15	113.5	6.4	521	1	CEA1_MOUSE	P31809 mus musculu
16	110.5	6.2	463	1	CD4_CANFA	P33705 canis famil
17	105.5	6.0	329	1	CD86_HUMAN	P42081 homo sapien
18	102.5	5.8	519	1	ECTO_RAT	P16573 rattus norv
19	101	5.7	349	1	CEA8_HUMAN	P31997 homo sapien
20	101	5.7	349	1	LACH_SCHAM	Q26474 schistocerc
21	101	5.7	588	1	C166_CHICK	P42292 gallus gall
22	100.5	5.7	555	1	C166_CARAU	Q90304 carassius a
23	99	5.6	417	1	PVR_CERAE	P32506 cercopithec
24	98.5	5.6	526	1	BUTY_BOVIN	P18892 bos taurus
25	98	5.5	347	1	CD2_HORSE	P37998 equus cabal
26	98	5.5	503	1	SHS1_HUMAN	P78324 h protein-t
27	98	5.5	1382	1	MET_RAT	P97523 rattus norv
28	97	5.5	773	1	PIGR_RABIT	P01832 oryctolagus
29	96	5.4	359	1	LACH_DROME	Q24372 drosophila
30	96	5.4	526	1	BUTY_HUMAN	Q13410 homo sapien
31	96	5.4	1087	1	PGDS_XENLA	P26619 xenopus lae
32	96	5.4	1451	1	MYM1_HUMAN	P52179 homo sapien
33	95.5	5.4	365	1	CXAR_MOUSE	P97792 mus musculu
34	95.5	5.4	700	1	PTPE_HUMAN	P23469 homo sapien
35	95.5	5.4	771	1	PIGR_MOUSE	O70570 mus musculu
36	95.5	5.4	822	1	CAN3_SHEEP	Q9tth8 ovis aries
37	94	5.3	233	1	GP42_RAT	P23505 rattus norv
38	94	5.3	1088	1	NCA1_XENLA	P16170 xenopus lae
39	93	5.2	419	1	PSG4_HUMAN	Q00888 homo sapien
40	93	5.2	419	1	PSG7_HUMAN	Q13046 homo sapien
41	93	5.2	535	1	PYRG_SPICI	P52200 spiroplasma
42	92.5	5.2	299	1	JAM1_HUMAN	Q9y624 homo sapien
43	92.5	5.2	330	1	CD86_RABIT	P42071 oryctolagus
44	92.5	5.2	564	1	C166_BRARE	Q90460 brachydanio
45	91	5.1	491	1	KCS3_RABIT	Q9tt17 oryctolagus
46	91	5.1	822	1	CAN3_BOVIN	P51186 bos taurus
47	91	5.1	1548	1	SMCY_MOUSE	Q62240 mus musculu
48	90.5	5.1	417	1	PVR_HUMAN	P15151 homo sapien
49	90.5	5.1	1905	1	Y659_PASMU	Q9cmz1 pasteurella
50	90	5.1	250	1	LFA3_HUMAN	P19256 homo sapien
51	90	5.1	419	1	PSG1_HUMAN	P11464 homo sapien
52	90	5.1	541	1	IR18_HUMAN	Q13478 homo sapien
53	89.5	5.1	243	1	CD48_HUMAN	P09326 homo sapien
54	89.5	5.1	349	1	OMPA_BUCAI	P57414 buchnera ap
55	89.5	5.1	821	1	CAN3_PIG	P43368 sus scrofa
56	89.5	5.1	1051	1	YC94_HUMAN	Q9p2q2 homo sapien
57	89	5.0	309	1	CD86_MOUSE	P42082 mus musculu
58	89	5.0	821	1	CAN3_HUMAN	P20807 homo sapien
59	88.5	5.0	271	1	OX2V_KSHV	P88963 kaposi's sa
60	88.5	5.0	327	1	MOXR_RAT	Q9es58 rattus norv
61	88.5	5.0	1390	1	MET_HUMAN	P08581 homo sapien
62	88	5.0	363	1	MURG_BORBU	O51708 borrelia bu
63	88	5.0	508	1	C6D5_DROME	Q9vfp1 drosophila
64	88	5.0	509	1	SHS1_RAT	P97710 r protein-t
65	88	5.0	530	1	PVR2_MOUSE	P32507 mus musculu
66	88	5.0	699	1	PTPE_MOUSE	P49446 mus musculu
67	88	5.0	821	1	CAN3_RAT	P16259 rattus norv
68	88	5.0	1092	1	NCA2_XENLA	P36335 xenopus lae
69	88	5.0	6669	1	NEBU_HUMAN	P20929 homo sapien
70	87.5	4.9	265	1	CEA7_HUMAN	Q14002 homo sapien
71	87.5	4.9	422	1	K3L1_RAT	P83556 rattus norv
72	87.5	4.9	769	1	PIGR_RAT	P15083 rattus norv
73	87	4.9	457	1	CD4_MOUSE	P06332 mus musculu
74	87	4.9	491	1	KCS3_HUMAN	Q9bq31 homo sapien
75	87	4.9	583	1	C166_HUMAN	Q13740 homo sapien
76	87	4.9	1666	1	MYM1_MOUSE	Q62234 mus musculu
77	87	4.9	3707	1	PGBM_MOUSE	Q05793 mus musculu
78	86.5	4.9	443	1	EX7L_VIBVU	Q8df05 vibrio vuln
79	86	4.9	348	1	KILO_RAT	Q9z0j8 rattus norv
80	86	4.9	354	1	VGLI_VZVD	P09258 varicella-z
81	85.5	4.8	978	1	KFMS_FSVMD	P00545 feline sarc
82	85.5	4.8	2491	1	MPRI_HUMAN	P11717 homo sapien
83	85	4.8	402	1	RAGE_RAT	Q63495 rattus norv
84	85	4.8	428	1	PSG3_HUMAN	Q16557 homo sapien
85	85	4.8	821	1	CAN3_MOUSE	Q64691 mus musculu
86	84.5	4.8	292	1	Y152_HUMAN	Q14165 homo sapien
87	84.5	4.8	583	1	C166_MOUSE	Q61490 mus musculu
88	84.5	4.8	1211	1	M10L_HUMAN	Q9bxt6 homo sapien
89	84	4.7	668	1	PBS2_YEAST	P08018 saccharomyc
90	84	4.7	1300	1	IRR_MOUSE	Q9wtl4 mus musculu
91	84	4.7	1379	1	MET_MOUSE	P16056 mus musculu
92	84	4.7	3034	1	CLR1_MOUSE	O35161 mus musculu
93	83.5	4.7	298	1	JAM2_HUMAN	P57087 homo sapien
94	83	4.7	463	1	STHA_PSEFL	O05139 pseudomonas
95	83	4.7	757	1	PIGR_BOVIN	P81265 bos taurus
96	83	4.7	873	1	LDVR_HUMAN	P98155 homo sapien
97	83	4.7	1106	1	ACLY_CAEEL	P53585 caenorhabdi
98	82.5	4.7	773	1	MES2_CAEEL	O17514 caenorhabdi
99	82	4.6	386	1	NATB_BACSU	P46904 bacillus su
100	82	4.6	609	1	HEMA_RINDR	P41355 rinderpest
101	82	4.6	880	1	TYO3_MOUSE	P55144 mus musculu
102	82	4.6	1007	1	GRD2_HUMAN	O43424 homo sapien
103	82	4.6	3562	1	PGCV_CHICK	Q90953 gallus gall
104	81.5	4.6	278	1	OX2G_RAT	P04218 rattus norv
105	81.5	4.6	302	1	ICOL_HUMAN	O75144 homo sapien
106	81.5	4.6	378	1	LEUK_RAT	P13838 rattus norv

107	81.5	4.6	497	1	GALT_CLOAB	Q97ez4	clostridium
108	81.5	4.6	709	1	Y939_SULTO	Q973g3	sulfolobus
109	81.5	4.6	815	1	CAN3_MACFA	Q9glg7	macaca fasc
110	81.5	4.6	925	1	W70T_HUMAN	P57737	homo sapien
111	81	4.6	338	1	LAMP_HUMAN	Q13449	homo sapien
112	81	4.6	489	1	C302_DROME	Q9ngx9	drosophila
113	81	4.6	760	1	YCE5_YEAST	P25574	saccharomyc
114	81	4.6	829	1	CAD3_HUMAN	P22223	homo sapien
115	81	4.6	1304	1	NRCA_HUMAN	Q92823	homo sapien
116	81	4.6	1941	1	UBR1_KLULA	O60014	kluyveromyc
117	80.5	4.5	346	1	EFB1_HUMAN	P98172	homo sapien
118	80.5	4.5	462	1	MURD_CLOAB	Q97eb9	clostridium
119	80.5	4.5	476	1	YCAM_ECOLI	P75835	escherichia
120	80.5	4.5	1364	1	BLM_XENLA	Q9dey9	xenopus lae
121	80.5	4.5	1948	1	PTN5_HUMAN	Q13332	homo sapien
122	80.5	4.5	3343	1	YOG7_CAEEL	P34616	caenorhabdi
123	80.5	4.5	3354	1	CADN_MOUSE	Q99pf4	mus musculu
124	80.5	4.5	3358	1	PGCV_MOUSE	Q62059	mus musculu
125	80.5	4.5	6632	1	UN89_CAEEL	O01761	caenorhabdi
126	80	4.5	338	1	LAMP_RAT	Q62813	rattus norv
127	80	4.5	341	1	K2L3_HUMAN	P43628	h killer ce
128	80	4.5	482	1	ARCD_PSEAE	P18275	pseudomonas
129	80	4.5	1040	1	AXO1_HUMAN	Q02246	homo sapien
130	80	4.5	1170	1	TSP1_MOUSE	P35441	mus musculu
131	79.5	4.5	249	1	MYP0_CHICK	P37301	gallus gall
132	79.5	4.5	328	1	CYS4_BRANA	P25251	brassica na
133	79.5	4.5	430	1	TPSN_CHICK	O73895	gallus gall
134	79.5	4.5	490	1	T1ME_ECOLI	Q47282	escherichia
135	79.5	4.5	740	1	PEC1_PIG	Q95242	sus scrofa
136	79.5	4.5	859	1	PMS2_MOUSE	P54279	mus musculu
137	79.5	4.5	873	1	LDVR_MOUSE	P98156	mus musculu
138	79.5	4.5	980	1	KFMS_FELCA	P13369	felis silve
139	79.5	4.5	1465	1	MYM2_HUMAN	P54296	homo sapien
140	79	4.5	438	1	YZ32_METJA	Q60289	methanococc
141	79	4.5	463	1	STHA_PSEPK	Q88ky8	pseudomonas
142	79	4.5	1228	1	ALA5_ARATH	Q9sgg3	arabidopsis
143	79	4.5	1361	1	GLI4_XENLA	Q91661	xenopus lae
144	78.5	4.4	429	1	EPC_RAT	P01855	rattus norv
145	78.5	4.4	467	1	SIL5_MOUSE	Q91y57	mus musculu
146	78.5	4.4	497	1	UBID_ECO57	P58194	escherichia
147	78.5	4.4	628	1	LU_HUMAN	P50895	homo sapien
148	78.5	4.4	831	1	SAS3_YEAST	P34218	saccharomyc
149	78.5	4.4	847	1	CD22_HUMAN	P20273	homo sapien
150	78.5	4.4	927	1	CDGD_HUMAN	Q9y5g3	homo sapien
151	78.5	4.4	1036	1	AXO1_CHICK	P28685	gallus gall
152	78	4.4	335	1	PSG5_HUMAN	Q15238	homo sapien
153	78	4.4	353	1	CEPU_CHICK	Q90773	gallus gall
154	78	4.4	609	1	HEMA_RINDK	P12567	rinderpest
155	78	4.4	761	1	NCA2_HUMAN	P13592	homo sapien
156	78	4.4	771	1	SM1A_DROME	Q24322	drosophila
157	78	4.4	848	1	NCA1_HUMAN	P13591	homo sapien
158	78	4.4	884	1	CADB_XENLA	P33152	xenopus lae
159	78	4.4	993	1	DSG3_MOUSE	O35902	mus musculu
160	77.5	4.4	236	1	YJL1_SCHPO	O74414	schizosacch
161	77.5	4.4	239	1	CD8A_FELCA	P41688	felis silve
162	77.5	4.4	333	1	C1B1_CAVPO	Q9qzz2	cavia porce
163	77.5	4.4	448	1	EX7L_STRR6	Q8dpm9	streptococc
164	77.5	4.4	490	1	CNA8_MOUSE	Q8bj63	mus musculu
165	77.5	4.4	491	1	SYT9_HUMAN	Q86ss6	homo sapien
166	77.5	4.4	510	1	MQO_WIGBR	Q8d1v2	wiggleswort
167	77.5	4.4	513	1	SHS1_MOUSE	P97797	m protein-t
168	77.5	4.4	650	1	LIB1_HUMAN	Q8nh16	h leukocyte
169	77.5	4.4	739	1	VCA1_HUMAN	P19320	homo sapien
170	77.5	4.4	757	1	DNM1_YEAST	P54861	saccharomyc
171	77.5	4.4	1912	1	PTPD_HUMAN	P23468	homo sapien
172	77.5	4.4	1950	1	UBR1_YEAST	P19812	saccharomyc
173	77	4.3	138	1	PSAD_NOSS8	P56596	nostoc sp.
174	77	4.3	278	1	OX2G_MOUSE	O54901	mus musculu
175	77	4.3	338	1	LAMP_CHICK	Q98919	gallus gall
176	77	4.3	491	1	KCS3_RAT	O88759	rattus norv
177	77	4.3	502	1	SKS1_YEAST	Q12505	saccharomyc
178	77	4.3	523	1	CP78_SOYBN	O48927	glycine max
179	77	4.3	873	1	LDVR_RABIT	P35953	oryctolagus
180	77	4.3	894	1	MTP_MOUSE	O08601	mus musculu
181	77	4.3	1041	1	EGT2_YEAST	P42835	saccharomyc
182	77	4.3	1448	1	PK3G_HUMAN	O75747	homo sapien
183	77	4.3	1897	1	PTPF_HUMAN	P10586	homo sapien
184	77	4.3	4870	1	RYR3_HUMAN	Q15413	homo sapien
185	76.5	4.3	191	1	MOBA_PYRAB	Q9v0d0	pyrococcus
186	76.5	4.3	426	1	PSG9_HUMAN	Q00887	homo sapien
187	76.5	4.3	458	1	CD4_MACNE	Q08340	macaca neme
188	76.5	4.3	497	1	UBID_ECOLI	P26615	escherichia
189	76.5	4.3	1071	1	SEF1_KLULA	P87164	kluyveromyc
190	76.5	4.3	1089	1	PGDS_HUMAN	P16234	homo sapien
191	76.5	4.3	1124	1	TCF8_HUMAN	P37275	homo sapien
192	76.5	4.3	1156	1	N133_HUMAN	Q8wum0	homo sapien
193	76.5	4.3	1328	1	HUS2_SCHPO	Q09811	schizosacch
194	76.5	4.3	1802	1	HKR1_YEAST	P41809	saccharomyc
195	76	4.3	138	1	PSAD_FREDI	P23808	fremyella d
196	76	4.3	262	1	YCJI_ECOLI	P51983	escherichia
197	76	4.3	316	1	DDL_ENTGA	Q47823	enterococcu
198	76	4.3	333	1	AMAL_DROME	P15364	drosophila
199	76	4.3	417	1	PGCB_FELCA	P41725	felis silve
200	76	4.3	487	1	DPD2_YEAST	P46957	saccharomyc
201	76	4.3	524	1	BUTY_MOUSE	Q62556	mus musculu
202	76	4.3	977	1	KFMS_MOUSE	P09581	mus musculu
203	76	4.3	978	1	KFMS_RAT	Q00495	rattus norv
204	76	4.3	2029	1	LAR_DROME	P16621	drosophila
205	75.5	4.3	246	1	MOG_BOVIN	P55803	bos taurus
206	75.5	4.3	321	1	TCB_FLV	P11364	feline leuk
207	75.5	4.3	421	1	MFR1_SCHPO	O94423	schizosacch
208	75.5	4.3	446	1	EX7L_STRPN	Q97qj8	streptococc
209	75.5	4.3	458	1	CD4_MACFA	P79185	macaca fasc
210	75.5	4.3	462	1	ALB3_ARATH	Q8lbp4	arabidopsis
211	75.5	4.3	498	1	MQO2_STAAW	Q8num4	staphylococ
212	75.5	4.3	699	1	UVRG_HUMAN	Q9p2y5	homo sapien
213	75.5	4.3	1020	1	CONT_MOUSE	P12960	mus musculu
214	75.5	4.3	1089	1	PGDS_MOUSE	P26618	mus musculu
215	75.5	4.3	2109	1	PGCA_CHICK	P07898	gallus gall
216	75.5	4.3	3317	1	CADN_RAT	P58365	rattus norv
217	75	4.2	208	1	TRPF_CHLTR	O84331	chlamydia t
218	75	4.2	239	1	CD8A_CANFA	P33706	canis famil
219	75	4.2	323	1	YAMB_THETU	P38541	thermoanaer
220	75	4.2	332	1	C1B3_CAVPO	Q9qzz0	cavia porce
221	75	4.2	543	1	EAA1_MOUSE	P56564	mus musculu
222	75	4.2	543	1	EAA1_RAT	P24942	rattus norv
223	75	4.2	641	1	CAN6_MOUSE	O35646	mus musculu
224	75	4.2	641	1	CAN6_RAT	O88501	rattus norv
225	75	4.2	686	1	EMAP_STRPU	Q26613	strongyloce
226	75	4.2	703	1	LAGD_LACLA	P59852	lactococcus
227	75	4.2	747	1	FHUA_ECOLI	P06971	escherichia
228	75	4.2	1091	1	NCA1_CHICK	P13590	gallus gall
229	75	4.2	1099	1	NKX1_HUMAN	O60721	homo sapien
230	75	4.2	1256	1	NRCA_MOUSE	Q810u4	mus musculu
231	75	4.2	1492	1	AT7A_RAT	P70705	rattus norv
232	75	4.2	3396	1	PGCV_HUMAN	P13611	homo sapien
233	74.5	4.2	146	1	RMP3_CAVPO	Q8r4c4	cavia porce
234	74.5	4.2	219	1	FLA4_PYRKO	Q9v2w8	pyrococcus
235	74.5	4.2	232	1	OVAX_CHICK	P01013	gallus gall
236	74.5	4.2	328	1	PDXA_VIBVU	Q8ded3	vibrio vuln
237	74.5	4.2	379	1	NLPD_ECOLI	P33648	escherichia
238	74.5	4.2	544	1	YES_XIPHE	P27447	xiphophorus
239	74.5	4.2	648	1	RCQ1_MOUSE	Q9z129	mus musculu
240	74.5	4.2	688	1	LIP_STAEP	Q02510	staphylococ
241	74.5	4.2	741	1	YBIO_ECOLI	P75783	escherichia
242	74.5	4.2	764	1	ICCR_DROME	Q08180	drosophila
243	74.5	4.2	881	1	ENV_SIVMK	P05884	simian immu
244	74.5	4.2	1007	1	GRD2_MOUSE	Q61625	mus musculu
245	74.5	4.2	1007	1	GRD2_RAT	Q63226	rattus norv
246	74.5	4.2	1178	1	RPOB_MYCLE	P30760	mycobacteri
247	74.5	4.2	1522	1	BAI3_HUMAN	O60242	homo sapien
248	74.5	4.2	1723	1	LY75_MOUSE	Q60767	mus musculu
249	74.5	4.2	2012	1	DSCA_HUMAN	O60469	homo sapien
250	74.5	4.2	2459	1	MAPB_RAT	P15205	rattus norv
251	74.5	4.2	4655	1	LRP2_HUMAN	P98164	homo sapien
252	74	4.2	148	1	RMP1_HUMAN	O60894	homo sapien

253	74	4.2	227	1	GPMA_CHLCV	Q821n6	chlamydophi
254	74	4.2	333	1	GCB_RAT	P20761	rattus norv
255	74	4.2	384	1	NRFF_HAEIN	P44942	haemophilus
256	74	4.2	403	1	CD33_MOUSE	Q63994	mus musculu
257	74	4.2	469	1	EC33_YEAST	P38248	saccharomyc
258	74	4.2	645	1	SKB1_SCHPO	P78963	schizosacch
259	74	4.2	687	1	TGM2_HUMAN	P21980	homo sapien
260	74	4.2	821	1	FGR2_MOUSE	P21803	mus musculu
261	74	4.2	862	1	CD22_MOUSE	P35329	mus musculu
262	74	4.2	862	1	SM4D_HUMAN	Q92854	homo sapien
263	74	4.2	910	1	RDL2_ARATH	Q8w3k3	arabidopsis
264	74	4.2	1063	1	CZCA_ALCEU	P13511	alcaligenes
265	74	4.2	1063	1	CZCA_ALCSP	P94177	alcaligenes
266	74	4.2	1165	1	CHS3_YEAST	P29465	saccharomyc
267	74	4.2	1561	1	Y34F_DROME	Q9w5d0	drosophila
268	74	4.2	1709	1	SN_HUMAN	Q9bzz2	homo sapien
269	74	4.2	4344	1	DYHC_EMENI	P45444	emericella
270	74	4.2	5217	1	HTS1_COCCA	Q01886	cochliobolu
271	74	4.2	6781	1	R1AB_PEDV7	Q91av2	p replicase
272	73.5	4.1	321	1	YOR4_ADEG1	P20746	avian adeno
273	73.5	4.1	364	1	CD33_HUMAN	P20138	homo sapien
274	73.5	4.1	428	1	PYRC_BACHD	Q9k9v7	bacillus ha
275	73.5	4.1	458	1	CD4_MACFU	P79184	macaca fusc
276	73.5	4.1	458	1	CD4_MACMU	P16003	macaca mula
277	73.5	4.1	695	1	VTXB_SYNVE	Q98993	synanceia v
278	73.5	4.1	850	1	NRG2_HUMAN	O14511	homo sapien
279	73.5	4.1	873	1	LDVR_RAT	P98166	rattus norv
280	73.5	4.1	880	1	ENV_SIVML	P11267	simian immu
281	73.5	4.1	1057	1	SEF1_YEAST	P34228	saccharomyc
282	73.5	4.1	1166	1	L2GL_DROPS	Q08470	drosophila
283	73.5	4.1	2301	1	POLG_TMEVD	P13899	t genome po
284	73.5	4.1	4544	1	LRP1_HUMAN	Q07954	homo sapien
285	73	4.1	175	1	RMP2_HUMAN	O60895	homo sapien
286	73	4.1	304	1	K2S2_HUMAN	P43631	homo sapien
287	73	4.1	322	1	YZ68_BACHD	Q9k706	bacillus ha
288	73	4.1	413	1	HEMO_HYACE	P25033	hyalophora
289	73	4.1	518	1	TT8_ARATH	Q9ft81	arabidopsis
290	73	4.1	543	1	EAA1_AMBTI	O57321	ambystoma t
291	73	4.1	576	1	IL1R_RAT	Q02955	rattus norv
292	73	4.1	666	1	NOD_DROME	P18105	drosophila
293	73	4.1	853	1	NCA1_BOVIN	P31836	bos taurus
294	73	4.1	853	1	PBPA_HAEIN	P31776	h penicilli
295	73	4.1	901	1	VP3_BTV13	Q65750	bluetongue
296	73	4.1	901	1	VP3_BTV17	P03539	bluetongue
297	73	4.1	1072	1	ITA6_CHICK	P26007	gallus gall
298	73	4.1	1515	1	YCF1_YEAST	P39109	saccharomyc
299	73	4.1	3788	1	LYST_MOUSE	P97412	mus musculu
300	72.5	4.1	399	1	YGV7_SCHPO	O43021	schizosacch
301	72.5	4.1	424	1	PSGA_HUMAN	Q15235	homo sapien
302	72.5	4.1	435	1	PSG6_HUMAN	Q00889	homo sapien
303	72.5	4.1	440	1	YMT6_YEAST	Q04215	saccharomyc
304	72.5	4.1	443	1	TOLB_BRUME	Q93tg4	brucella me
305	72.5	4.1	443	1	TOLB_BRUSU	Q8fz07	brucella su
306	72.5	4.1	485	1	DLTA_STAEP	Q8ct93	staphylococ
307	72.5	4.1	657	1	MM15_MOUSE	O54732	mus musculu
308	72.5	4.1	666	1	SLY1_YEAST	P22213	saccharomyc
309	72.5	4.1	686	1	IPL2_MOUSE	Q9ers6	mus musculu
310	72.5	4.1	851	1	NCL1_CAEEL	P34611	caenorhabdi
311	72.5	4.1	867	1	ENV_HV1J3	P12489	human immun
312	72.5	4.1	895	1	SECA_CYACA	O19911	cyanidium c
313	72.5	4.1	909	1	DDR1_PANTR	Q7yr43	pan troglod
314	72.5	4.1	913	1	DDR1_HUMAN	Q08345	h epithelia
315	72.5	4.1	1013	1	SCA4_RICRH	Q9aj81	rickettsia
316	72.5	4.1	1021	1	CONT_RAT	Q63198	rattus norv
317	72.5	4.1	1165	1	LEPR_PIG	O02671	sus scrofa
318	72.5	4.1	1214	1	NRCA_RAT	P97686	rattus norv
319	72.5	4.1	1369	1	NFAS_CHICK	O42414	gallus gall
320	72.5	4.1	1434	1	PTC1_MOUSE	Q61115	mus musculu
321	72.5	4.1	2333	1	PGCA_CANFA	Q28343	canis famil
322	72.5	4.1	2696	1	NSD1_HUMAN	Q96173	homo sapien
323	72.5	4.1	4367	1	DYHC_NEUCR	P45443	neurospora
324	72	4.1	384	1	Z183_CAEEL	O17917	caenorhabdi
325	72	4.1	394	1	Z193_HUMAN	O15535	homo sapien
326	72	4.1	463	1	STHA_PSESM	Q884i6	pseudomonas
327	72	4.1	469	1	GABP_BACSU	P46349	bacillus su
328	72	4.1	510	1	PUSH_ARATH	O22928	arabidopsis
329	72	4.1	517	1	PVR1_HUMAN	Q15223	homo sapien
330	72	4.1	548	1	5EAS_TOBAC	Q40577	nicotiana t
331	72	4.1	585	1	YHD9_YEAST	P38732	saccharomyc
332	72	4.1	643	1	CD93_RAT	Q9et61	rattus norv
333	72	4.1	646	1	MU18_HUMAN	P43121	homo sapien
334	72	4.1	670	1	S213_HUMAN	P46721	homo sapien
335	72	4.1	776	1	AD28_MACFA	Q9xsl6	macaca fasc
336	72	4.1	778	1	GCR_SAISC	O46567	saimiri sci
337	72	4.1	840	1	HS74_HUMAN	P34932	homo sapien
338	72	4.1	840	1	ORC1_MOUSE	Q9z1n2	mus musculu
339	72	4.1	868	1	NRG2_RAT	O35569	rattus norv
340	72	4.1	901	1	VP3_BTV10	P12435	bluetongue
341	72	4.1	901	1	VP3_BTV11	Q65749	bluetongue
342	72	4.1	901	1	VP3_BTV1S	P56582	bluetongue
343	72	4.1	901	1	VP3_BTV2A	Q65748	bluetongue
344	72	4.1	1159	1	SOR2_HUMAN	Q96pq0	homo sapien
345	72	4.1	1186	1	SYLC_CAEEL	Q09996	caenorhabdi
346	72	4.1	1348	1	VGR2_COTJA	P52583	coturnix co
347	72	4.1	1906	1	KMLS_CHICK	P11799	gallus gall
348	72	4.1	2358	1	YEEJ_ECOLI	P76347	escherichia
349	71.5	4.0	229	1	VV_P14HA	P21739	human parai
350	71.5	4.0	291	1	HTPX_BUCBP	P59559	buchnera ap
351	71.5	4.0	299	1	YJG8_YEAST	P40363	saccharomyc
352	71.5	4.0	312	1	YC90_METJA	Q58686	methanococc
353	71.5	4.0	338	1	RTCA_METJA	Q60335	methanococc
354	71.5	4.0	339	1	MDH_METFE	P16142	methanother
355	71.5	4.0	403	1	RAGE_MOUSE	Q62151	mus musculu
356	71.5	4.0	496	1	C71F_ARATH	P58046	arabidopsis
357	71.5	4.0	498	1	MQO2_STAAM	Q99r30	staphylococ
358	71.5	4.0	500	1	RT03_PROWI	P46740	prototheca
359	71.5	4.0	515	1	GMI1_METAC	Q8tmi6	methanosarc
360	71.5	4.0	526	1	SRC_RSVSR	P00524	rous sarcom
361	71.5	4.0	527	1	MM19_MOUSE	Q9jhi0	mus musculu
362	71.5	4.0	537	1	PYRG_CHLCV	Q822t2	chlamydophi
363	71.5	4.0	733	1	ERG7_RAT	P48450	rattus norv
364	71.5	4.0	764	1	PIGR_HUMAN	P01833	homo sapien
365	71.5	4.0	919	1	HEX_ADE12	P19900	human adeno
366	71.5	4.0	923	1	ODO1_BUCAP	Q8k9n3	buchnera ap
367	71.5	4.0	1032	1	Y895_HAEIN	Q57124	haemophilus
368	71.5	4.0	1374	1	YQ3D_SCHPO	Q09884	schizosacch
369	71.5	4.0	1377	1	RPOC_BORBU	O51349	borrelia bu
370	71.5	4.0	1693	1	SAS_DROME	Q04164	drosophila
371	71.5	4.0	2126	1	PKDR_MOUSE	Q9z0t6	mus musculu
372	71.5	4.0	2468	1	MAPB_HUMAN	P46821	homo sapien
373	71.5	4.0	3063	1	CA1C_HUMAN	Q99715	homo sapien
374	71	4.0	258	1	Y256_MYCPN	P75421	mycoplasma
375	71	4.0	334	1	EFB1_CHICK	O73612	gallus gall
376	71	4.0	343	1	G3P_SULTO	Q971k2	sulfolobus
377	71	4.0	344	1	NTRI_MOUSE	Q99pj0	mus musculu
378	71	4.0	344	1	NTRI_RAT	Q62718	rattus norv
379	71	4.0	345	1	EFB1_MOUSE	P52795	mus musculu
380	71	4.0	389	1	CYB_DICDI	Q37311	dictyosteli
381	71	4.0	417	1	GATD_PYRAE	Q8zy04	pyrobaculum
382	71	4.0	455	1	YM18_YEAST	P40208	saccharomyc
383	71	4.0	462	1	RD21_ARATH	P43297	arabidopsis
384	71	4.0	509	1	VMT9_MYXVL	P08073	myxoma viru
385	71	4.0	522	1	YL8J_SCHPO	Q9utal	schizosacch
386	71	4.0	551	1	HAS2_XENLA	O57427	xenopus lae
387	71	4.0	605	1	COG6_HUMAN	Q9y2v7	homo sapien
388	71	4.0	690	1	LIP_STAAU	P10335	staphylococ
389	71	4.0	690	1	LIP_STAAW	Q8nyc2	staphylococ
390	71	4.0	727	1	PEC1_MOUSE	Q08481	mus musculu
391	71	4.0	821	1	FGR2_HUMAN	P21802	homo sapien
392	71	4.0	905	1	XPF_HUMAN	Q92889	homo sapien
393	71	4.0	922	1	W70T_MOUSE	Q9d2v7	mus musculu
394	71	4.0	956	1	SYI_AQUAE	O66651	aquifex aeo
395	71	4.0	1018	1	CONT_HUMAN	Q12860	homo sapien
396	71	4.0	1082	1	RGR1_YEAST	P19263	saccharomyc
397	71	4.0	1240	1	YQU3_CAEEL	Q09550	caenorhabdi
398	71	4.0	1338	1	VGR1_HUMAN	P17948	h vascular

399	71	4.0	4391	1	PGBM_HUMAN	P98160	homo sapien
400	70.5	4.0	203	1	FLA1_ARCFU	O29208	archaeoglob
401	70.5	4.0	311	1	HTX1_SULTO	Q973r2	sulfolobus
402	70.5	4.0	332	1	PDXA_VIBPA	Q87st5	vibrio para
403	70.5	4.0	333	1	MDHC_HUMAN	P40925	homo sapien
404	70.5	4.0	338	1	MDHM_HUMAN	P40926	homo sapien
405	70.5	4.0	338	1	MDHM_RAT	P04636	rattus norv
406	70.5	4.0	429	1	ARSB_STAXY	Q01255	staphylococ
407	70.5	4.0	455	1	K3L2_HUMAN	P43630	homo sapien
408	70.5	4.0	526	1	SRC_AVISR	P00525	avian sarco
409	70.5	4.0	532	1	SRC_CHICK	P00523	gallus gall
410	70.5	4.0	537	1	YES_XENLA	P10936	xenopus lae
411	70.5	4.0	545	1	FGR_FSVGR	P00544	feline sarc
412	70.5	4.0	547	1	TFH1_MOUSE	Q9dba9	mus musculu
413	70.5	4.0	557	1	SRC_AVIST	P14085	avian sarco
414	70.5	4.0	558	1	VP10_RBSDV	P19898	rice black
415	70.5	4.0	568	1	SRC_AVISS	P14084	avian sarco
416	70.5	4.0	569	1	CYSP_PLAFA	P25805	plasmodium
417	70.5	4.0	587	1	SRC_AVIS2	P15054	avian sarco
418	70.5	4.0	610	1	CALG_HUMAN	O14967	homo sapien
419	70.5	4.0	627	1	MUTL_BACSU	P49850	bacillus su
420	70.5	4.0	630	1	MUC1_MOUSE	Q02496	mus musculu
421	70.5	4.0	641	1	CAN6_HUMAN	Q9y6q1	homo sapien
422	70.5	4.0	648	1	GYRB_MYCGA	P47720	mycoplasma
423	70.5	4.0	686	1	IPL2_HUMAN	Q9np60	h x-linked
424	70.5	4.0	787	1	OBP_HSV7J	P52379	human herpe
425	70.5	4.0	793	1	YEA8_SCHPO	O14073	schizosacch
426	70.5	4.0	843	1	EF2_DROME	P13060	drosophila
427	70.5	4.0	877	1	CAD2_BOVIN	P19534	bos taurus
428	70.5	4.0	895	1	MTP_MESAU	P55158	mesocricetu
429	70.5	4.0	906	1	CAD2_MOUSE	P15116	mus musculu
430	70.5	4.0	906	1	CAD2_RAT	Q9z1y3	rattus norv
431	70.5	4.0	928	1	PM10_CHLPN	Q9rb65	chlamydia p
432	70.5	4.0	938	1	PM15_CHLPN	Q9z883	chlamydia p
433	70.5	4.0	984	1	SEN7_HUMAN	Q9bqf6	homo sapien
434	70.5	4.0	1200	1	HYAL_STRPU	O76536	strongyloce
435	70.5	4.0	1356	1	VGR2_HUMAN	P35968	homo sapien
436	70.5	4.0	1454	1	CPSA_CAEEL	Q9n4c2	caenorhabdi
437	70.5	4.0	1694	1	SN_MOUSE	Q62230	mus musculu
438	70.5	4.0	2298	1	CU05_HUMAN	Q9y3r5	homo sapien
439	70.5	4.0	2303	1	POLG_TMEVG	P08545	t genome po
440	70.5	4.0	2464	1	MAPB_MOUSE	P14873	mus musculu
441	70.5	4.0	2738	1	PGCV_RAT	Q9erb4	rattus norv
442	70	4.0	115	1	KV5F_MOUSE	P01638	mus musculu
443	70	4.0	224	1	CM35_HUMAN	Q08708	homo sapien
444	70	4.0	262	1	RPC_BP163	P15238	bacteriopha
445	70	4.0	298	1	JAM1_BOVIN	Q9xt56	bos taurus
446	70	4.0	403	1	TRPB_ACICA	P16706	acinetobact
447	70	4.0	421	1	EPC_MOUSE	P06336	mus musculu
448	70	4.0	536	1	YEN1_SCHPO	O13695	schizosacch
449	70	4.0	542	1	EAA1_BOVIN	P46411	bos taurus
450	70	4.0	576	1	IL1R_MOUSE	P13504	mus musculu
451	70	4.0	611	1	VE1_PAPVE	P11328	european el
452	70	4.0	742	1	NU88_RAT	O08658	rattus norv
453	70	4.0	810	1	CAN3_CHICK	Q92177	gallus gall
454	70	4.0	837	1	GCSR_MOUSE	P40223	mus musculu
455	70	4.0	1040	1	AXO1_RAT	P22063	rattus norv
456	70	4.0	1097	1	PGDR_RAT	Q05030	rattus norv
457	70	4.0	1162	1	LEPR_MOUSE	P48356	mus musculu
458	70	4.0	1214	1	SIP1_HUMAN	O60315	homo sapien
459	70	4.0	1215	1	SIP1_MOUSE	Q9r0g7	mus musculu
460	70	4.0	1456	1	RRPO_PVXHB	Q07630	potato viru
461	70	4.0	1456	1	RRPO_PVXX3	P17779	potato viru
462	70	4.0	1461	1	NEO1_HUMAN	Q92859	homo sapien
463	70	4.0	1657	1	ALS2_HUMAN	Q96q42	homo sapien
464	70	4.0	1722	1	LY75_MESAU	Q920p9	mesocricetu
465	70	4.0	2004	1	YP73_YERPE	Q8zdj2	yersinia pe
466	69.5	3.9	270	1	NFAM_HUMAN	Q8net5	homo sapien
467	69.5	3.9	284	1	SUHA_HUMAN	Q06520	homo sapien
468	69.5	3.9	295	1	AROE_CHLTE	Q8kbh8	chlorobium
469	69.5	3.9	327	1	EFB1_XENLA	O13097	xenopus lae
470	69.5	3.9	332	1	Y614_PYRHO	O58348	pyrococcus
471	69.5	3.9	338	1	MDHM_MOUSE	P08249	mus musculu
472	69.5	3.9	346	1	NRL3_ARATH	P46010	arabidopsis
473	69.5	3.9	429	1	ARSB_STAEP	Q8cqf4	staphylococ
474	69.5	3.9	437	1	PUR8_AQUAE	O66856	aquifex aeo
475	69.5	3.9	444	1	TOLB_RICCN	Q92il4	rickettsia
476	69.5	3.9	497	1	ANSP_SALTY	P40812	salmonella
477	69.5	3.9	503	1	WSC2_YEAST	P53832	saccharomyc
478	69.5	3.9	523	1	SRC_RSVPA	P31693	rous sarcom
479	69.5	3.9	535	1	SRC_RAT	Q9wud9	rattus norv
480	69.5	3.9	548	1	AMDS_EMENI	P08158	emericella
481	69.5	3.9	548	1	TFH1_HUMAN	P32780	homo sapien
482	69.5	3.9	568	1	ULP1_SCHPO	O42957	schizosacch
483	69.5	3.9	585	1	KNC1_RAT	P25122	rattus norv
484	69.5	3.9	616	1	Y396_HELPY	O25157	helicobacte
485	69.5	3.9	633	1	AGP1_YEAST	P25376	saccharomyc
486	69.5	3.9	682	1	PRC_ECOLI	P23865	escherichia
487	69.5	3.9	718	1	COAT_MUMIM	P07302	murine minu
488	69.5	3.9	736	1	ME27_SCHPO	O94713	schizosacch
489	69.5	3.9	751	1	FOH1_PIG	O77564	s glutamate
490	69.5	3.9	776	1	POLG_LANVY	P29838	langat viru
491	69.5	3.9	849	1	VNCS_AEDEV	P27454	aedes denso
492	69.5	3.9	1033	1	CIS1_MOUSE	Q8r4b8	mus musculu
493	69.5	3.9	1062	1	NAL2_HUMAN	Q9nx02	homo sapien
494	69.5	3.9	1178	1	RPOB_MYCTU	P47766	mycobacteri
495	69.5	3.9	1260	1	CAML_MOUSE	P11627	mus musculu
496	69.5	3.9	1604	1	UB32_HUMAN	Q8nfa0	homo sapien
497	69.5	3.9	1722	1	LY75_HUMAN	O60449	homo sapien
498	69.5	3.9	3414	1	POLG_LANVT	P29837	l genome po
499	69	3.9	139	1	PSAD_ANASP	P58573	anabaena sp
500	69	3.9	217	1	ALGF_PSEFL	P59791	pseudomonas
501	69	3.9	327	1	I12B_MARMO	Q61729	marmota mon
502	69	3.9	344	1	NTRI_HUMAN	Q9p121	homo sapien
503	69	3.9	357	1	YOJ1_CAEEL	P34624	caenorhabdi
504	69	3.9	390	1	Y109_NPVAC	P41662	autographa
505	69	3.9	394	1	IDI2_PYRFU	Q8u2h9	pyrococcus
506	69	3.9	458	1	PRTC_RABIT	Q28661	oryctolagus
507	69	3.9	490	1	CPC7_RAT	P05179	rattus norv
508	69	3.9	497	1	VL1_BPV2	P06458	bovine papi
509	69	3.9	505	1	ATPA_SYNP6	P08449	synechococc
510	69	3.9	506	1	SHS1_BOVIN	O46631	bos taurus
511	69	3.9	515	1	PVR1_PIG	Q9gl76	sus scrofa
512	69	3.9	523	1	C756_CAMME	O04773	campanula m
513	69	3.9	537	1	IR18_MOUSE	Q61098	mus musculu
514	69	3.9	542	1	EAA1_HUMAN	P43003	homo sapien
515	69	3.9	557	1	ILVD_BACAA	Q81s26	bacillus an
516	69	3.9	584	1	MA6S_YEAST	P07265	saccharomyc
517	69	3.9	597	1	SILL_PANTR	Q95lh0	pan troglod
518	69	3.9	644	1	HOBO_DROME	P12258	drosophila
519	69	3.9	661	1	NKX2_HUMAN	Q9ui40	homo sapien
520	69	3.9	715	1	ADSV_MOUSE	Q60604	mus musculu
521	69	3.9	741	1	NU88_HUMAN	Q99567	homo sapien
522	69	3.9	756	1	NRG2_MOUSE	P56974	mus musculu
523	69	3.9	919	1	INCE_HUMAN	Q9nqs7	homo sapien
524	69	3.9	1049	1	VP39_YEAST	Q07468	saccharomyc
525	69	3.9	1068	1	HMDH_ASPTE	Q9y7d2	aspergillus
526	69	3.9	1109	1	TCF8_RAT	Q62947	rattus norv
527	69	3.9	1327	1	TNK1_HUMAN	O95271	homo sapien
528	69	3.9	1442	1	PTC1_CHICK	Q90693	gallus gall
529	69	3.9	1656	1	ATC8_YEAST	Q12674	saccharomyc
530	69	3.9	2132	1	PGCA_MOUSE	Q61282	mus musculu
531	69	3.9	2196	1	MOR2_SCHPO	Q9hdv6	schizosacch
532	69	3.9	4563	1	APB_HUMAN	P04114	homo sapien
533	68.5	3.9	240	1	CD7_HUMAN	P09564	homo sapien
534	68.5	3.9	268	1	YHC6_YEAST	P38740	saccharomyc
535	68.5	3.9	296	1	YFCI_ECOLI	P77768	escherichia
536	68.5	3.9	310	1	SDC1_HUMAN	P18827	homo sapien
537	68.5	3.9	329	1	YQG1_CAEEL	Q09272	caenorhabdi
538	68.5	3.9	335	1	PSG2_HUMAN	P11465	homo sapien
539	68.5	3.9	338	1	MDHM_PIG	P00346	sus scrofa
540	68.5	3.9	366	1	OXAA_MYCTU	Q7tvc3	mycobacteri
541	68.5	3.9	407	1	LMP1_CRIGR	P49129	cricetulus
542	68.5	3.9	423	1	LMB1_YERPE	Q8zas9	yersinia pe
543	68.5	3.9	448	1	EX7L_BACSU	P54521	bacillus su
544	68.5	3.9	453	1	TRME_BUCMP	O51830	buchnera ap

545	68.5	3.9	458	1	CD4_CERAE	Q08338	cercopithec
546	68.5	3.9	458	1	CD4_HUMAN	P01730	homo sapien
547	68.5	3.9	459	1	SPAK_BACSU	P33113	bacillus su
548	68.5	3.9	464	1	RCAA_HORVU	Q40073	hordeum vul
549	68.5	3.9	497	1	KCS1_MOUSE	O35173	mus musculu
550	68.5	3.9	524	1	MQO_CANBF	Q7vrs0	candidatus
551	68.5	3.9	542	1	IMA1_YEAST	Q02821	saccharomyc
552	68.5	3.9	555	1	ILVD_AQUAE	O67009	aquifex aeo
553	68.5	3.9	561	1	BIO5_YEAST	P53744	saccharomyc
554	68.5	3.9	584	1	RYK2_DROME	Q9v422	drosophila
555	68.5	3.9	592	1	PU92_YEAST	P38009	s bifunctio
556	68.5	3.9	601	1	MUTL_LISMO	Q8y788	listeria mo
557	68.5	3.9	626	1	HTPG_BUCBP	Q89a93	buchnera ap
558	68.5	3.9	654	1	MCPC_BACSU	P54576	bacillus su
559	68.5	3.9	711	1	LCFD_HUMAN	O60488	homo sapien
560	68.5	3.9	789	1	SHE4_YEAST	P51534	saccharomyc
561	68.5	3.9	827	1	CSG_HALVO	P25062	halobacteri
562	68.5	3.9	831	1	PRLR_CHICK	Q04594	gallus gall
563	68.5	3.9	906	1	CAD2_HUMAN	P19022	homo sapien
564	68.5	3.9	968	1	CTD1_HUMAN	O60716	homo sapien
565	68.5	3.9	972	1	KFMS_HUMAN	P07333	homo sapien
566	68.5	3.9	976	1	AMY_BUTFI	P30269	butyrivibri
567	68.5	3.9	1043	1	TCF8_MESAU	Q60542	mesocricetu
568	68.5	3.9	1134	1	YML7_YEAST	Q03735	saccharomyc
569	68.5	3.9	1248	1	DIA1_HUMAN	O60610	homo sapien
570	68.5	3.9	1257	1	CAML_HUMAN	P32004	homo sapien
571	68.5	3.9	1466	1	SPA2_YEAST	P23201	saccharomyc
572	68.5	3.9	1520	1	PMPD_CHLMU	Q9plb0	chlamydia m
573	68.5	3.9	1704	1	VILD_DICDI	Q8wq85	dictyosteli
574	68.5	3.9	3354	1	CADN_HUMAN	Q9h251	homo sapien
575	68.5	3.9	4349	1	DYHC_FUSSO	P78716	fusarium so
576	68	3.8	155	1	PCP_HAEIN	P10325	haemophilus
577	68	3.8	157	1	PR1_MEDSA	Q43560	medicago sa
578	68	3.8	167	1	Y741_RICPR	O05960	rickettsia
579	68	3.8	221	1	YB31_MYCPN	P75267	mycoplasma
580	68	3.8	231	1	YC93_METJA	Q58689	methanococc
581	68	3.8	262	1	CAHD_HUMAN	Q8n1q1	homo sapien
582	68	3.8	275	1	ICA2_HUMAN	P13598	homo sapien
583	68	3.8	298	1	HTPX_STRP3	Q8k8k2	streptococc
584	68	3.8	298	1	HTPX_STRP8	Q8p2k0	streptococc
585	68	3.8	298	1	HTPX_STRPY	Q9a1d5	streptococc
586	68	3.8	340	1	PFTA_ARATH	Q9lx33	a protein f
587	68	3.8	371	1	DP3B_TREPA	O83048	treponema p
588	68	3.8	395	1	SYT8_MOUSE	Q9r0n6	mus musculu
589	68	3.8	401	1	ASSY_STAAM	Q99vc7	staphylococ
590	68	3.8	401	1	ASSY_STAAW	Q8nxf2	staphylococ
591	68	3.8	409	1	F16P_WHEAT	P09195	triticum ae
592	68	3.8	431	1	ORDL_HAEIN	P44732	haemophilus
593	68	3.8	514	1	C11A_DASAM	Q92045	dasyatis am
594	68	3.8	520	1	LEU1_BRAJA	Q89gb0	bradyrhizob
595	68	3.8	521	1	ICEA_HUMAN	Q92851	homo sapien
596	68	3.8	526	1	VP5_BTV10	P07389	bluetongue
597	68	3.8	528	1	YE19_SCHPO	O13874	schizosacch
598	68	3.8	584	1	MA3S_YEAST	P38158	saccharomyc
599	68	3.8	595	1	SILL_HUMAN	Q96pq1	homo sapien
600	68	3.8	632	1	CSX1_SCHPO	O13759	schizosacch
601	68	3.8	640	1	GYRB_SPICI	P34031	spiroplasma
602	68	3.8	649	1	GUND_CLOTM	P04954	clostridium
603	68	3.8	656	1	Y691_RICPR	Q9zcn2	rickettsia
604	68	3.8	688	1	EFG_APPPP	Q9zeu4	apple proli
605	68	3.8	690	1	PTRB_MORLA	Q59536	moraxella l
606	68	3.8	756	1	RPC2_MOUSE	P59470	mus musculu
607	68	3.8	789	1	AD07_RAT	Q63180	rattus norv
608	68	3.8	796	1	COPP_SCHPO	O42937	schizosacch
609	68	3.8	814	1	SEFC_SALEN	P33388	salmonella
610	68	3.8	896	1	RPOP_NEUCR	P33540	neurospora
611	68	3.8	901	1	VP3_BTV1A	P20608	bluetongue
612	68	3.8	906	1	CADO_XENLA	P33147	xenopus lae
613	68	3.8	912	1	PGCB_BOVIN	Q28062	bos taurus
614	68	3.8	962	1	GUNA_PSEFL	P10476	pseudomonas
615	68	3.8	963	1	IRE2_RAT	Q62751	rattus norv
616	68	3.8	994	1	MERK_RAT	P57097	rattus norv
617	68	3.8	997	1	YPX2_CAEEL	Q20256	caenorhabdi
618	68	3.8	1147	1	KIN2_YEAST	P13186	saccharomyc
619	68	3.8	1174	1	PTNL_HUMAN	Q16825	homo sapien
620	68	3.8	1195	1	CHS4_NEUCR	Q01285	neurospora
621	68	3.8	1271	1	YC81_CAEEL	Q19981	caenorhabdi
622	68	3.8	1281	1	MDR3_CRIGR	P23174	cricetulus
623	68	3.8	1458	1	PHLX_RABIT	Q05017	oryctolagus
624	68	3.8	1522	1	MRP3_RAT	O88563	rattus norv
625	68	3.8	1786	1	UVRA_CHLTR	O84337	chlamydia t
626	68	3.8	2124	1	PGCA_RAT	P07897	rattus norv
627	68	3.8	3341	1	POLG_MCFA	P33515	m genome po
628	67.5	3.8	134	1	CYB5_BRAOL	P40934	brassica ol
629	67.5	3.8	148	1	RMP3_HUMAN	O60896	homo sapien
630	67.5	3.8	212	1	BROM_ANACO	P14518	ananas como
631	67.5	3.8	215	1	CIB3_MOUSE	Q8bhk2	mus musculu
632	67.5	3.8	221	1	VA36_VACCV	P21059	vaccinia vi
633	67.5	3.8	261	1	YJY1_YEAST	P47086	saccharomyc
634	67.5	3.8	322	1	ICOL_MOUSE	Q9jhj8	mus musculu
635	67.5	3.8	329	1	GC2_CAVPO	P01862	cavia porce
636	67.5	3.8	345	1	EFB1_RAT	P52796	rattus norv
637	67.5	3.8	348	1	K2L2_HUMAN	P43627	homo sapien
638	67.5	3.8	348	1	OMB1_NEIGO	P18195	neisseria g
639	67.5	3.8	348	1	Y479_MYCTU	Q11145	mycobacteri
640	67.5	3.8	361	1	SERC_BACHD	Q9kdm4	bacillus ha
641	67.5	3.8	450	1	PUR8_PYRHO	O58582	pyrococcus
642	67.5	3.8	491	1	SYT9_MOUSE	Q9r0n9	mus musculu
643	67.5	3.8	491	1	SYT9_RAT	Q925c0	rattus norv
644	67.5	3.8	497	1	KCS1_RAT	O88758	rattus norv
645	67.5	3.8	511	1	KNC1_HUMAN	P48547	homo sapien
646	67.5	3.8	511	1	KNC1_MOUSE	P15388	mus musculu
647	67.5	3.8	535	1	SRC_HUMAN	P12931	homo sapien
648	67.5	3.8	540	1	SRC_MOUSE	P05480	mus musculu
649	67.5	3.8	547	1	CD19_MOUSE	P25918	mus musculu
650	67.5	3.8	567	1	IRL1_MOUSE	P14719	mus musculu
651	67.5	3.8	569	1	YE59_MYCPN	P75324	mycoplasma
652	67.5	3.8	570	1	DFA5_ANASP	Q8z0c1	anabaena sp
653	67.5	3.8	571	1	ASN2_YEAST	P49090	saccharomyc
654	67.5	3.8	581	1	HPCL_MOUSE	Q9qxe0	mus musculu
655	67.5	3.8	584	1	DAK1_YEAST	P54838	saccharomyc
656	67.5	3.8	587	1	CO8B_ONCMY	Q90x85	oncorhynchu
657	67.5	3.8	615	1	YSPK_CAEEL	Q19425	caenorhabdi
658	67.5	3.8	621	1	Y344_CHLPN	Q9k275	chlamydia p
659	67.5	3.8	660	1	PKN1_COREF	Q8fui5	corynebacte
660	67.5	3.8	697	1	NANB_STRPN	Q54727	streptococc
661	67.5	3.8	703	1	CNA1_MOUSE	Q8bmd6	mus musculu
662	67.5	3.8	732	1	ACPH_PIG	P19205	sus scrofa
663	67.5	3.8	748	1	SM3B_MOUSE	Q62177	mus musculu
664	67.5	3.8	790	1	CADI_HUMAN	Q13634	homo sapien
665	67.5	3.8	795	1	TLR1_MOUSE	Q9epq1	mus musculu
666	67.5	3.8	837	1	NCM2_HUMAN	O15394	homo sapien
667	67.5	3.8	879	1	YE07_MYCPN	P75377	mycoplasma
668	67.5	3.8	886	1	DSC1_MOUSE	P55849	mus musculu
669	67.5	3.8	944	1	CHS2_NEUCR	P30589	neurospora
670	67.5	3.8	956	1	GLK4_HUMAN	Q16099	homo sapien
671	67.5	3.8	1036	1	HPI2_DEIRA	P13126	deinococcus
672	67.5	3.8	1062	1	YA13_HUMAN	Q9y216	homo sapien
673	67.5	3.8	1070	1	PTK7_HUMAN	Q13308	homo sapien
674	67.5	3.8	1072	1	CARB_THETN	Q8rbk0	thermoanaer
675	67.5	3.8	1460	1	PCX1_MOUSE	Q9qyc1	mus musculu
676	67.5	3.8	1527	1	ARHB_RAT	Q9e867	rattus norv
677	67.5	3.8	1928	1	LPH_RAT	Q02401	rattus norv
678	67.5	3.8	2144	1	BP28_HUMAN	Q9h583	homo sapien
679	67.5	3.8	2208	1	POLN_MANCV	Q69014	manchester
680	67.5	3.8	4660	1	LRP2_RAT	P98158	rattus norv
681	67	3.8	131	1	IL13_MOUSE	P20109	mus musculu
682	67	3.8	135	1	CYS5_TOBAC	P49099	nicotiana t
683	67	3.8	156	1	L18B_LUPLU	P52779	lupinus lut
684	67	3.8	189	1	CD3E_MOUSE	P22646	mus musculu
685	67	3.8	214	1	FLA4_PYRHO	O58285	pyrococcus
686	67	3.8	255	1	DAPB_CLOTE	Q891s2	clostridium
687	67	3.8	255	1	YQIX_BACSU	P54535	bacillus su
688	67	3.8	282	1	ISPA_BUCAI	P57537	buchnera ap
689	67	3.8	300	1	NANK_HAEIN	P44541	haemophilus
690	67	3.8	316	1	RSP4_TRIGR	P38980	tripneustes

691	67	3.8	320	1	RLUB_VIBVU	Q8d8c0 vibrio vuln
692	67	3.8	358	1	BIOB_METJA	Q58692 methanococc
693	67	3.8	371	1	CRL2_HUMAN	Q9hc73 homo sapien
694	67	3.8	373	1	REP1_YEAST	P03871 saccharomyc
695	67	3.8	401	1	ASSY_STAEP	Q8cpu3 staphylococ
696	67	3.8	413	1	HEMO_MANSE	P31398 manduca sex
697	67	3.8	495	1	CD5_HUMAN	P06127 homo sapien
698	67	3.8	501	1	CPJ5_MOUSE	O54749 mus musculu
699	67	3.8	524	1	Y395_MYCGE	P47635 mycoplasma
700	67	3.8	542	1	IMA1_SCHPO	O14063 schizosacch

ALIGNMENTS

```
RESULT 1
LY9_MOUSE
ID   LY9_MOUSE      STANDARD;      PRT;   654 AA.
AC   Q01965; Q9ES29; Q9ES35; Q9ES36;
DT   01-JUN-1994 (Rel. 29, Created)
DT   28-FEB-2003 (Rel. 41, Last sequence update)
DT   10-OCT-2003 (Rel. 42, Last annotation update)
DE   T-lymphocyte surface antigen Ly-9 precursor (Lymphocyte antigen 9)
DE   (Cell-surface molecule Ly-9).
GN   LY9 OR LY-9.
OS   Mus musculus (Mouse).
OC   Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC   Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus.
OX   NCBI_TaxID=10090;
RN   [1]
RP   SEQUENCE FROM N.A., AND POLYMORPHISM.
RC   STRAIN=129/Sv, BALB/c, and C57BL/6; TISSUE=Spleen;
RX   MEDLINE=20424510; PubMed=10970093;
RA   Tovar V., de la Fuente M.A., Pizcueta P., Bosch J., Engel P.;
RT   "Gene structure of the mouse leukocyte cell surface molecule Ly9.";
RL   Immunogenetics 51:788-793(2000).
RN   [2]
RP   SEQUENCE OF 22-654 FROM N.A., AND SEQUENCE OF 48-59.
RX   MEDLINE=92373005; PubMed=1506686;
RA   Sandrin M.S., Gumley T.P., Henning M.M., Vaughan H.A., Gonez L.J.,
RA   Trapani J.A., McKenzie I.F.C.;
RT   "Isolation and characterization of cDNA clones for mouse Ly-9.";
RL   J. Immunol. 149:1636-1641(1992).
CC   -!- FUNCTION: May participate in adhesion reactions between T
CC       lymphocytes and accessory cells by homophilic interaction.
CC   -!- SUBCELLULAR LOCATION: Type I membrane protein.
CC   -!- TISSUE SPECIFICITY: LYMPHOCYTES.
CC   -!- SIMILARITY: Contains 2 immunoglobulin-like C2-type domains.
CC   -!- SIMILARITY: Contains 2 immunoglobulin-like V-type domains.
CC   ----------------------------------------------------------------------
CC   This SWISS-PROT entry is copyright. It is produced through a collaboration
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CC   or send an email to license@isb-sib.ch).
CC   ----------------------------------------------------------------------
DR   EMBL; AF244131; AAG14997.1; -.
DR   EMBL; AF244130; AAG14996.1; -.
DR   EMBL; AF246701; AAG13268.2; -.
DR   EMBL; AF245117; AAG13268.2; JOINED.
DR   EMBL; AF245506; AAG13268.2; JOINED.
DR   EMBL; AF245118; AAG13268.2; JOINED.
DR   EMBL; AF245507; AAG13268.2; JOINED.
DR   EMBL; AF245508; AAG13268.2; JOINED.
DR   EMBL; AF245509; AAG13268.2; JOINED.
DR   EMBL; AF245510; AAG13268.2; JOINED.
DR   EMBL; AF246699; AAG13268.2; JOINED.
DR   EMBL; AF246700; AAG13268.2; JOINED.
DR   EMBL; M84412; AAA39468.1; -.
DR   HSSP; P08921; 1HNG.
DR   MGD; MGI:96885; Ly9.
DR   InterPro; IPR007110; Ig-like.
DR   InterPro; IPR003599; Ig.
DR   Pfam; PF00047; ig; 2.
DR   SMART; SM00409; IG; 2.
DR   PROSITE; PS50835; IG_LIKE; 2.
KW   Cell adhesion; Antigen; Signal; Transmembrane; Glycoprotein;
KW   Immunoglobulin domain; Repeat; Polymorphism.
FT   SIGNAL        1     47
FT   CHAIN        48    654       T-LYMPHOCYTE SURFACE ANTIGEN LY-9.
FT   DOMAIN       48    453       EXTRACELLULAR (POTENTIAL).
FT   TRANSMEM    454    474       POTENTIAL.
FT   DOMAIN      475    654       CYTOPLASMIC (POTENTIAL).
FT   DOMAIN       48    158       IG-LIKE V-TYPE 1.
FT   DOMAIN      159    243       IG-LIKE C2-TYPE 1.
FT   DOMAIN      250    362       IG-LIKE V-TYPE 2.
FT   DOMAIN      353    453       IG-LIKE C2-TYPE 2.
FT   DISULFID    172    242       POTENTIAL.
FT   DISULFID    178    222       POTENTIAL.
FT   DISULFID    376    445       POTENTIAL.
FT   DISULFID    382    426       POTENTIAL.
FT   CARBOHYD     68     68       N-LINKED (GLCNAC. . .) (POTENTIAL).
FT   CARBOHYD    120    120       N-LINKED (GLCNAC. . .) (POTENTIAL).
FT   CARBOHYD    231    231       N-LINKED (GLCNAC. . .) (POTENTIAL).
FT   CARBOHYD    284    284       N-LINKED (GLCNAC. . .) (POTENTIAL).
FT   CARBOHYD    390    390       N-LINKED (GLCNAC. . .) (POTENTIAL).
FT   CARBOHYD    412    412       N-LINKED (GLCNAC. . .) (POTENTIAL).
FT   CARBOHYD    423    423       N-LINKED (GLCNAC. . .) (POTENTIAL).
FT   CARBOHYD    434    434       N-LINKED (GLCNAC. . .) (POTENTIAL).
FT   VARIANT      10     10       D -> G (IN LY9-1).
FT   VARIANT      14     14       G -> S (IN LY9-1).
FT   VARIANT      79     79       I -> T (IN LY9-1).
FT   VARIANT      91     91       F -> S (IN LY9-1).
FT   VARIANT     130    130       H -> Y (IN LY9-1).
FT   VARIANT     139    139       I -> T (IN LY9-1).
FT   VARIANT     362    362       P -> S.
FT   VARIANT     366    366       K -> N (IN LY9-1).
FT   VARIANT     377    377       E -> K (IN LY9-1).
FT   VARIANT     550    550       M -> I (IN LY9-1).
FT   VARIANT     592    592       G -> E (IN LY9-1).
FT   CONFLICT    283    283       F -> L (IN REF. 2).
FT   CONFLICT    499    499       T -> P (IN REF. 2).
FT   CONFLICT    560    560       V -> L (IN REF. 2).
FT   CONFLICT    647    654       TPTYENFT -> SPYL (IN REF. 2).
SQ   SEQUENCE   654 AA;  73142 MW;  1CBBE99708AE8EE7 CRC64;

  Query Match           20.0%;  Score 354.5;  DB 1;  Length 654;
  Best Local Similarity   27.6%;  Pred. No. 6.8e-22;
  Matches  118;  Conservative   52;  Mismatches  138;  Indels  119;  Gaps   16;

Qy         14 LWQL-TGSA----ASGPVKELVGSVGGAVTFPLKSK-VKQVDSIVWTFNTTPLVTIQPEG 67
              :||  ||::    |:|  | :|| :|  || ||: :  :   ::|| |||:  |  |
Db        238 IWQFCTGASRRKTAAG--KTVVGILGEPVTLPLEFRATRATKNVVWVFNTS--VISQERR 293

Qy         68 GTIIVTQNR-----NRERVDFPDGGYSLKLSKLKKNDSGIYYVGIYSSSLQQPSTQEYVL 122
              |       |          ||   |   |||:|:||  |:| |:  : | : : || : : |
Db        294 GAATADSRRKPKGSEERRVRTSDQDQSLKISQLKMEDAGPYHAYVCSEASRDPSVRHFTL 353

Qy        123 HVYEHLSKPKVTMGLQSNKNGTCVTNLTCCMEHGEEDVIYTWKALGQAANESHNGSILPI 182
              ||: | || ||        || |   ||| :: |  :| |||  |   |  |   | | :
Db        354 LVYKRLEKPSVTKSPVHMMNGICEVVLTCSVDGGGNNVTYTWMPLQNKAVMSQGKSHLNV 413

Qy        183 SWRWGESDMTFICVARNPVSRNFSSPILARKLCEGAADDPDSSMVLLCLLLVPLLLSLFV 242
              ||  ||    | | | |||| | ||   :  :| |   |: :    |||: ||| : :
Db        414 SWESGEHLPNFTCTAHNPVS-NSSSQFSSGTICSG----PERNKRFWLLLLLVLLLLMLI 468

Qy        243 LGLFLWFLKRE--------RQEEYIEE----------------KKRVDICRETPNICP- 276
              | |:   |::         || |   |                    :::|:  :|    |
Db        469 GGYFILRKKKQCSSLATRYRQAEVPAEIPETPTGHGQFSVLSQRYEKLDMSAKTTRHQPT 528

Qy        277 ----------------------HSGENTE---YDTIPHTN---------------------- 291
                                   ||  |:    || : | :
Db        529 PTSDTSSESSATTEEDDEKTRMHSTANSRNQVYDLVTHQDIAHALAYEGQVEYEAITPYD 588
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Qy        292 ----------------------RTIL--KEDPANTVYSTVEIPKK-MENPHSLLTMPDTP 326
                                     | |  |:: :||:| :|: |||  : |      |:||
Db        589 KVDGSMDEEDMAYIQVSLNVQGETPLPQKKEDSNTIYCSVQKPKKTAQTPQQDAESPETP 648

Qy        327 RLFAYEN 333
                  |||
Db        649 ---TYEN 652


RESULT 2
LY9_HUMAN
ID   LY9_HUMAN      STANDARD;      PRT;   655 AA.
AC   Q9HBG7; Q14775; Q9H4N5; Q9NQ24;
DT   28-FEB-2003 (Rel. 41, Created)
DT   28-FEB-2003 (Rel. 41, Last sequence update)
DT   10-OCT-2003 (Rel. 42, Last annotation update)
DE   T-lymphocyte surface antigen Ly-9 precursor (Lymphocyte antigen 9)
DE   (Cell-surface molecule Ly-9) (CD229 antigen).
GN   LY9.
OS   Homo sapiens (Human).
OC   Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC   Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
OX   NCBI_TaxID=9606;
RN   [1]
RP   SEQUENCE FROM N.A. (ISOFORM 1).
RX   MEDLINE=20424510; PubMed=10970093;
RA   Tovar V., de la Fuente M.A., Pizcueta P., Bosch J., Engel P.;
RT   "Gene structure of the mouse leukocyte cell surface molecule Ly9.";
RL   Immunogenetics 51:788-793(2000).
RN   [2]
RP   SEQUENCE OF 32-654 FROM N.A. (ISOFORM 2).
RX   MEDLINE=96128248; PubMed=8537117;
RA   Sandrin M.S., Henning M.M., Lo M.F., Baker E., Sutherland G.R.,
RA   McKenzie I.F.;
RT   "Isolation and characterization of cDNA clones for Humly9: the human
RT   homologue of mouse Ly9.";
RL   Immunogenetics 43:13-19(1996).
RN   [3]
RP   SEQUENCE OF 1-151 FROM N.A.
RA   Bates K.;
RL   Submitted (APR-2000) to the EMBL/GenBank/DDBJ databases.
RN   [4]
RP   SEQUENCE OF 99-655 FROM N.A. (ISOFORM 3).
RA   Zhou J., Yu W., Tang H., Mei G., Tsang Y.T.M., Bouck J., Gibbs R.A.,
RA   Margolin J.F.;
RL   Submitted (JUL-2000) to the EMBL/GenBank/DDBJ databases.
CC   -!- FUNCTION: May participate in adhesion reactions between T
CC       lymphocytes and accessory cells by homophilic interaction.
CC   -!- SUBCELLULAR LOCATION: Type I membrane protein.
CC   -!- ALTERNATIVE PRODUCTS:
CC       Event=Alternative splicing; Named isoforms=3;
CC         Comment=Experimental confirmation may be lacking for some
CC         isoforms;
CC       Name=1;
CC         IsoId=Q9HBG7-1; Sequence=Displayed;
CC       Name=2;
CC         IsoId=Q9HBG7-2; Sequence=VSP_002525;
CC       Name=3;
CC         IsoId=Q9HBG7-3; Sequence=VSP_002524, VSP_002525, VSP_002526;
CC   -!- SIMILARITY: Contains 2 immunoglobulin-like C2-type domains.
CC   -!- SIMILARITY: Contains 2 immunoglobulin-like V-type domains.
CC   ----------------------------------------------------------------------
CC   This SWISS-PROT entry is copyright. It is produced through a collaboration
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CC   or send an email to license@isb-sib.ch).
CC   ----------------------------------------------------------------------
DR   EMBL; AF244129; AAG14995.1; -.
DR   EMBL; L42621; AAA92623.1; -.
DR   EMBL; AL121985; CAC00580.1; -.
DR   EMBL; AY007142; AAG02002.1; -.
DR   Genew; HGNC:6730; LY9.
DR   MIM; 600684; -.
DR   GO; GO:0005887; C:integral to plasma membrane; ISS.
DR   GO; GO:0016064; P:humoral defense mechanism (sensu Vertebrata); NAS.
DR   InterPro; IPR007110; Ig-like.
DR   InterPro; IPR003599; Ig.
DR   Pfam; PF00047; ig; 2.
DR   SMART; SM00409; IG; 2.
DR   PROSITE; PS50835; IG_LIKE; 2.
KW   Cell adhesion; Antigen; Signal; Transmembrane; Glycoprotein;
KW   Immunoglobulin domain; Repeat; Alternative splicing.
FT   SIGNAL        1     47       POTENTIAL.
FT   CHAIN        48    655       T-LYMPHOCYTE SURFACE ANTIGEN LY-9.
FT   DOMAIN       48    454       EXTRACELLULAR (POTENTIAL).
FT   TRANSMEM    455    476       POTENTIAL.
FT   DOMAIN      477    655       CYTOPLASMIC (POTENTIAL).
FT   DOMAIN       48    158       IG-LIKE V-TYPE 1.
FT   DOMAIN      159    235       IG-LIKE C2-TYPE 1.
FT   DOMAIN      251    363       IG-LIKE V-TYPE 2.
FT   DOMAIN      364    452       IG-LIKE C2-TYPE 2.
FT   DISULFID    172    242       POTENTIAL.
FT   DISULFID    178    222       POTENTIAL.
FT   DISULFID    377    446       POTENTIAL.
FT   DISULFID    383    427       POTENTIAL.
FT   CARBOHYD     68     68       N-LINKED (GLCNAC. . .) (POTENTIAL).
FT   CARBOHYD     95     95       N-LINKED (GLCNAC. . .) (POTENTIAL).
FT   CARBOHYD    120    120       N-LINKED (GLCNAC. . .) (POTENTIAL).
FT   CARBOHYD    169    169       N-LINKED (GLCNAC. . .) (POTENTIAL).
FT   CARBOHYD    173    173       N-LINKED (GLCNAC. . .) (POTENTIAL).
FT   CARBOHYD    285    285       N-LINKED (GLCNAC. . .) (POTENTIAL).
FT   CARBOHYD    413    413       N-LINKED (GLCNAC. . .) (POTENTIAL).
FT   CARBOHYD    424    424       N-LINKED (GLCNAC. . .) (POTENTIAL).
FT   VARSPLIC    359    448       Missing (in isoform 3).
FT                                /FTId=VSP_002524.
FT   VARSPLIC    500    513       Missing (in isoform 2 and isoform 3).
FT                                /FTId=VSP_002525.
FT   VARSPLIC    524    554       PARQQPTPTSDSSSDSNLTTEEDEDRPEVHK -> Q (in
FT                                isoform 3).
FT                                /FTId=VSP_002526.
FT   CONFLICT    171    171       MISSING (IN REF. 1).
FT   CONFLICT    602    602       V -> M (IN REF. 4).
SQ   SEQUENCE   655 AA;  72107 MW;  9FB0A3056D79F80A CRC64;

  Query Match             17.9%;  Score 318;  DB 1;  Length 655;
  Best Local Similarity   30.3%;  Pred. No. 7.6e-19;
  Matches   91;  Conservative   49;  Mismatches  128;  Indels   32;  Gaps   10;

Qy         19 GSAASGPVKE-LVGSVGGAVTFPLK-SKVKQVDSIVWTFNTTPLVTIQPEGGT---IIVT 73
              |:: |   | :|| :|  || ||     :  : :|| |||: :   : |  |   :| :
Db        246 GASRGGTTGETVVGVLGEPVTLPLALPACRDTEKVVWLFNTSIISKEREEAATADPLIKS 305

Qy         74 QNRNRERVDFPDGGYSLKLSKLKKNDSGIYYVGIYSSSLQQPSTQEYVLHVYEHLSKPKV 133
              ::  : ||       |||:|:||  |:| |:  : | :    |      | :|  | |||:
Db        306 RDPYKNRVWVSSQDCSLKISQLKIEDAGPYHAYVCSEASSVTSMTHVTLLIYRRLRKPKI 365

Qy        134 TMGLQSNKNGTCVTNLTCCMEHGEEDVIYTWKALGQAANESHNGSILPISWRWGESDMTF 193
              |  |: :::| |  :||| :| |   |:||| | : |  |   | | :|||  |:
Db        366 TWSLRHSEDGICRISLTCSVEDGGNTVMYTWTPLQKEAVVSQGESHLNVSWRSSENHPNL 425

Qy        194 ICVARNPVSRNFSSPILARKLCEGAADDPDSSMVLLCLLLVPLLLSLFVLGLFLWFLKRE 253
              | | |||||: |   |:  :| | |   |: :  |   |   |:: |  :|:| | :
Db        426 TCTASNPVSRS-SHQFLSENICSG----PERNTKLWIGLF--LMVCLLCVGIFSWCI--- 475

Qy        254 RQEEYIEEKKRVDICRETPNICPHSGE---NTEYDTIPHTNRTILKEDPANTVYSTVEIP 310
                  ||   |  | |    |  :|  | ||  ::| :      |  :: |
Db        476 --------WKRKGRC-SVPAFCSSQAEAPADTPEPTAGHTLYSVLSQG-----YEKLDTP 521


RESULT 3
SLAM_MOUSE
ID   SLAM_MOUSE     STANDARD;      PRT;   343 AA.
AC   Q9QUM4; Q9QXZ3;
```

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DT   16-OCT-2001 (Rel. 40, Created)
DT   16-OCT-2001 (Rel. 40, Last sequence update)
DT   15-MAR-2004 (Rel. 43, Last annotation update)
DE   Signaling lymphocytic activation molecule precursor.
GN   SLAMF1 OR SLAM.
OS   Mus musculus (Mouse).
OC   Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC   Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus.
OX   NCBI_TaxID=10090;
RN   [1]
RP   SEQUENCE FROM N.A. (ISOFORMS LONG AND SHORT).
RC   STRAIN=BALB/c;
RX   MEDLINE=20040375; PubMed=10570270;
RA   Castro A.G., Hauser T.M., Cocks B.G., Abrams J., Zurawski S.,
RA   Churakova T., Zonin F., Robinson D., Tangye S.G., Aversa G.,
RA   Nichols K.E., de Vries J.E., Lanier L.L., O'Garra A.;
RT   "Molecular and functional characterization of mouse signaling
RT   lymphocytic activation molecule (SLAM): differential expression and
RT   responsiveness in Th1 and Th2 cells.";
RL   J. Immunol. 163:5860-5870(1999).
RN   [2]
RP   SEQUENCE FROM N.A. (ISOFORM LONG).
RA   Wang N., Wu C., Sayos J., Terhorst C.;
RT   "Genomic organization of murine SLAM.";
RL   Submitted (JUL-1999) to the EMBL/GenBank/DDBJ databases.
CC   -!- FUNCTION: HIGH-AFFINITY SELF-LIGAND CONSIDERED TO BE IMPORTANT IN
CC       BIDIRECTIONAL T <-> B-CELL STIMULATION. SLAM-INDUCED SIGNAL-
CC       TRANSDUCTION EVENTS IN T LYMPHOCYTES ARE DIFFERENT FROM THOSE IN B
CC       CELLS. TWO MODES OF SLAM SIGNALING ARE LIKELY TO EXIST: ONE IN
CC       WHICH THE INHIBITOR SH2D1A ACTS AS A NEGATIVE REGULATOR AND
CC       ANOTHER IN WHICH PROTEIN-TYROSINE PHOSPHATASE 2C (PTPN11)-
CC       DEPENDENT SIGNAL TRANSDUCTION OPERATES.
CC   -!- SUBUNIT: ITS CYTOPLASMIC DOMAIN INTERACTS WITH SH2 DOMAIN PROTEIN
CC       1A (SH2D1A) THROUGH PART OF ITS SH2 DOMAIN, AND UPON TYROSINE
CC       PHOSPHORYLATION WITH PTPN11, BUT NOT WITH SHP-1.
CC   -!- SUBCELLULAR LOCATION: Type I membrane protein; present on the
CC       surface of B and T cells.
CC   -!- ALTERNATIVE PRODUCTS:
CC       Event=Alternative splicing; Named isoforms=2;
CC       Name=Long;
CC         IsoId=Q9QUM4-1; Sequence=Displayed;
CC       Name=Short;
CC         IsoId=Q9QUM4-2; Sequence=VSP_002570;
CC   -!- PTM: Phosphorylated.
CC   -!- SIMILARITY: Contains 1 immunoglobulin-like V-type domain.
CC   -!- SIMILARITY: Contains 1 immunoglobulin-like C2-type domain.
CC   ---------------------------------------------------------------------
CC   This SWISS-PROT entry is copyright. It is produced through a collaboration
CC   between the Swiss Institute of Bioinformatics and the EMBL outstation -
CC   the European Bioinformatics Institute. There are no restrictions on its
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CC   or send an email to license@isb-sib.ch).
CC   ---------------------------------------------------------------------
DR   EMBL; AF149791; AAF22231.1; -.
DR   EMBL; AF149792; AAF22232.1; -.
DR   EMBL; AF164523; AAF13818.1; -.
DR   EMBL; AF164519; AAF13818.1; JOINED.
DR   EMBL; AF164520; AAF13818.1; JOINED.
DR   EMBL; AF164521; AAF13818.1; JOINED.
DR   EMBL; AF164522; AAF13818.1; JOINED.
DR   EMBL; AF160990; AAF14535.1; -.
DR   MGD; MGI:1351314; Slam.
DR   InterPro; IPR007110; Ig-like.
DR   PROSITE; PS50835; IG_LIKE; 1.
KW   Receptor; Signal; Transmembrane; T-cell; Glycoprotein; Repeat;
KW   Immunoglobulin domain; Phosphorylation; Alternative splicing.
FT   SIGNAL        1     24       POTENTIAL.
FT   CHAIN        25    343       SIGNALING LYMPHOCYTIC ACTIVATION
FT                                 MOLECULE.
FT   DOMAIN       25    242       EXTRACELLULAR (POTENTIAL).
FT   TRANSMEM    243    265       POTENTIAL.
FT   DOMAIN      266    343       CYTOPLASMIC (POTENTIAL).
FT   DOMAIN        ?    153       IG-LIKE V-TYPE.
FT   DOMAIN      145    228       IG-LIKE C2-TYPE.
FT   DISULFID    161    232       BY SIMILARITY.
FT   DISULFID    167    212       BY SIMILARITY.
FT   SITE        286    291       SH2-BINDING (POTENTIAL).
FT   SITE        313    318       SH2-BINDING (POTENTIAL).
FT   SITE        333    338       SH2-BINDING (POTENTIAL).
FT   CARBOHYD     54     54       N-LINKED (GLCNAC. . .) (POTENTIAL).
FT   CARBOHYD     58     58       N-LINKED (GLCNAC. . .) (POTENTIAL).
FT   CARBOHYD    103    103       N-LINKED (GLCNAC. . .) (POTENTIAL).
FT   CARBOHYD    126    126       N-LINKED (GLCNAC. . .) (POTENTIAL).
FT   CARBOHYD    151    151       N-LINKED (GLCNAC. . .) (POTENTIAL).
FT   CARBOHYD    158    158       N-LINKED (GLCNAC. . .) (POTENTIAL).
FT   CARBOHYD    192    192       N-LINKED (GLCNAC. . .) (POTENTIAL).
FT   CARBOHYD    211    211       N-LINKED (GLCNAC. . .) (POTENTIAL).
FT   CARBOHYD    226    226       N-LINKED (GLCNAC. . .) (POTENTIAL).
FT   VARSPLIC    296    343       PQEKKLHDALTDQDPCTTIYVAATEPAPESVQEPNPTTVYA
FT                                SVTLPES -> VRSMPHLAGVSVIFRTGFLIAALHTTMVLQ
FT                                GLLE (in isoform Short).
FT                                /FTId=VSP_002570.
SQ   SEQUENCE   343 AA;  38094 MW;  798047057E834C4 CRC64;

  Query Match             10.5%;  Score 186;  DB 1;  Length 343;
  Best Local Similarity   24.3%;  Pred. No. 3.7e-08;
  Matches   89;  Conservative   64;  Mismatches  130;  Indels   84;  Gaps   21;

Qy          8 LTLIYILWQLTGSAASG----PVKELVGSVGGAVTFPL-------KSKVKQVDSIVWTFN 56
              |  : : ::|:     |    ||  ::  :|     ||       ||  | |  :| |
Db         12 LLFLSLAFELSYGTGGGVMDCPV--ILQKLGQDTWLPLTNEHQINKSVNKSVRILV-TMA 68

Qy         57 TTPLVTIQPEGGTIIVTQNRNRERVDF-------PD---GGY-------SLKLSKLKKND 99
              |:|           |:: | |      ||    ||      |||:   ::
Db         69 TSP------------GSKSNKKIVSFDLSKGSYPDHLEDGYHFQSKNLSLKILGNRRES 115

Qy        100 SGIYYVGIYSS-SLQQPSTQEYVLHVYEHLSKP--KVTMGLQSNKNGTCVTNLTCCMEHG 156
              | | | :  : |:||   |   | :|| :| |  ||    | |:||||   | | :: |
Db        116 EGWYLVSVEENVSVQQFCKQ---LKLYEQVSPPEIKVLNKTQENENGTCSLLLACTVKKG 172

Qy        157 EEDVIYTWK-----ALGQAANESHNGSILPISWRWGESDMTFICVARNPV---SRNFSSP 208
              :  | |:|       |   || ||   :| |:      | : | | |||   || |:
Db        173 DH-VTYSWSDEAGTHLLSRANRSH---LLHITLSNQHQDSIYNCTASNPVSSISRTFN-- 226

Qy        209 ILARKLCEGAADDPDSSMVLLCLLLVPLLLSLFVLGLFLWFLKRERQEEYIE---EKKRV 265
              |: : |:  :    |  :   |: : :::   ::   :  :||: :  : :   |:| :
Db        227 -LSSQACKQESSSESSPWMQYTLVPLGVVIIFILVFTAIIMMKRQGKSNHCQPPVEEKSL 285

Qy        266 DICRETPNICPHSGENTEYDTIPHTNRTILKEDPANTVY--STVEIPKKMENP-----HS 318
              |  :    |   |  :|       :  :||  |:|  :|   |: :: |     ::
Db        286 TIYAQVQKSGPQ--EKKLHD-------ALTDQDPCTTIYVAATEPAPESVQEPNPTTVYA 336

Qy        319 LLTMPDT 325
              :|:|::
Db        337 SVTLPES 343


RESULT 4
SLAM_HUMAN
ID   SLAM_HUMAN     STANDARD;      PRT;   335 AA.
AC   Q13291;
DT   16-OCT-2001 (Rel. 40, Created)
DT   16-OCT-2001 (Rel. 40, Last sequence update)
DT   15-MAR-2004 (Rel. 43, Last annotation update)
DE   Signaling lymphocytic activation molecule precursor (IPO-3) (CD150
DE   antigen) (CDw150).
GN   SLAMF1 OR SLAM.
OS   Homo sapiens (Human).
OC   Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC   Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
OX   NCBI_TaxID=9606;
RN   [1]
RP   SEQUENCE FROM N.A. (ISOFORMS 1; 2 AND 3).
RC   TISSUE=T-cell;
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RX   MEDLINE=95342241; PubMed=7617038;
RA   Cocks B.G., Chang C.-C.J., Carballido J.M., Yssel H., de Vries J.E.,
RA   Aversa G.;
RT   "A novel receptor involved in T-cell activation.";
RL   Nature 376:260-263(1995).
CC   -!- FUNCTION: HIGH-AFFINITY SELF-LIGAND CONSIDERED TO BE IMPORTANT IN
CC       BIDIRECTIONAL T <-> B-CELL STIMULATION. SLAM-INDUCED SIGNAL-
CC       TRANSDUCTION EVENTS IN T LYMPHOCYTES ARE DIFFERENT FROM THOSE IN B
CC       CELLS. TWO MODES OF SLAM SIGNALING ARE LIKELY TO EXIST: ONE IN
CC       WHICH THE INHIBITOR SH2D1A ACTS AS A NEGATIVE REGULATOR AND
CC       ANOTHER IN WHICH PROTEIN-TYROSINE PHOSPHATASE 2C (PTPN11)-
CC       DEPENDENT SIGNAL TRANSDUCTION OPERATES.
CC   -!- SUBUNIT: ITS CYTOPLASMIC DOMAIN INTERACTS WITH SH2 DOMAIN PROTEIN
CC       1A (SH2D1A) THROUGH PART OF ITS SH2 DOMAIN, AND WITH PTPN11.
CC   -!- SUBCELLULAR LOCATION: Type I membrane protein; present on the
CC       surface of B and T cells.
CC   -!- ALTERNATIVE PRODUCTS:
CC       Event=Alternative splicing; Named isoforms=3;
CC       Name=1; Synonyms=Long;
CC         IsoId=Q13291-1; Sequence=Displayed;
CC       Name=2; Synonyms=Short;
CC         IsoId=Q13291-2; Sequence=VSP_002568, VSP_002569;
CC       Name=3; Synonyms=Secreted;
CC         IsoId=Q13291-3; Sequence=VSP_002567;
CC   -!- TISSUE SPECIFICITY: Constitutively expressed on peripheral blood
CC       memory T cells, T-cell clones, immature thymocytes, and a
CC       proportion of B-cells, and is rapidly induced on naive T cells
CC       after activation.
CC   -!- DOMAIN: SH2 DOMAINS USE TO BIND TO PHOSPHOTYROSINE RESIDUES IN A
CC       SEQUENCE-SPECIFIC MANNER. IN THIS CASE, HOWEVER, THE SPECIFIC
CC       SH2D1A-BINDING SITE IS AROUND THE MOST MEMBRANE-PROXIMAL TYROSINE
CC       RESIDUE (TYR-281) OF THE CYTOPLASMIC TAIL, AND PHOSPHORYLATION OF
CC       TYR-281 IS NOT REQUIRED FOR BINDING.
CC   -!- PTM: PHOSPHORYLATED BY FYN.
CC   -!- SIMILARITY: Contains 1 immunoglobulin-like V-type domain.
CC   -!- SIMILARITY: Contains 1 immunoglobulin-like C2-type domain.
CC   -!- DATABASE: NAME=PROW; NOTE=CD guide CDw150 entry;
CC       WWW="http://www.ncbi.nlm.nih.gov/prow/cd/cdw150.htm".
CC   ---------------------------------------------------------------------
CC   This SWISS-PROT entry is copyright. It is produced through a collaboration
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CC   the European Bioinformatics Institute. There are no restrictions on its
CC   use by non-profit institutions as long as its content is in no way
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CC   entities requires a license agreement (See http://www.isb-sib.ch/announce/
CC   or send an email to license@isb-sib.ch).
CC   ---------------------------------------------------------------------
DR   EMBL; U33017; AAA75380.1; -.
DR   PIR; S58892; S58892.
DR   PDB; 1D4T; 10-APR-00.
DR   PDB; 1D4W; 04-APR-00.
DR   PDB; 1KA6; 28-AUG-02.
DR   PDB; 1KA7; 28-AUG-02.
DR   Genew; HGNC:10903; SLAMF1.
DR   MIM; 603492; -.
DR   GO; GO:0003823; F:antigen binding; TAS.
DR   GO; GO:0004888; F:transmembrane receptor activity; TAS.
DR   GO; GO:0006960; P:antimicrobial humoral response (sensu Inver. . .; TAS.
DR   GO; GO:0008284; P:positive regulation of cell proliferation; TAS.
DR   InterPro; IPR007110; Ig-like.
DR   PROSITE; PS50835; IG_LIKE; 1.
KW   Receptor; Signal; Transmembrane; T-cell; Antigen; Glycoprotein;
KW   Repeat; Immunoglobulin domain; Phosphorylation; Alternative splicing;
KW   3D-structure.
FT   SIGNAL       1     20       POTENTIAL.
FT   CHAIN       21    335       SIGNALING LYMPHOCYTIC ACTIVATION
FT                               MOLECULE.
FT   DOMAIN       21    237       EXTRACELLULAR (POTENTIAL).
FT   TRANSMEM    238    258       POTENTIAL.
FT   DOMAIN      259    335       CYTOPLASMIC (POTENTIAL).
FT   DOMAIN        ?    152       IG-LIKE V-TYPE.
FT   DOMAIN      144    223       IG-LIKE C2-TYPE.
FT   DISULFID    158    228       BY SIMILARITY.
FT   DISULFID    164    209       BY SIMILARITY.
FT   SITE        281    286       SH2-BINDING (POTENTIAL).
FT   SITE        307    312       SH2-BINDING (POTENTIAL).
FT   SITE        327    332       SH2-BINDING (POTENTIAL).
FT   CARBOHYD     53     53       N-LINKED (GLCNAC. . .) (POTENTIAL).
FT   CARBOHYD     57     57       N-LINKED (GLCNAC. . .) (POTENTIAL).
FT   CARBOHYD    102    102       N-LINKED (GLCNAC. . .) (POTENTIAL).
FT   CARBOHYD    125    125       N-LINKED (GLCNAC. . .) (POTENTIAL).
FT   CARBOHYD    150    150       N-LINKED (GLCNAC. . .) (POTENTIAL).
FT   CARBOHYD    155    155       N-LINKED (GLCNAC. . .) (POTENTIAL).
FT   CARBOHYD    189    189       N-LINKED (GLCNAC. . .) (POTENTIAL).
FT   CARBOHYD    217    217       N-LINKED (GLCNAC. . .) (POTENTIAL).
FT   VARSPLIC    234    263       Missing (in isoform 3).
FT                               /FTId=VSP_002567.
FT   VARSPLIC    289    298       PLQKKLDSFP -> DTHHQTSDLF (in isoform 2).
FT                               /FTId=VSP_002568.
FT   VARSPLIC    299    335       Missing (in isoform 2).
FT                               /FTId=VSP_002569.
SQ   SEQUENCE   335 AA;  37231 MW;  BFB0F27EA31D8C04 CRC64;

  Query Match             10.3%;  Score 182.5;  DB 1;  Length 335;
  Best Local Similarity   22.5%;  Pred. No. 7e-08;
  Matches   82;  Conservative   72;  Mismatches  129;  Indels   81;  Gaps   19;

Qy          8 LTLIYILW-QLTGSAASGP------VKELVGSVGGAVTFPL------KSKVKQVDSIVWT 54
              |:| ::|:  |   |: |          :::  :|  |  ||      ||  | :  :|
Db          7 LSLTFVLFLSLAFGASYGTGGRMMNCPKILRQLGSKVLLPLTYERINKSMNKSIHIVVTM 66

Qy         55 FNT------TPLVTIQP-EGGTIIVTQNRNRERVDFPDGGYSLKLSKLKKNDSGIYYVGI 107
                :        :|:: | | |           :|  |      :| : : :| | | | : :
Db         67 AKSLENSVENKIVSLDPSEAG----PPRYLGDRYKFYLENLTLGIRESRKEDEGWYLMTL 122

Qy        108 YSS-SLQQPSTQEYVLHVYEHLSKPKVTMGLQSNKNGTCVTNLTCCMEHGEEDVIYTW-- 164
              : |:|:   |   | :|| :| |:: :  :: :||||   | | :| |:  | |:|
Db        123 EKNVSVQRFCLQ---LRLYEQVSTPEIKVLNKTQENGTCTLILGCTVEKGDH-VAYSWSE 178

Qy        165 KALGQAANESHNGSILPISWRWGESDMTFICVARNPVSRNFS--SPILARKLCEGAADDP 222
              ||      | :::  :| ::     :|  :||   ||:| |    ||        |   ||
Db        179 KAGTHPLNPANSSHLLSLTLGPQHADNIYICTVSNPISNNSQTFSP------WPGCRTDP 232

Qy        223 DSSM-----------VLLCLLLVPLLLSLFVLGLFLWFLKRERQEEYIE---EKKRVDIC 268
                :             |:: |::| :|             |:|  :  : :   ||| : |
Db        233 SETKPWAVYAGLLGGVIMILIMVVILQ----------LRRRGKTNHYQTTVEKKSLTIY 281

Qy        269 RETPNICPHSGENTEYDTIPHTNRTILKEDPANTVY--STVEIPKKMENPHSL-----LT 321
              :     |     : |: |         :||  |:|  :|  :|: ::  :|:      :|
Db        282 AQVQKPGP---LQKKLDSFP-------AQDPCTTIYVAATEPVPESVQETNSITVYASVT 331

Qy        322 MPDT 325
              :|::
Db        332 LPES 335


RESULT 5
CD2_MOUSE
ID   CD2_MOUSE      STANDARD;      PRT;   344 AA.
AC   P08920; Q61394;
DT   01-NOV-1988 (Rel. 09, Created)
DT   01-NOV-1988 (Rel. 09, Last sequence update)
DT   15-MAR-2004 (Rel. 43, Last annotation update)
DE   T-cell surface antigen CD2 precursor (T-cell surface antigen
DE   T11/Leu-5) (LFA-2) (LFA-3 receptor).
GN   CD2.
OS   Mus musculus (Mouse).
OC   Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC   Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus.
OX   NCBI_TaxID=10090;
RN   [1]
RP   SEQUENCE FROM N.A.
RC   STRAIN=B10.A;
RX   MEDLINE=87276135; PubMed=2440689;
RA   Sewell W.A., Brown M.H., Fink P.J., Kozak C.A., Crumpton M.J.;
RT   "The murine homologue of the T lymphocyte CD2 antigen: molecular
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RT   cloning, chromosome assignment and cell surface expression.";
RL   Eur. J. Immunol. 17:1015-1020(1987).
RN   [2]
RP   SEQUENCE FROM N.A.
RX   MEDLINE=88004738; PubMed=2820751;
RA   Clayton L.K., Sayre P.H., Novotny J., Reinherz E.L.;
RT   "Murine and human T11 (CD2) cDNA sequences suggest a common signal
RT   transduction mechanism.";
RL   Eur. J. Immunol. 17:1367-1370(1987).
RN   [3]
RP   SEQUENCE FROM N.A.
RC   STRAIN=BALB/c; TISSUE=Liver;
RX   MEDLINE=88144486; PubMed=2894031;
RA   Diamond D.J., Clayton L.K., Sayre P.H., Reinherz E.L.;
RT   "Exon-intron organization and sequence comparison of human and murine
RT   T11 (CD2) genes.";
RL   Proc. Natl. Acad. Sci. U.S.A. 85:1615-1619(1988).
RN   [4]
RP   SEQUENCE FROM N.A.
RX   MEDLINE=88140313; PubMed=3257775;
RA   Yagita H., Okumura K., Nakauchi H.;
RT   "Molecular cloning of the murine homologue of CD2. Homology of the
RT   molecule to its human counterpart T11.";
RL   J. Immunol. 140:1321-1326(1988).
RN   [5]
RP   SEQUENCE FROM N.A.
RC   STRAIN=C57BL/6; TISSUE=Hematopoietic;
RX   MEDLINE=22388257; PubMed=12477932;
RA   Strausberg R.L., Feingold E.A., Grouse L.H., Derge J.G.,
RA   Klausner R.D., Collins F.S., Wagner L., Shenmen C.M., Schuler G.D.,
RA   Altschul S.F., Zeeberg B., Buetow K.H., Schaefer C.F., Bhat N.K.,
RA   Hopkins R.F., Jordan H., Moore T., Max S.I., Wang J., Hsieh F.,
RA   Diatchenko L., Marusina K., Farmer A.A., Rubin G.M., Hong L.,
RA   Stapleton M., Soares M.B., Bonaldo M.F., Casavant T.L., Scheetz T.E.,
RA   Brownstein M.J., Usdin T.B., Toshiyuki S., Carninci P., Prange C.,
RA   Raha S.S., Loquellano N.A., Peters G.J., Abramson R.D., Mullahy S.J.,
RA   Bosak S.A., McEwan P.J., McKernan K.J., Malek J.A., Gunaratne P.H.,
RA   Richards S., Worley K.C., Hale S., Garcia A.M., Gay L.J., Hulyk S.W.,
RA   Villalon D.K., Muzny D.M., Sodergren E.J., Lu X., Gibbs R.A.,
RA   Fahey J., Helton E., Ketteman M., Madan A., Rodrigues S., Sanchez A.,
RA   Whiting M., Madan A., Young A.C., Shevchenko Y., Bouffard G.G.,
RA   Blakesley R.W., Touchman J.W., Green E.D., Dickson M.C.,
RA   Rodriguez A.C., Grimwood J., Schmutz J., Myers R.M.,
RA   Butterfield Y.S.N., Krzywinski M.I., Skalska U., Smailus D.E.,
RA   Schnerch A., Schein J.E., Jones S.J.M., Marra M.A.;
RT   "Generation and initial analysis of more than 15,000 full-length
RT   human and mouse cDNA sequences.";
RL   Proc. Natl. Acad. Sci. U.S.A. 99:16899-16903(2002).
RN   [6]
RP   INTERACTION WITH CD2AP.
RX   MEDLINE=98412662; PubMed=9741631;
RA   Dustin M.L., Olszowy M.W., Holdorf A.D., Li J., Bromley S., Desai N.,
RA   Widder P., Rosenberger F., van der Merwe P.A., Allen P.M., Shaw A.S.;
RT   "A novel adaptor protein orchestrates receptor patterning and
RT   cytoskeletal polarity in T-cell contacts.";
RL   Cell 94:667-677(1998).
CC   -!- FUNCTION: CD2 interacts with lymphocyte function-associated
CC       antigen (LFA-3) and CD48/BCM1 to mediate adhesion between T
CC       cells and other cell types. CD2 is implicated in the triggerring
CC       of T-cells, the cytoplasmic domain is implicated in the
CC       signaling function.
CC   -!- SUBUNIT: Interacts with CD2AP.
CC   -!- SUBCELLULAR LOCATION: Type I membrane protein.
CC   -!- SIMILARITY: Contains 1 immunoglobulin-like V-type domain.
CC   -!- SIMILARITY: Contains 1 immunoglobulin-like C2-type domain.
CC   ---------------------------------------------------------------------
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CC   use by non-profit institutions as long as its content is in no way
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CC   entities requires a license agreement (See http://www.isb-sib.ch/announce/
CC   or send an email to license@isb-sib.ch).
CC   ---------------------------------------------------------------------
DR   EMBL; Y00023; CAA68258.1; -.
DR   EMBL; X06143; CAA29500.1; -.
DR   EMBL; M19807; AAA37393.1; -.
DR   EMBL; M19799; AAA37393.1; JOINED.
DR   EMBL; M19801; AAA37393.1; JOINED.
DR   EMBL; M19803; AAA37393.1; JOINED.
DR   EMBL; M19805; AAA37393.1; JOINED.
DR   EMBL; M18934; AAA37397.1; -.
DR   EMBL; BC053731; AAH53731.1; -.
DR   PIR; I49585; I49585.
DR   HSSP; P08921; 1A64.
DR   MGD; MGI:88320; Cd2.
DR   GO; GO:0005515; F:protein binding; ISS.
DR   GO; GO:0004872; F:receptor activity; ISS.
DR   InterPro; IPR008424; CD2.
DR   InterPro; IPR007110; Ig-like.
DR   Pfam; PF05790; CD2; 1.
DR   PROSITE; PS50835; IG_LIKE; FALSE_NEG.
KW   Immunoglobulin domain; T-cell; Glycoprotein; Antigen; Transmembrane;
KW   Cell adhesion; Repeat; Signal.
FT   SIGNAL        1     22
FT   CHAIN        23    344       T-CELL SURFACE ANTIGEN CD2.
FT   DOMAIN       23    203       EXTRACELLULAR (POTENTIAL).
FT   TRANSMEM    204    229       POTENTIAL.
FT   DOMAIN      230    344       CYTOPLASMIC (POTENTIAL).
FT   DOMAIN       23    121       IG-LIKE V-TYPE.
FT   DOMAIN      122    202       IG-LIKE C2-TYPE.
FT   DOMAIN      276    343       PRO-RICH.
FT   DISULFID    133    197       BY SIMILARITY.
FT   DISULFID    140    180       BY SIMILARITY.
FT   CARBOHYD     82     82       N-LINKED (GLCNAC. . .) (POTENTIAL).
FT   CARBOHYD     94     94       N-LINKED (GLCNAC. . .) (POTENTIAL).
FT   CARBOHYD    135    135       N-LINKED (GLCNAC. . .) (POTENTIAL).
FT   CARBOHYD    166    166       N-LINKED (GLCNAC. . .) (POTENTIAL).
FT   CONFLICT     99     99       Y -> T (IN REF. 3).
FT   CONFLICT    128    128       M -> V (IN REF. 3 AND 4).
FT   CONFLICT    139    139       T -> I (IN REF. 4).
FT   CONFLICT    175    175       N -> A (IN REF. 3).
FT   CONFLICT    175    175       N -> S (IN REF. 4).
FT   CONFLICT    191    191       K -> N (IN REF. 2).
FT   CONFLICT    192    192       M -> T (IN REF. 3 AND 4).
SQ   SEQUENCE   344 AA;  38414 MW;  CFD12FCBD1444450 CRC64;

  Query Match             8.1%;  Score 144;  DB 1;  Length 344;
  Best Local Similarity   21.4%;  Pred. No. 0.00012;
  Matches   72;  Conservative   56;  Mismatches  132;  Indels   76;  Gaps   16;

Qy         12 YILWQLTGSAASGPVKELV-GSVGGAVT--FPLKSKVKQVDSIVWTFNTTPLVTIQPEGG 68
              ::|: |:|  |      | : | :|  :|  |       :| : |          |
Db         10 FLLFSLSGKGADCRDNETIWGVLGHGITLNIPNFQMTDDIDEVRWV----------RRG 58

Qy         69 TIIVTQNRNR------ERVDFPDGGYSLKLSK-LKKNDSGIYYVGIYSSSLQQPSTQEYV 121
              |::    | :      |  :    | |||: | : :|||| | | :| ::      ::
Db         59 TLVAEFKRKKPPFLISETYEVLANG-SLKIKKPMMRNDSGTYNVMVYGTNGMTRLEKDLD 117

Qy        122 LHVYEHLSKPKVTMGLQSNKNGTCV-TNLTCCMEHGEEDVIYTWKALGQAANESHNGSIL 180
              : : | :||| :          :  | | ||| :  | :  :  ::  |:    |     |
Db        118 VRILERVSKPMI--------HWECPNTTLTCAVLQGTDFELKLYQ--GETLLNS-----L 162

Qy        181 P---ISWRWGESDMTFICVARNPVSRNFSSPILARKLCEGAADDPDSSMVLLCL------ 231
              |   :|::|   :  | | | ||||:    ::        : |: :
Db        163 PQKNMSYQWTNLNAPFKCEAINPVSKESKMEVV---------NCPEKGLSFYVTVGVGAG 213

Qy        232 -LLVPLLLSLFVLGLFLWFLKRERQEEYIEEKKRVDICRETPNICPHSGENTEYDTIPHT 290
               ||: ||::||:   |    :|:|     :|:  :   | :           |    ||:
Db        214 GLLLVLLVALFI---FCICKRRKRNRRRKDEELEIKASRTS---------TVERGPKPHS 261

Qy        291 NRTILKEDPANTVYSTVEIPKKMENPHSLLTMPDTP 326
                      ||    ::| :       | | |    |
Db        262 T-------PAAAAQNSVALQAPPPPGHHLQTPGHRP 290
```

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RESULT 6
CD48_RAT
ID   CD48_RAT       STANDARD;      PRT;   240 AA.
AC   P10252;
DT   01-MAR-1989 (Rel. 10, Created)
DT   01-MAR-1989 (Rel. 10, Last sequence update)
DT   10-OCT-2003 (Rel. 42, Last annotation update)
DE   MRC OX-45 surface antigen precursor (BCM1 surface antigen) (BLAST-1)
DE   (CD48).
GN   CD48 OR BCM-1.
OS   Rattus norvegicus (Rat).
OC   Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC   Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Rattus.
OX   NCBI_TaxID=10116;
RN   [1]
RP   SEQUENCE FROM N.A.
RX   MEDLINE=89030603; PubMed=3181129;
RA   Killeen N., Moessner R., Arvieux J., Willis A., Williams A.F.;
RT   "The MRC OX-45 antigen of rat leukocytes and endothelium is in a
RT   subset of the immunoglobulin superfamily with CD2, LFA-3 and
RT   carcinoembryonic antigens.";
RL   EMBO J. 7:3087-3091(1988).
CC   -!- FUNCTION: LIGAND FOR CD2. MIGHT FACILITATE INTERACTION BETWEEN
CC       ACTIVATED LYMPHOCYTES. PROBABLY INVOLVED IN REGULATING T-CELL
CC       ACTIVATION.
CC   -!- SUBCELLULAR LOCATION: Attached to the membrane by a GPI-anchor.
CC   -!- SIMILARITY: Contains 1 immunoglobulin-like C2-type domain.
CC   -!- SIMILARITY: Contains 1 immunoglobulin-like V-type domain.
CC   ---------------------------------------------------------------------
CC   This SWISS-PROT entry is copyright. It is produced through a collaboration
CC   between the Swiss Institute of Bioinformatics and the EMBL outstation -
CC   the European Bioinformatics Institute. There are no restrictions on its
CC   use by non-profit institutions as long as its content is in no way
CC   modified and this statement is not removed. Usage by and for commercial
CC   entities requires a license agreement (See http://www.isb-sib.ch/announce/
CC   or send an email to license@isb-sib.ch).
CC   ---------------------------------------------------------------------
DR   EMBL; X13016; CAA31438.1; -.
DR   PIR; S01299; S01299.
DR   GlycoSuiteDB; P10252; -.
DR   InterPro; IPR007110; Ig-like.
DR   InterPro; IPR003599; Ig.
DR   Pfam; PF00047; ig; 1.
DR   SMART; SM00409; IG; 1.
DR   PROSITE; PS50835; IG_LIKE; 1.
KW   Immunoglobulin domain; T-cell; Antigen; Glycoprotein; GPI-anchor;
KW   Signal; Repeat; Lipoprotein.
FT   SIGNAL        1    22
FT   CHAIN        23   217       MRC OX-45 SURFACE ANTIGEN.
FT   PROPEP      218   240       REMOVED IN MATURE FORM.
FT   DOMAIN       29   127       IG-LIKE C2-TYPE 1.
FT   DOMAIN      131   207       IG-LIKE C2-TYPE 2.
FT   LIPID       217   217       GPI-anchor amidated serine.
FT   CARBOHYD     38    38       N-LINKED (GLCNAC. . .) (POTENTIAL).
FT   CARBOHYD     97    97       N-LINKED (GLCNAC. . .) (POTENTIAL).
FT   CARBOHYD    140   140       N-LINKED (GLCNAC. . .) (POTENTIAL).
FT   CARBOHYD    186   186       N-LINKED (GLCNAC. . .) (POTENTIAL).
FT   CARBOHYD    203   203       N-LINKED (GLCNAC. . .) (POTENTIAL).
SQ   SEQUENCE   240 AA;  27680 MW;  42CBBF9947A0E437 CRC64;

  Query Match             7.6%;  Score 134;  DB 1;  Length 240;
  Best Local Similarity   24.6%;  Pred. No. 0.00053;
  Matches   48;  Conservative   33;  Mismatches  104;  Indels   10;  Gaps    4;

Qy         13 ILWQLTGSAASGPVKELVGSV----GGAVTFP-LKSKVKQVDSIVWTFNTTPLVTIQPEG 67
              ||  |  |  :|   :  | :|    |  ||   ||  :    : |   |   :
Db         11 ILESLLLSLVTGFQDQSVPNVNAITGSNVTLTILKHPLASYQRLTWLHTTNQKILEYFPN 70

Qy         68 GTIIVTQNRNRERVDFPDGGYSLKLSKLKKNDSGIYYVGIYSSSLQQPSTQEYVLHVYEH 127
              |   | ::  ::|||      :|::  : | | | ||: :   :  |   :  : ||:
Db         71 GKKTVFESVFKDRVDLDKTNGALRIYNVSKEDRGDYYMRMLHETEDQ---WKITMEVYDL 127

Qy        128 LSKPKVTMGLQSNKNGTCVTNLTCCMEHGEEDVIYTWKALGQAANESHNGSILPISWRWG 187
                :||| : :    |   :|   |:| :|  :: | |||        : : | :| |:
Db        128 VSKPAIKIEKTKNLTDSCHLRLSCKVE--DQGVDYTWYEDSGPFPQRNPGYVLEITITPH 185

Qy        188 ESDMTFICVARNPVS 202
                     : |   ||||
Db        186 NKSTFYTCQVSNPVS 200


RESULT 7
CD2_HUMAN
ID   CD2_HUMAN      STANDARD;      PRT;   351 AA.
AC   P06729; Q96TE5;
DT   01-JAN-1988 (Rel. 06, Created)
DT   01-NOV-1988 (Rel. 09, Last sequence update)
DT   10-OCT-2003 (Rel. 42, Last annotation update)
DE   T-cell surface antigen CD2 precursor (T-cell surface antigen
DE   T11/Leu-5) (LFA-2) (LFA-3 receptor) (Erythrocyte receptor) (Rosette
DE   receptor).
GN   CD2.
OS   Homo sapiens (Human).
OC   Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC   Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
OX   NCBI_TaxID=9606;
RN   [1]
RP   SEQUENCE FROM N.A., AND VARIANT HIS-266.
RX   MEDLINE=88144486; PubMed=2894031;
RA   Diamond D.J., Clayton L.K., Sayre P.H., Reinherz E.L.;
RT   "Exon-intron organization and sequence comparison of human and murine
RT   T11 (CD2) genes.";
RL   Proc. Natl. Acad. Sci. U.S.A. 85:1615-1619(1988).
RN   [2]
RP   SEQUENCE FROM N.A.
RX   MEDLINE=87204137; PubMed=2437578;
RA   Seed B., Aruffo A.;
RT   "Molecular cloning of the CD2 antigen, the T-cell erythrocyte
RT   receptor, by a rapid immunoselection procedure.";
RL   Proc. Natl. Acad. Sci. U.S.A. 84:3365-3369(1987).
RN   [3]
RP   SEQUENCE FROM N.A., AND VARIANT HIS-266.
RX   MEDLINE=87041523; PubMed=3490670;
RA   Sewell W.A., Brown M.H., Dunne J., Owen M.J., Crumpton M.J.;
RT   "Molecular cloning of the human T-lymphocyte surface CD2 (T11)
RT   antigen.";
RL   Proc. Natl. Acad. Sci. U.S.A. 83:8718-8722(1986).
RN   [4]
RP   REVISIONS.
RA   Sewell W.A., Brown M.H., Dunne J., Owen M.J., Crumpton M.J.;
RL   Proc. Natl. Acad. Sci. U.S.A. 84:7256-7256(1987).
RN   [5]
RP   SEQUENCE FROM N.A.
RX   MEDLINE=87204243; PubMed=2883656;
RA   Sayre P.H., Chang H.-C., Hussey R.E., Brown N.R., Richardson N.E.,
RA   Spagnoli G., Clayton L.K., Reinherz E.L.;
RT   "Molecular cloning and expression of T11 cDNAs reveal a receptor-like
RT   structure on human T lymphocytes.";
RL   Proc. Natl. Acad. Sci. U.S.A. 84:2941-2945(1987).
RN   [6]
RP   SEQUENCE FROM N.A., AND VARIANT HIS-266.
RX   MEDLINE=89005055; PubMed=2901953;
RA   Lang G., Wotton D., Owen M.J., Sewell W.A., Brown M.H., Mason D.Y.,
RA   Crumpton M.J., Kioussis D.;
RT   "The structure of the human CD2 gene and its expression in transgenic
RT   mice.";
RL   EMBO J. 7:1675-1682(1988).
RN   [7]
RP   SEQUENCE FROM N.A., AND VARIANT HIS-266.
RA   Hall R.;
RL   Submitted (APR-2000) to the EMBL/GenBank/DDBJ databases.
RN   [8]
RP   SEQUENCE FROM N.A.
RC   TISSUE=Pancreas, and Spleen;
RX   MEDLINE=22388257; PubMed=12477932;
RA   Strausberg R.L., Feingold E.A., Grouse L.H., Derge J.G.,
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RA   Klausner R.D., Collins F.S., Wagner L., Shenmen C.M., Schuler G.D.,
RA   Altschul S.F., Zeeberg B., Buetow K.H., Schaefer C.F., Bhat N.K.,
RA   Hopkins R.F., Jordan H., Moore T., Max S.I., Wang J., Hsieh F.,
RA   Diatchenko L., Marusina K., Farmer A.A., Rubin G.M., Hong L.,
RA   Stapleton M., Soares M.B., Bonaldo M.F., Casavant T.L., Scheetz T.E.,
RA   Brownstein M.J., Usdin T.B., Toshiyuki S., Carninci P., Prange C.,
RA   Raha S.S., Loquellano N.A., Peters G.J., Abramson R.D., Mullahy S.J.,
RA   Bosak S.A., McEwan P.J., McKernan K.J., Malek J.A., Gunaratne P.H.,
RA   Richards S., Worley K.C., Hale S., Garcia A.M., Gay L.J., Hulyk S.W.,
RA   Villalon D.K., Muzny D.M., Sodergren E.J., Lu X., Gibbs R.A.,
RA   Fahey J., Helton E., Ketteman M., Madan A., Rodrigues S., Sanchez A.,
RA   Whiting M., Madan A., Young A.C., Shevchenko Y., Bouffard G.G.,
RA   Blakesley R.W., Touchman J.W., Green E.D., Dickson M.C.,
RA   Rodriguez A.C., Grimwood J., Schmutz J., Myers R.M.,
RA   Butterfield Y.S.N., Krzywinski M.I., Skalska U., Smailus D.E.,
RA   Schnerch A., Schein J.E., Jones S.J.M., Marra M.A.;
RT   "Generation and initial analysis of more than 15,000 full-length
RT   human and mouse cDNA sequences.";
RL   Proc. Natl. Acad. Sci. U.S.A. 99:16899-16903(2002).
RN   [9]
RP   X-RAY CRYSTALLOGRAPHY (2.5 ANGSTROMS) OF 25-206.
RX   MEDLINE=95086863; PubMed=7994575;
RA   Bodian D.L., Jones E.Y., Harlos K., Stuart D.I., Davis S.J.;
RT   "Crystal structure of the extracellular region of the human cell
RT   adhesion molecule CD2 at 2.5-A resolution.";
RL   Structure 2:755-766(1994).
RN   [10]
RP   STRUCTURE BY NMR OF 25-129.
RX   MEDLINE=94348865; PubMed=7915183;
RA   Withka J.M., Wyss D.F., Wagner G., Arulanandam A.R.N., Reinherz E.L.,
RA   Recny M.A.;
RT   "Structure of the glycosylated adhesion domain of human T lymphocyte
RT   glycoprotein CD2.";
RL   Structure 1:69-81(1993).
RN   [11]
RP   STRUCTURE BY NMR OF 25-129.
RX   MEDLINE=95381065; PubMed=7544493;
RA   Wyss D.F., Choi J.S., Li J., Knoppers M.H., Willis K.J.,
RA   Arulanandam A.R., Smolyar A., Reinherz E.L., Wagner G.;
RT   "Conformation and function of the N-linked glycan in the adhesion
RT   domain of human CD2.";
RL   Science 269:1273-1278(1995).
RN   [12]
RP   MUTAGENESIS.
RX   MEDLINE=88039075; PubMed=2444890;
RA   Peterson A., Seed B.;
RT   "Monoclonal antibody and ligand binding sites of the T cell
RT   erythrocyte receptor (CD2).";
RL   Nature 329:842-846(1987).
RN   [13]
RP   CD59-BINDING DATA.
RX   MEDLINE=92311658; PubMed=1377404;
RA   Hahn W.C., Menu E., Bothwell A.L.M., Sims P.J., Bierer B.E.;
RT   "Overlapping but nonidentical binding sites on CD2 for CD58 and a
RT   second ligand CD59.";
RL   Science 256:1805-1807(1992).
CC   -!- FUNCTION: CD2 interacts with lymphocyte function-associated
CC       antigen (LFA-3) and CD48/BCM1 to mediate adhesion between T
CC       cells and other cell types. CD2 is implicated in the triggerring
CC       of T-cells, the cytoplasmic domain is implicated in the
CC       signaling function.
CC   -!- SUBUNIT: Interacts with CD2AP (By similarity).
CC   -!- SUBCELLULAR LOCATION: Type I membrane protein.
CC   -!- SIMILARITY: Contains 1 immunoglobulin-like V-type domain.
CC   -!- SIMILARITY: Contains 1 immunoglobulin-like C2-type domain.
CC   -!- DATABASE: NAME=PROW; NOTE=CD guide CD2 entry;
CC       WWW="http://www.ncbi.nlm.nih.gov/prow/cd/cd2.htm".
CC   ---------------------------------------------------------------------
CC   This SWISS-PROT entry is copyright. It is produced through a collaboration
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CC   or send an email to license@isb-sib.ch).
CC   ---------------------------------------------------------------------
DR   EMBL; M16445; AAA51738.1; -.
DR   EMBL; M14362; AAA35571.1; -.
DR   EMBL; M16336; AAA51946.1; -.
DR   EMBL; M19806; AAA53095.1; -.
DR   EMBL; M19798; AAA53095.1; JOINED.
DR   EMBL; M19800; AAA53095.1; JOINED.
DR   EMBL; M19802; AAA53095.1; JOINED.
DR   EMBL; M19804; AAA53095.1; JOINED.
DR   EMBL; X07871; CAA30721.1; -.
DR   EMBL; X07872; CAA30721.1; JOINED.
DR   EMBL; X07873; CAA30721.1; JOINED.
DR   EMBL; X07874; CAA30721.1; JOINED.
DR   EMBL; AL135798; CAC14840.1; -.
DR   EMBL; BC033583; AAH33583.1; -.
DR   PIR; A28967; RWHUC2.
DR   PDB; 1CDB; 15-OCT-94.
DR   PDB; 1HNF; 07-FEB-95.
DR   PDB; 1GYA; 08-NOV-96.
DR   PDB; 1L2Z; 20-NOV-02.
DR   GlycoSuiteDB; P06729; -.
DR   Genew; HGNC:1639; CD2.
DR   MIM; 186990; -.
DR   GO; GO:0005887; C:integral to plasma membrane; NAS.
DR   GO; GO:0005515; F:protein binding; IPI.
DR   GO; GO:0004872; F:receptor activity; NAS.
DR   GO; GO:0007166; P:cell surface receptor linked signal transdu. . .; TAS.
DR   GO; GO:0016337; P:cell-cell adhesion; NAS.
DR   GO; GO:0006917; P:induction of apoptosis; TAS.
DR   GO; GO:0045768; P:positive regulation of anti-apoptosis; NAS.
DR   GO; GO:0045580; P:regulation of T-cell differentiation; NAS.
DR   GO; GO:0042110; P:T-cell activation; TAS.
DR   InterPro; IPR008424; CD2.
DR   InterPro; IPR007110; Ig-like.
DR   Pfam; PF05790; CD2; 1.
DR   PROSITE; PS50835; IG_LIKE; FALSE_NEG.
KW   Immunoglobulin domain; T-cell; Glycoprotein; Antigen; Transmembrane;
KW   Cell adhesion; Repeat; Signal; Polymorphism; 3D-structure.
FT   SIGNAL       1     24
FT   CHAIN       25    351       T-CELL SURFACE ANTIGEN CD2.
FT   DOMAIN      25    209       EXTRACELLULAR (POTENTIAL).
FT   TRANSMEM   210    235       POTENTIAL.
FT   DOMAIN     236    351       CYTOPLASMIC (POTENTIAL).
FT   DOMAIN      25    128       IG-LIKE V-TYPE.
FT   DOMAIN     129    209       IG-LIKE C2-TYPE.
FT   DOMAIN      61     75       LFA-3 (CD58) BINDING REGION 1.
FT   DOMAIN     106    120       LFA-3 (CD58) BINDING REGION 2.
FT   DOMAIN     282    338       PRO-RICH.
FT   DISULFID   139    203       BY SIMILARITY.
FT   DISULFID   146    186       BY SIMILARITY.
FT   CARBOHYD    89     89       N-LINKED (GLCNAC. . .).
FT   CARBOHYD   141    141       N-LINKED (GLCNAC. . .) (POTENTIAL).
FT   CARBOHYD   150    150       N-LINKED (GLCNAC. . .) (POTENTIAL).
FT   VARIANT    266    266       Q -> H (in dbSNP:699738).
FT                               /FTId=VAR_017104.
FT   MUTAGEN     67     67       K->R: LOSS OF LFA-3 BINDING.
FT   MUTAGEN     70     70       Q->K: LOSS OF LFA-3 BINDING.
FT   MUTAGEN    110    110       Y->D: LOSS OF LFA-3 AND CD59 BINDING.
FT   MUTAGEN    111    111       D->H: LOSS OF LFA-3 AND CD59 BINDING.
FT   CONFLICT   287    287       G -> A (IN REF. 3).
FT   CONFLICT   339    351       HGAAENSLSPSSN -> MGQQKTHCPLPLIKKDRNCLFQ
FT                               (IN REF. 3).

  Query Match             7.5%;  Score 133.5;  DB 1;  Length 351;
  Best Local Similarity   22.7%;  Pred. No. 0.00093;
  Matches   68;  Conservative   52;  Mismatches  105;  Indels   75;  Gaps   15;

Qy         28 ELVGSVGGAVTFPLKS--KVKQVDSIVW--TFNTTPLVTIQPEGGTIIVTQNRNRERVDF 83
              |  |::|  :   : |      :| | |  | :   :   : | |    : ::  :: |
Db         32 ETWGALGQDINLDIPSFQMSDDIDDIKWEKTSDKKKIAQFRKEKETF---KEKDTYKL-F 87
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Qy          84 PDGGYSLKLSKLKKNDSGIYYVGIYSSSLQQPSTQEYVLHVYEHLSKPKVTMGLQSNKNG 143
               :|  :||:  || :|  || | || :  :    : : | : | :||||::
Db          88 KNG--TLKIKHLKTDDQDIYKVSIYDTKGKNVLEKIFDLKIQERVSKPKISW-------- 137

Qy         144 TCV-TNLTCCMEHGEEDVIYTWKALGQAANESHNGSILPISWR-----WGES-DMTFICV 196
               ||: | ||| : :| :  :           |   :|  | :| |     |  |    | |
Db         138 TCINTTLTCEVMNGTDPEL----------NLYQDGKHLKLSQRVITHKWTTSLSAKFKCT 187

Qy         197 ARNPVSRNFS-SPI----------LARKLCEGAADDPDSSMVLLCLLLVPLLLSLFVLGL 245
               | | ||:  |  |:          |   :| | :                  || :||  |
Db         188 AGNKVSKESSVEPVSCPEKGLDIYLIIGICGGGS----------------LLMVFVALL 230

Qy         246 FLWFLKRERQ-----EEYIEEK-------KRVDICRETPNICPHSGENTEYDTIPHTNRT 293
                 :  ||::|     :| :| :       :|    :: |    | :   :::   |  :|:
Db         231 VFYITKRKKQRSRRNDEELETRAHRVATEERGRKPQQIPASTPQNPATSQHPPPPPGHRS 290
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RESULT 8
CD2_RAT
ID CD2_RAT STANDARD; PRT; 344 AA.
AC P08921;
DT 01-NOV-1988 (Rel. 09, Created)
DT 01-NOV-1988 (Rel. 09, Last sequence update)
DT 10-OCT-2003 (Rel. 42, Last annotation update)
DE T-cell surface antigen CD2 precursor (T-cell surface antigen
DE T11/Leu-5) (LFA-2) (LFA-3 receptor) (OX-34 antigen).
GN CD2.
OS Rattus norvegicus (Rat).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Rattus.
OX NCBI_TaxID=10116;
RN [1]
RP SEQUENCE OF 42-344 FROM N.A., AND PARTIAL SEQUENCE.
RC STRAIN=AO;
RX MEDLINE=87139793; PubMed=3102667;
RA Williams A.F., Barclay A.N., Clark S.J., Paterson D.J., Willis A.C.;
RT "Similarities in sequences and cellular expression between rat CD2
RT and CD4 antigens.";
RL J. Exp. Med. 165:368-380(1987).
RN [2]
RP SEQUENCE FROM N.A.
RC STRAIN=AO;
RA Barclay A.N., Williams A.F.;
RL Submitted (MAY-1987) to the EMBL/GenBank/DDBJ databases.
RN [3]
RP IMPORTANCE OF C-TERMINAL IN SIGNALING.
RX MEDLINE=88327862; PubMed=2901293;
RA He Q., Beyers A.D., Barclay A.N., Williams A.F.;
RT "A role in transmembrane signaling for the cytoplasmic domain of the
RT CD2 T lymphocyte surface antigen.";
RL Cell 54:979-984(1988).
RN [4]
RP X-RAY CRYSTALLOGRAPHY (2.8 ANGSTROMS) OF 23-198.
RX MEDLINE=93063364; PubMed=1279440;
RA Jones E.Y., Davis S.J., Williams A.F., Harlos K., Stuart D.I.;
RT "Crystal structure at 2.8-A resolution of a soluble form of the cell
RT adhesion molecule CD2.";
RL Nature 360:232-239(1992).
RN [5]
RP X-RAY CRYSTALLOGRAPHY (2.0 ANGSTROMS) OF 23-121.
RX MEDLINE=95365363; PubMed=7638192;
RA Murray A.J., Lewis S.J., Barclay A.N., Brady R.L.;
RT "One sequence, two folds: a metastable structure of CD2.";
RL Proc. Natl. Acad. Sci. U.S.A. 92:7337-7341(1995).
RN [6]
RP X-RAY CRYSTALLOGRAPHY (2.0 ANGSTROMS) OF 23-121.
RX MEDLINE=98400497; PubMed=9731771;
RA Murray A.J., Head J.G., Barker J.J., Brady R.L.;
RT "Engineering an intertwined form of CD2 for stability and assembly.";
RL Nat. Struct. Biol. 5:778-782(1998).
RN [7]
RP STRUCTURE BY NMR OF 23-121.
RX MEDLINE=92049704; PubMed=1682812;
RA Driscoll P.C., Cyster J.G., Campbell I.D., Williams A.F.;
RT "Structure of domain 1 of rat T lymphocyte CD2 antigen.";
RL Nature 353:762-765(1991).
CC -!- FUNCTION: CD2 interacts with lymphocyte function-associated
CC antigen (LFA-3) and CD48/BCM1 to mediate adhesion between T
CC cells and other cell types. CD2 is implicated in the triggerring
CC of T-cells, the cytoplasmic domain is implicated in the
CC signaling function.
CC -!- SUBUNIT: Interacts with CD2AP (By similarity).
CC -!- SUBCELLULAR LOCATION: Type I membrane protein.
CC -!- SIMILARITY: Contains 1 immunoglobulin-like V-type domain.
CC -!- SIMILARITY: Contains 1 immunoglobulin-like C2-type domain.
CC ---

CC ---
DR EMBL; X05111; CAA28757.1; -.
DR PDB; 1CDC; 15-SEP-95.
DR PDB; 1HNG; 07-FEB-95.
DR PDB; 1A64; 27-MAY-98.
DR PDB; 1A6P; 17-JUN-98.
DR PDB; 1A7B; 17-JUN-98.
DR GO; GO:0005515; F:protein binding; ISS.
DR GO; GO:0004872; F:receptor activity; ISS.
DR InterPro; IPR008424; CD2.
DR InterPro; IPR007110; Ig-like.
DR InterPro; IPR003599; Ig.
DR Pfam; PF05790; CD2; 1.
DR SMART; SM00409; IG; 1.
DR PROSITE; PS50835; IG_LIKE; FALSE_NEG.
KW Immunoglobulin domain; T-cell; Glycoprotein; Antigen; Transmembrane;
KW Cell adhesion; Repeat; Signal; 3D-structure.

FT	SIGNAL	1	22
FT	CHAIN	23	344 T-CELL SURFACE ANTIGEN CD2.
FT	DOMAIN	23	202 EXTRACELLULAR (POTENTIAL).
FT	TRANSMEM	203	228 POTENTIAL.
FT	DOMAIN	229	344 CYTOPLASMIC (POTENTIAL).
FT	DOMAIN	23	121 IG-LIKE V-TYPE.
FT	DOMAIN	122	202 IG-LIKE C2-TYPE.
FT	DOMAIN	277	343 PRO-RICH.
FT	DISULFID	132	196
FT	DISULFID	139	179
FT	CARBOHYD	99	99 N-LINKED (GLCNAC. . .).
FT	CARBOHYD	106	106 N-LINKED (GLCNAC. . .).
FT	CARBOHYD	134	134 N-LINKED (GLCNAC. . .).
FT	STRAND	25	31
FT	TURN	32	33
FT	STRAND	36	38
FT	TURN	41	42
FT	TURN	47	48
FT	STRAND	49	56
FT	TURN	57	58
FT	STRAND	59	65
FT	STRAND	71	72
FT	TURN	75	76
FT	STRAND	77	79
FT	TURN	81	82
FT	STRAND	85	87
FT	HELIX	92	94
FT	STRAND	96	104
FT	STRAND	109	120
FT	STRAND	127	131
FT	TURN	132	135
FT	STRAND	136	140
FT	STRAND	148	153
FT	TURN	154	155
FT	STRAND	156	161
FT	STRAND	165	169

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FT   STRAND       177    183
FT   TURN         184    185
FT   STRAND       186    192
SQ   SEQUENCE   344 AA;  38414 MW;  41BAED392CE16356 CRC64;

  Query Match             7.3%;  Score 130;  DB 1;  Length 344;
  Best Local Similarity   22.4%;  Pred. No. 0.0018;
  Matches   65;  Conservative   51;  Mismatches  112;  Indels   62;  Gaps   13;

Qy         12 YILWQLTGSAA----SGPVKELVGSVGGAVTFPLKSKVKQVDSIVWTFNTTPLVTIQPEG 67
              ::|: |:   |    || |   :|  |  :  |       :| : |           |
Db         10 FLLFSLSSKGADCRDSGTVWGALGH-GINLNIPNFQMTDDIDEVRW----------ER 56

Qy         68 GTIIVTQNRNRERVDFPDGGY------SLKLSKLKKNDSGIYYVGIYSSSLQQPSTQEYV 121
              |: :| : : : :     | :       ||:  | ::||| | | :||::  :  :
Db         57 GSTLVAEFKRKMKPFLKSGAFEILANGDLKIKNLTRDDSGTYNVTVYSTNGTRILDKALD 116

Qy        122 LHVYEHLSKPKVTMGLQSNKNGTCV----TNLTCCMEHGEEDVIYTWKALGQAANESHNG 177
              | : | :||| :     ||   ||     |::   :  |:| :    ::| |
Db        117 LRILEMVSKPMIYWEC-SNATLTCEVLEGTDVELKLYQGKEHL----RSLRQKT------ 165

Qy        178 SILPISWRWGESDMTFICVARNPVSRNFSSPILARKLCEGAADDPDSSMVLLCLLLVPL- 236
                :|::|      | | | | ||:     ::         : |:  : |  :: |
Db        166 ----MSYQWTNLRAPFKCKAVNRVSQESEMEVV---------NCPEKGLPLYLIVGVSAG 212

Qy        237 -LLSLFVLGLFLWFL------KRERQEEYIEEK-KRVDICRETPNICPHS 278
               ||.:|   ||:: :       | |: | :| |  |:      |   |||
Db        213 GLLLVFFGALFIFCICKRKKRNRRRKGEELEIKASRMSTVERGPK--PHS 260


RESULT 9
CD48_MOUSE
ID   CD48_MOUSE     STANDARD;      PRT;   240 AA.
AC   P18181;
DT   01-NOV-1990 (Rel. 16, Created)
DT   01-NOV-1990 (Rel. 16, Last sequence update)
DT   15-MAR-2004 (Rel. 43, Last annotation update)
DE   MRC OX-45 surface antigen precursor (BCM1 surface antigen) (BLAST-1)
DE   (CD48) (HM48-1).
GN   CD48 OR BCM-1.
OS   Mus musculus (Mouse).
OC   Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC   Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus.
OX   NCBI_TaxID=10090;
RN   [1]
RP   SEQUENCE FROM N.A.
RC   STRAIN=BALB/c;
RX   MEDLINE=90278362; PubMed=1693656;
RA   Wong Y.W., Williams A.F., Kingsmore S.F., Seldin M.F.;
RT   "Structure, expression, and genetic linkage of the mouse BCM1 (OX45
RT   or Blast-1) antigen. Evidence for genetic duplication giving rise to
RT   the BCM1 region on mouse chromosome 1 and the CD2/LFA3 region on
RT   mouse chromosome 3.";
RL   J. Exp. Med. 171:2115-2130(1990).
RN   [2]
RP   SEQUENCE OF 23-40.
RX   MEDLINE=93018850; PubMed=1383383;
RA   Kato K., Koyanagi M., Okada H., Takanahi T., Wong Y.W., Williams A.F.,
RA   Okumura K., Yagita H.;
RT   "CD48 is a counter-receptor for mouse CD2 and is involved in T cell
RT   activation.";
RL   J. Exp. Med. 176:1241-1249(1992).
CC   -!- FUNCTION: LIGAND FOR CD2. MIGHT FACILITATE INTERACTION BETWEEN
CC       ACTIVATED LYMPHOCYTES. PROBABLY INVOLVED IN REGULATING T-CELL
CC       ACTIVATION.
CC   -!- SUBCELLULAR LOCATION: Attached to the membrane by a GPI-anchor.
CC   -!- SIMILARITY: Contains 1 immunoglobulin-like C2-type domain.
CC   -!- SIMILARITY: Contains 1 immunoglobulin-like V-type domain.
CC   ---------------------------------------------------------------------
CC   This SWISS-PROT entry is copyright. It is produced through a collaboration
CC   between the Swiss Institute of Bioinformatics and the EMBL outstation -
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CC   or send an email to license@isb-sib.ch).
CC   ---------------------------------------------------------------------
DR   EMBL; X53526; CAA37604.1; -.
DR   EMBL; X17501; CAA35542.1; -.
DR   PIR; JL0143; JL0143.
DR   MGD; MGI:88339; Cd48.
DR   InterPro; IPR007110; Ig-like.
DR   InterPro; IPR003599; Ig.
DR   Pfam; PF00047; ig; 1.
DR   SMART; SM00409; IG; 1.
DR   PROSITE; PS50835; IG_LIKE; 1.
KW   Antigen; Repeat; Signal; Immunoglobulin domain; Glycoprotein;
KW   Lipoprotein; GPI-anchor.
FT   SIGNAL        1     22
FT   CHAIN        23    217       MRC OX-45 SURFACE ANTIGEN.
FT   PROPEP      218    240       REMOVED IN MATURE FORM.
FT   DOMAIN       29    125       IG-LIKE C2-TYPE 1.
FT   DOMAIN      129    209       IG-LIKE C2-TYPE 2.
FT   LIPID       217    217       GPI-anchor amidated serine.
FT   DISULFID    151    193       POTENTIAL.
FT   CARBOHYD     32     32       N-LINKED (GLCNAC. . .) (POTENTIAL).
FT   CARBOHYD     38     38       N-LINKED (GLCNAC. . .) (POTENTIAL).
FT   CARBOHYD     70     70       N-LINKED (GLCNAC. . .) (POTENTIAL).
FT   CARBOHYD    136    136       N-LINKED (GLCNAC. . .) (POTENTIAL).
FT   CARBOHYD    186    186       N-LINKED (GLCNAC. . .) (POTENTIAL).
FT   CARBOHYD    203    203       N-LINKED (GLCNAC. . .) (POTENTIAL).
SQ   SEQUENCE   240 AA;  27383 MW;  F3BF6987A9E9C71E CRC64;

  Query Match             7.1%;  Score 126.5;  DB 1;  Length 240;
  Best Local Similarity   21.4%;  Pred. No. 0.0022;
  Matches   52;  Conservative   45;  Mismatches  125;  Indels   21;  Gaps    8;

Qy          7 CLTLIYILWQLTGSAASGPVKELVGSVGGAVTFPL-KSKVKQVDSIVWTFNTTPLVTIQP 65
              || |  :|  |          : ::  : |  ||  : |  :      | |       :
Db          9 CLVLELLLLPLGTGFQGHSIPDINATTGSNVTLKIHKDPLGPYKRITWLHTKNQKILEYN 68

Qy         66 EGGTIIVTQNRNRERVDFPDGGYSLKLSKLKKNDSGIYYVGIYSSSLQQPSTQ-EYVLHV 124
                 | : ::  : ||    :   :| :|.::| | | ||: :    |::   : :  | |
Db         69 YNSTKTIFESEFKGRVYLEENNGALHISNVRKEDKGTYYMRV----LRETENELKITLEV 124

Qy        125 YEHLSKPKVTMGLQSNKNGTCVTNLTCCMEHGEEDVIYTWKALGQAANESHNGSILPISW 184
              :: : || : :         :|   |:|  |  :: | |||         :   | :| :
Db        125 FDPVPKPSIEINKTEASTDSCHLRLSC--EVKDQHVDYTWYESSGPFPKKSPGYVLDLIV 182

Qy        185 RWGESDMTFICVARNPVSRN-----FSSPI-LARK--LCEGAADDPDSSMVLLCLLLVPL 236
                    : |   ||||       |: |  |||   :|  |      : :|:  |::  :
Db        183 TPQNKSTFYTCQVSNPVSSKNDTVYFTLPCDLARSSGVCWTA-----TWLVVTTLIIHRI 237

Qy        237 LLS 239
               ||:
Db        238 LLT 240


RESULT 10
CEA1_HUMAN
ID   CEA1_HUMAN     STANDARD;      PRT;   526 AA.
AC   P13688;
DT   01-JAN-1990 (Rel. 13, Created)
DT   01-JUL-1993 (Rel. 26, Last sequence update)
DT   10-OCT-2003 (Rel. 42, Last annotation update)
DE   Carcinoembryonic antigen-related cell adhesion molecule 1 precursor
DE   (Biliary glycoprotein 1) (BGP-1) (Antigen CD66) (CD66a antigen).
GN   CEACAM1 OR BGP OR BGP1.
OS   Homo sapiens (Human).
OC   Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC   Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
OX   NCBI_TaxID=9606;
RN   [1]
RP   SEQUENCE FROM N.A., AND PARTIAL SEQUENCE.
RX   MEDLINE=88320555; PubMed=2457922;
RA   Hinoda Y., Neumaier M., Hefta S.A., Drzeniek Z., Wagener C.,
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RA   Shively L., Hefta L.J.F., Shively J.E., Paxton R.J.;
RT   "Molecular cloning of a cDNA coding biliary glycoprotein I: primary
RT   structure of a glycoprotein immunologically crossreactive with
RT   carcinoembryonic antigen.";
RL   Proc. Natl. Acad. Sci. U.S.A. 85:6959-6963(1988).
RN   [2]
RP   REVISION.
RA   Hinoda Y., Neumaier M., Hefta S.A., Drzeniek Z., Wagener C.,
RA   Shively L., Hefta L.J.F., Shively J.E., Paxton R.J.;
RL   Proc. Natl. Acad. Sci. U.S.A. 86:1668-1668(1989).
RN   [3]
RP   SEQUENCE FROM N.A.
RX   MEDLINE=89139550; PubMed=2537311;
RA   Barnett T.R., Kretschmer A., Austen D.A., Goebel S.J., Hart J.T.,
RA   Elting J.J., Kamarck M.E.;
RT   "Carcinoembryonic antigens: alternative splicing accounts for the
RT   multiple mRNAs that code for novel members of the carcinoembryonic
RT   antigen family.";
RL   J. Cell Biol. 108:267-276(1989).
RN   [4]
RP   SEQUENCE FROM N.A.
RC   TISSUE=Leukocyte;
RX   MEDLINE=91222218; PubMed=2025273;
RA   Kuroki M., Arakawa F., Matsuo Y., Oikawa S., Nakazato H.,
RA   Matsuoka Y.;
RT   "Three novel molecular forms of biliary glycoprotein deduced from
RT   cDNA clones from a human leukocyte library.";
RL   Biochem. Biophys. Res. Commun. 176:578-585(1991).
RN   [5]
RP   SEQUENCE FROM N.A.
RA   Lamerdin J.E., McCready P.M., Skowronski E., Adamson A.W.,
RA   Burkhart-Schultz K., Gordon L., Kyle A., Ramirez M., Stilwagen S.,
RA   Phan H., Velasco N., Do L., Regala W., Terry A., Garnes J.,
RA   Danganan L., Poundstone P., Christensen M., Georgescu A., Avila J.,
RA   Liu S., Attix C., Andreise T., Trankheim M., Amico-Keller G.,
RA   Coefield J., Duarte S., Lucas S., Bruce R., Thomas P., Quan G.,
RA   Kronmiller B., Arellano A., Montgomery M., Ow D., Nolan M., Trong S.,
RA   Kobayashi A., Olsen A.S., Carrano A.V.;
RL   Submitted (JUN-1998) to the EMBL/GenBank/DDBJ databases.
CC   -!- SUBCELLULAR LOCATION: Type I membrane protein (isoform A).
CC       Secreted (isoforms G, H and I).
CC   -!- ALTERNATIVE PRODUCTS:
CC       Event=Alternative splicing; Named isoforms=4;
CC       Name=A;
CC         IsoId=P13688-1; Sequence=Displayed;
CC       Name=G;
CC         IsoId=P13688-2; Sequence=VSP_002482, VSP_002483;
CC       Name=H;
CC         IsoId=P13688-3; Sequence=VSP_002478, VSP_002479;
CC       Name=I;
CC         IsoId=P13688-4; Sequence=VSP_002480, VSP_002481;
CC   -!- DISEASE: Increased serum levels of BGP-1 are found in individuals
CC       suffering from hepatic disorders.
CC   -!- SIMILARITY: Belongs to the immunoglobulin superfamily. CEA
CC       family.
CC   -!- SIMILARITY: Contains 1 immunoglobulin-like V-type domain.
CC   -!- SIMILARITY: Contains 3 immunoglobulin-like C2-type domains.
CC   -!- DATABASE: NAME=PROW; NOTE=CD guide CD66a entry;
CC       WWW="http://www.ncbi.nlm.nih.gov/prow/cd/cd66a.htm".
CC   ---------------------------------------------------------------------
CC   This SWISS-PROT entry is copyright. It is produced through a collaboration
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CC   ---------------------------------------------------------------------
DR   EMBL; X16354; CAA34404.1; -.
DR   EMBL; J03858; AAA51826.1; -.
DR   EMBL; D90311; BAA14341.1; -.
DR   EMBL; D90312; BAA14342.1; -.
DR   EMBL; D90313; BAA14343.1; -.
DR   EMBL; M69176; AAA51825.1; -.
DR   EMBL; M72238; AAA58393.1; -.
DR   EMBL; M72238; AAA58394.1; -.
DR   EMBL; AC004785; AAC18434.1; -.
DR   EMBL; AC004785; AAC18437.1; -.
DR   EMBL; AC004785; AAC18438.1; -.
DR   EMBL; AC004785; AAC18439.1; -.
DR   PIR; A32164; A32164.
DR   PIR; JH0394; JH0394.
DR   PIR; JH0395; JH0395.
DR   PIR; JH0396; JH0396.
DR   Genew; HGNC:1814; CEACAM1.
DR   MIM; 109770; -.
DR   GO; GO:0005887; C:integral to plasma membrane; TAS.
DR   GO; GO:0005624; C:membrane fraction; TAS.
DR   InterPro; IPR007110; Ig-like.
DR   Pfam; PF00047; ig; 4.
DR   PROSITE; PS50835; IG_LIKE; 3.
KW   Immunoglobulin domain; Glycoprotein; Transmembrane; Signal; Repeat;
KW   Alternative splicing; Pyrrolidone carboxylic acid.
FT   SIGNAL       1    34
FT   CHAIN       35   526       CARCINOEMBRYONIC ANTIGEN-RELATED CELL
FT                               ADHESION MOLECULE 1.
FT   DOMAIN       35   428       EXTRACELLULAR (POTENTIAL).
FT   TRANSMEM    429   452       POTENTIAL.
FT   DOMAIN      453   526       CYTOPLASMIC (POTENTIAL).
FT   DOMAIN       35   142       IG-LIKE V-TYPE.
FT   DOMAIN      145   232       IG-LIKE C2-TYPE 1.
FT   DOMAIN      237   317       IG-LIKE C2-TYPE 2.
FT   DOMAIN      323   413       IG-LIKE C2-TYPE 3.
FT   DISULFID    167   215       PROBABLE.
FT   DISULFID    259   299       PROBABLE.
FT   DISULFID    348   396       PROBABLE.
FT   MOD_RES      35    35       PYRROLIDONE CARBOXYLIC ACID.
FT   CARBOHYD    104   104       N-LINKED (GLCNAC. . .).
FT   CARBOHYD    111   111       N-LINKED (GLCNAC. . .).
FT   CARBOHYD    115   115       N-LINKED (GLCNAC. . .).
FT   CARBOHYD    152   152       N-LINKED (GLCNAC. . .).
FT   CARBOHYD    182   182       N-LINKED (GLCNAC. . .) (POTENTIAL).
FT   CARBOHYD    197   197       N-LINKED (GLCNAC. . .) (POTENTIAL).
FT   CARBOHYD    208   208       N-LINKED (GLCNAC. . .) (POTENTIAL).
FT   CARBOHYD    224   224       N-LINKED (GLCNAC. . .) (POTENTIAL).
FT   CARBOHYD    232   232       N-LINKED (GLCNAC. . .) (POTENTIAL).
FT   CARBOHYD    254   254       N-LINKED (GLCNAC. . .).
FT   CARBOHYD    274   274       N-LINKED (GLCNAC. . .) (POTENTIAL).
FT   CARBOHYD    288   288       N-LINKED (GLCNAC. . .) (POTENTIAL).
FT   CARBOHYD    292   292       N-LINKED (GLCNAC. . .) (POTENTIAL).
FT   CARBOHYD    302   302       N-LINKED (GLCNAC. . .) (POTENTIAL).
FT   CARBOHYD    309   309       N-LINKED (GLCNAC. . .) (POTENTIAL).
FT   CARBOHYD    345   345       N-LINKED (GLCNAC. . .) (POTENTIAL).
FT   CARBOHYD    351   351       N-LINKED (GLCNAC. . .) (POTENTIAL).
FT   CARBOHYD    363   363       N-LINKED (GLCNAC. . .) (POTENTIAL).
FT   CARBOHYD    378   378       N-LINKED (GLCNAC. . .) (POTENTIAL).
FT   CARBOHYD    405   405       N-LINKED (GLCNAC. . .) (POTENTIAL).
FT   VARSPLIC    320   321       EL -> GK (in isoform H).
FT                               /FTId=VSP_002478.
FT   VARSPLIC    322   526       Missing (in isoform H).
FT                               /FTId=VSP_002479.
FT   VARSPLIC    321   351       LSPVVAKPQIKASKTTVTGDKDSVNLTCSTN -> SPVLGE
FT                               DEAVPGQHHPQHKPCQEGGCWDVLV (in isoform I).
FT                               /FTId=VSP_002480.
FT   VARSPLIC    352   526       Missing (in isoform I).
FT                               /FTId=VSP_002481.
FT   VARSPLIC    416   417       YN -> CK (in isoform G).
FT                               /FTId=VSP_002482.
FT   VARSPLIC    418   526       Missing (in isoform G).
FT                               /FTId=VSP_002483.
SQ   SEQUENCE   526 AA;  57560 MW;  CAD1B2328D069AF8 CRC64;

  Query Match             7.1%;  Score 125.5;  DB 1;  Length 526;
  Best Local Similarity   25.1%;  Pred. No. 0.0071;
  Matches   67;  Conservative   36;  Mismatches   93;  Indels   71;  Gaps   17;
```

```
Qy          68 GTIIVTQ-------NRNRERVDFPDGGYSLKLSKLKKNDSGIYYVGIYSSSL-QQPSTQE 119
               |  | ||       |  || : :|:   || :  : :||:| | : :  | |  : :| :
Db          81 GYAIGTQQATPGPANSGRETI-YPNA--SLLIQNVTQNDTGFYTLQVIKSDLVNEEATGQ 137

Qy         120 YVLHVYEHLSKPKVTMGLQSNKNGTCVTNLTCCMEHGEEDVIYTWKALGQAANESHNGSI 179
               :  |||  | || ::    :           ||  |   :|  | |             |
Db         138 F--HVYPELPKPSISSNNSNPVEDKDAVAFTC--EPETQDTTYLWWI---------NNQS 184

Qy         180 LPISWRW----GESDMTFICVAR----------NPVSRNFSSPILARKLCEG------A 218
               ||:| |     |   :| : | |          ||||  | | |:    :  |      :
Db         185 LPVSPRLQLSNGNRTLTLLSVTRNDTGPYECEIQNPVSANRSDPV-TLNVTYGPDTPTIS 243

Qy         219 ADD----PDSSMVLLCLLL--VPLLLSLFVLGLFLWFLKRERQEEYIEEKKRVDICRETP 272
               |     | ::: | |       |   |  : | |    ::  || :|             |
Db         244 PSDTYYRPGANLSLSCYAASNPPAQYSWLINGTF----QQSTQELFI-----------P 287

Qy         273 NI-CPHSGENTEY--DTIPHTNRTILK 296
               ||   :||  | :  :::   ||| :|
Db         288 NITVNNSGSYTCHANNSVTGCNRTTVK 314
```

RESULT 11
CEA6_HUMAN
ID CEA6_HUMAN STANDARD; PRT; 344 AA.
AC P40199; Q14920;
DT 01-FEB-1995 (Rel. 31, Created)
DT 28-FEB-2003 (Rel. 41, Last sequence update)
DT 10-OCT-2003 (Rel. 42, Last annotation update)
DE Carcinoembryonic antigen-related cell adhesion molecule 6 precursor
DE (Normal cross-reacting antigen) (Nonspecific crossreacting antigen)
DE (CD66c antigen).
GN CEACAM6 OR NCA.
OS Homo sapiens (Human).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
OX NCBI_TaxID=9606;
RN [1]
RP SEQUENCE FROM N.A.
RX MEDLINE=89122014; PubMed=3220478;
RA Barnett T., Goebel S.J., Nothdurft M.A., Elting J.J.;
RT "Carcinoembryonic antigen family: characterization of cDNAs coding
RT for NCA and CEA and suggestion of nonrandom sequence variation in
RT their conserved loop-domains.";
RL Genomics 3:59-66(1988).
RN [2]
RP SEQUENCE FROM N.A.
RC TISSUE=Lung carcinoma;
RX MEDLINE=88106638; PubMed=3337731;
RA Tawaragi Y., Oikawa S., Matsuoka Y., Kosaki G., Nakazato H.;
RT "Primary structure of nonspecific crossreacting antigen (NCA), a
RT member of carcinoembryonic antigen (CEA) gene family, deduced from
RT cDNA sequence.";
RL Biochem. Biophys. Res. Commun. 150:89-96(1988).
RN [3]
RP SEQUENCE FROM N.A.
RC TISSUE=Pancreas;
RX MEDLINE=22388257; PubMed=12477932;
RA Strausberg R.L., Feingold E.A., Grouse L.H., Derge J.G.,
RA Klausner R.D., Collins F.S., Wagner L., Shenmen C.M., Schuler G.D.,
RA Altschul S.F., Zeeberg B., Buetow K.H., Schaefer C.F., Bhat N.K.,
RA Hopkins R.F., Jordan H., Moore T., Max S.I., Wang J., Hsieh F.,
RA Diatchenko L., Marusina K., Farmer A.A., Rubin G.M., Hong L.,
RA Stapleton M., Soares M.B., Bonaldo M.F., Casavant T.L., Scheetz T.E.,
RA Brownstein M.J., Usdin T.B., Toshiyuki S., Carninci P., Prange C.,
RA Raha S.S., Loquellano N.A., Peters G.J., Abramson R.D., Mullahy S.J.,
RA Bosak S.A., McEwan P.J., McKernan K.J., Malek J.A., Gunaratne P.H.,
RA Richards S., Worley K.C., Hale S., Garcia A.M., Gay L.J., Hulyk S.W.,
RA Villalon D.K., Muzny D.M., Sodergren E.J., Lu X., Gibbs R.A.,
RA Fahey J., Helton E., Ketteman M., Madan A., Rodrigues S., Sanchez A.,
RA Whiting M., Madan A., Young A.C., Shevchenko Y., Bouffard G.G.,
RA Blakesley R.W., Touchman J.W., Green E.D., Dickson M.C.,
RA Rodriguez A.C., Grimwood J., Schmutz J., Myers R.M.,
RA Butterfield Y.S.N., Krzywinski M.I., Skalska U., Smailus D.E.,
RA Schnerch A., Schein J.E., Jones S.J.M., Marra M.A.;
RT "Generation and initial analysis of more than 15,000 full-length
RT human and mouse cDNA sequences.";
RL Proc. Natl. Acad. Sci. U.S.A. 99:16899-16903(2002).
CC -!- SUBCELLULAR LOCATION: Attached to the membrane by a GPI-anchor.
CC -!- SIMILARITY: Belongs to the immunoglobulin superfamily. CEA family.
CC -!- SIMILARITY: Contains 1 immunoglobulin-like V-type domain.
CC -!- SIMILARITY: Contains 2 immunoglobulin-like C2-type domains.
CC -!- DATABASE: NAME=PROW; NOTE=CD guide CD66c entry;
CC WWW="http://www.ncbi.nlm.nih.gov/prow/cd/cd66c.htm".
CC ---
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CC or send an email to license@isb-sib.ch).
CC ---
DR EMBL; M29541; AAA59915.1; -.
DR EMBL; M18728; AAA59907.1; -.
DR EMBL; BC005008; AAH05008.1; -.
DR Genew; HGNC:1818; CEACAM6.
DR MIM; 163980; -.
DR GO; GO:0005887; C:integral to plasma membrane; TAS.
DR GO; GO:0007267; P:cell-cell signaling; TAS.
DR GO; GO:0007165; P:signal transduction; TAS.
DR InterPro; IPR007110; Ig-like.
DR InterPro; IPR003598; Ig_c2.
DR Pfam; PF00047; ig; 3.
DR SMART; SM00408; IGc2; 1.
DR PROSITE; PS50835; IG_LIKE; 2.
KW Immunoglobulin domain; Antigen; Signal; Glycoprotein; GPI-anchor;
KW Repeat; Lipoprotein.

FT	SIGNAL	1	34	BY SIMILARITY.
FT	CHAIN	35	320	CARCINOEMBRYONIC ANTIGEN-RELATED CELL
FT				ADHESION MOLECULE 6.
FT	PROPEP	321	344	REMOVED IN MATURE FORM (BY SIMILARITY).
FT	LIPID	320	320	GPI-anchor amidated glycine (By
FT				similarity).
FT	DOMAIN	35	142	IG-LIKE V-TYPE.
FT	DOMAIN	145	232	IG-LIKE C2-TYPE 1.
FT	DOMAIN	237	314	IG-LIKE C2-TYPE 2.
FT	DISULFID	167	215	PROBABLE.
FT	DISULFID	259	299	PROBABLE.
FT	CARBOHYD	104	104	N-LINKED (GLCNAC. . .) (POTENTIAL).
FT	CARBOHYD	111	111	N-LINKED (GLCNAC. . .) (POTENTIAL).
FT	CARBOHYD	115	115	N-LINKED (GLCNAC. . .) (POTENTIAL).
FT	CARBOHYD	152	152	N-LINKED (GLCNAC. . .) (POTENTIAL).
FT	CARBOHYD	173	173	N-LINKED (GLCNAC. . .) (POTENTIAL).
FT	CARBOHYD	197	197	N-LINKED (GLCNAC. . .) (POTENTIAL).
FT	CARBOHYD	224	224	N-LINKED (GLCNAC. . .) (POTENTIAL).
FT	CARBOHYD	256	256	N-LINKED (GLCNAC. . .) (POTENTIAL).
FT	CARBOHYD	274	274	N-LINKED (GLCNAC. . .) (POTENTIAL).
FT	CARBOHYD	288	288	N-LINKED (GLCNAC. . .) (POTENTIAL).
FT	CARBOHYD	292	292	N-LINKED (GLCNAC. . .) (POTENTIAL).
FT	CARBOHYD	309	309	N-LINKED (GLCNAC. . .) (POTENTIAL).
FT	CONFLICT	138	138	F -> L (IN REF. 1).
FT	CONFLICT	239	239	V -> G (IN REF. 1).

SQ SEQUENCE 344 AA; 37237 MW; 4322C5D6E25849F5 CRC64;

Query Match 7.0%; Score 124.5; DB 1; Length 344;
Best Local Similarity 22.4%; Pred. No. 0.0051;
Matches 75; Conservative 35; Mismatches 118; Indels 107; Gaps 16;

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Qy          53 WTFNTTPLVTIQ------PEGGTII-----VTQNR------NRERVD------------ 82
               |   ||  :||:       ||  ::     : |||       ||||
Db          28 WNPPTTAKLTIESTPFNVAEGKEVLLLAHNLPQNRIGYSWYKGERVDGNSLIVGYVIGTQ 87

Qy          83 --FPDGGY----------SLKLSKLKKNDSGIYYVGIYSSSL-QQPSTQEYVLHVYEHLS 129
                 |   |          || :  : :||:| | : :  | |  : :| ::  |||  |
Db          88 QATPGPAYSGRETIYPNASLLIQNVTQNDTGFYTLQVIKSDLVNEEATGQF--HVYPELP 145
```

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Qy        130 KPKVTMGLQSNKNGTCVTNLTCCMEHGEEDVIYTWKALGQAANESHNGSILPISWRW--- 186
              || ::    :          ||  |   ::  | |          ||  ||:| |
Db        146 KPSISSNNSNPVEDKDAVAFTC--EPEVQNTTYLWWV---------NGQSLPVSPRLQLS 194

Qy        187 -GESDMTFI-----------CVARNPVSRNFSSPILARKLC---------EGAADDPDSS 225
               |   :| :           |  :|| | | | |:    |           |   | :
Db        195 NGNMTLTLLSVKRNDAGSYECEIQNPASANRSDPVTLNVLYGPDVPTISPSKANYRPGEN 254

Qy        226 MVLLCLLL--VPLLLSLFVLGLFLWFLKRERQEEYIEEKKRVDICRETPNI--------- 274
              : | |      |  | |: | |     ::  || :|          |||
Db        255 LNLSCHAASNPPAQYSWFINGTF----QQSTQELFI-----------PNITVNNSGSYM 298

Qy        275 CPHSGENTEYDTIPHTNRTILKEDPANTVYSTVEI 309
              |      |  :    |  |:    |  :  :|| |
Db        299 CQAHNSATGLNRTTVTMITVSGSAPVLSAVATVGI 333
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RESULT 12
CXAR_HUMAN
ID   CXAR_HUMAN     STANDARD;      PRT;   365 AA.
AC   P78310; O00694;
DT   30-MAY-2000 (Rel. 39, Created)
DT   30-MAY-2000 (Rel. 39, Last sequence update)
DT   10-OCT-2003 (Rel. 42, Last annotation update)
DE   Coxsackievirus and adenovirus receptor precursor (Coxsackievirus B-
DE   adenovirus receptor) (hCAR) (CVB3 binding protein).
GN   CXADR OR CAR.
OS   Homo sapiens (Human).
OC   Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC   Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
OX   NCBI_TaxID=9606;
RN   [1]
RP   SEQUENCE FROM N.A.
RX   MEDLINE=97190109; PubMed=9036860;
RA   Bergelson J.M., Cunningham J.A., Droguett G., Kurt-Jones E.,
RA   Krithivas A., Hong J.S., Horwitz M.S., Crowell R.L., Finberg R.W.;
RT   "Isolation of a common receptor for Coxsackie B viruses and
RT   adenoviruses 2 and 5.";
RL   Science 275:1320-1323(1997).
RN   [2]
RP   SEQUENCE FROM N.A.
RX   MEDLINE=97250541; PubMed=9096397;
RA   Tomko R.P., Xu R., Philipson L.;
RT   "HCAR and MCAR: the human and mouse cellular receptors for subgroup C
RT   adenoviruses and group B coxsackieviruses.";
RL   Proc. Natl. Acad. Sci. U.S.A. 94:3352-3356(1997).
RN   [3]
RP   SEQUENCE FROM N.A.
RX   MEDLINE=20008750; PubMed=10543405;
RA   Bowles K.R., Gibson J., Wu J., Shaffer L.G., Towbin J.A.,
RA   Bowles N.E.;
RT   "Genomic organization and chromosomal localization of the human
RT   Coxsackievirus B-adenovirus receptor gene.";
RL   Hum. Genet. 105:354-359(1999).
RN   [4]
RP   SEQUENCE FROM N.A.
RA   Anderson C.W., Kieleczawa J., Dunn J.J., Freimuth P.;
RT   "Sequence and expression of CXADR, the human gene for the
RT   coxsackievirus and adenovirus receptor.";
RL   Submitted (OCT-1999) to the EMBL/GenBank/DDBJ databases.
RN   [5]
RP   SEQUENCE FROM N.A.
RA   Andersson B., Tomko R., Andersson K., Darban H., Oncu D., Mizra M.,
RA   Sollerbrant K., Sonnhammer E., Philipson L.;
RT   "Putative regulatory domains in the human and mouse CAR genes.";
RL   Submitted (MAR-2000) to the EMBL/GenBank/DDBJ databases.
RN   [6]
RP   SEQUENCE FROM N.A.
RC   TISSUE=Cervix;
RX   MEDLINE=22388257; PubMed=12477932;
RA   Strausberg R.L., Feingold E.A., Grouse L.H., Derge J.G.,
RA   Klausner R.D., Collins F.S., Wagner L., Shenmen C.M., Schuler G.D.,
RA   Altschul S.F., Zeeberg B., Buetow K.H., Schaefer C.F., Bhat N.K.,
RA   Hopkins R.F., Jordan H., Moore T., Max S.I., Wang J., Hsieh F.,
RA   Diatchenko L., Marusina K., Farmer A.A., Rubin G.M., Hong L.,
RA   Stapleton M., Soares M.B., Bonaldo M.F., Casavant T.L., Scheetz T.E.,
RA   Brownstein M.J., Usdin T.B., Toshiyuki S., Carninci P., Prange C.,
RA   Raha S.S., Loquellano N.A., Peters G.J., Abramson R.D., Mullahy S.J.,
RA   Bosak S.A., McEwan P.J., McKernan K.J., Malek J.A., Gunaratne P.H.,
RA   Richards S., Worley K.C., Hale S., Garcia A.M., Gay L.J., Hulyk S.W.,
RA   Villalon D.K., Muzny D.M., Sodergren E.J., Lu X., Gibbs R.A.,
RA   Fahey J., Helton E., Ketteman M., Madan A., Rodrigues S., Sanchez A.,
RA   Whiting M., Madan A., Young A.C., Shevchenko Y., Bouffard G.G.,
RA   Blakesley R.W., Touchman J.W., Green E.D., Dickson M.C.,
RA   Rodriguez A.C., Grimwood J., Schmutz J., Myers R.M.,
RA   Butterfield Y.S.N., Krzywinski M.I., Skalska U., Smailus D.E.,
RA   Schnerch A., Schein J.E., Jones S.J.M., Marra M.A.;
RT   "Generation and initial analysis of more than 15,000 full-length
RT   human and mouse cDNA sequences.";
RL   Proc. Natl. Acad. Sci. U.S.A. 99:16899-16903(2002).
CC   -!- FUNCTION: SERVES AS A RECEPTOR FOR GROUP B COXSACKIEVIRUSES AND
CC       SUBGROUP C OF ADENOVIRUSES (AD2 AND AD5).
CC   -!- SUBCELLULAR LOCATION: Type I membrane protein.
CC   -!- SIMILARITY: Contains 2 immunoglobulin-like C2-type domains.
CC   ---------------------------------------------------------------------
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CC   or send an email to license@isb-sib.ch).
CC   ---------------------------------------------------------------------
DR   EMBL; Y07593; CAA68868.1; -.
DR   EMBL; U90716; AAC51234.1; -.
DR   EMBL; AF169366; AAF05908.1; -.
DR   EMBL; AF169360; AAF05908.1; JOINED.
DR   EMBL; AF169361; AAF05908.1; JOINED.
DR   EMBL; AF169362; AAF05908.1; JOINED.
DR   EMBL; AF169363; AAF05908.1; JOINED.
DR   EMBL; AF169364; AAF05908.1; JOINED.
DR   EMBL; AF169365; AAF05908.1; JOINED.
DR   EMBL; AF200465; AAF24344.1; -.
DR   EMBL; AF242865; AAG01088.1; -.
DR   EMBL; AF242862; AAG01088.1; JOINED.
DR   EMBL; AF242864; AAG01088.1; JOINED.
DR   EMBL; BC003684; AAH03684.1; -.
DR   EMBL; BC010536; AAH10536.1; -.
DR   PDB; 1EAJ; 13-JUL-01.
DR   PDB; 1F5W; 08-NOV-00.
DR   PDB; 1KAC; 24-NOV-99.
DR   Genew; HGNC:2559; CXADR.
DR   MIM; 602621; -.
DR   GO; GO:0005887; C:integral to plasma membrane; TAS.
DR   GO; GO:0004872; F:receptor activity; TAS.
DR   InterPro; IPR007110; Ig-like.
DR   InterPro; IPR003598; Ig_c2.
DR   Pfam; PF00047; ig; 2.
DR   SMART; SM00408; IGc2; 1.
DR   PROSITE; PS50835; IG_LIKE; 2.
KW   Immunoglobulin domain; Receptor; Transmembrane; Glycoprotein; Signal;
KW   Repeat; 3D-structure.
FT   SIGNAL       1    19       POTENTIAL.
FT   CHAIN       20   365       COXSACKIEVIRUS AND ADENOVIRUS RECEPTOR.
FT   DOMAIN      20   237       EXTRACELLULAR (POTENTIAL).
FT   TRANSMEM   238   258       POTENTIAL.
FT   DOMAIN     259   365       CYTOPLASMIC (POTENTIAL).
FT   DOMAIN      20   134       IG-LIKE C2-TYPE 1.
FT   DOMAIN     141   228       IG-LIKE C2-TYPE 2.
FT   DISULFID    41   120       BY SIMILARITY.
FT   DISULFID   162   212       BY SIMILARITY.
FT   CARBOHYD   106   106       N-LINKED (GLCNAC. . .) (POTENTIAL).
FT   CARBOHYD   201   201       N-LINKED (GLCNAC. . .) (POTENTIAL).
SQ   SEQUENCE   365 AA;  40029 MW;  AB01C6346CB7FE64 CRC64;

  Query Match             6.7%;  Score 119.5;  DB 1;  Length 365;
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  Best Local Similarity   21.2%;  Pred. No. 0.014;
  Matches   62;  Conservative   47;  Mismatches  124;  Indels   59;  Gaps   12;

Qy         68 GTIIVTQNRNRERVDFPDGGYSLKLSKLKKNDSGIYYVGIYSSSLQQPSTQEYVLHVYEH 127
              | :  | ||       |   |  |: :: |: :| | |   :  :     |      :|:
Db         89 GRVHFTSN------DLKSGDASINVTNLQLSDIGTYQCKVKKA----PGVANKKIHLVV- 137

Qy        128 LSKPKVTMGLQSNKNGT----CVTNLTCCMEHGEEDVIYTWKALGQAANESHNGSILPIS 183
              | ||    | :   :|:        : |  : |   : | |: | :  :          :| |
Db        138 LVKPS---GARCYVDGSEEIGSDFKIKCEPKEGSLPLQYEWQKLSDSQK-------MPTS 187

Qy        184 W-------------RWGESDMTFICVARNPVSRNFSSPILARKLCEGAADDPDSSMVLLC 230
              |             |   |: |  || |    |   | ||        | :   |:
Db        188 WLAEMTSSVISVKNASSEYSGTYSCTVRNRVG---SDQCLLRL----NVVPPSNKAGLIA 240

Qy        231 LLLVPLLLSLFVLGLFLWFLKRERQEEYIEEKKRVDICRETPNICPHSGENTEYDTIPHT 290
                ::  ||:| ::|| ::  :::|:||  |::   ||  : |   | | :|    |
Db        241 GAIIGTLLALALIGLIIFCCRKKRREEKYEKEVHHDIREDVPP--PKSRTSTARSYIGSN 298

Qy        291 NRTILKEDPAN------TVYSTV------EIPKKMENPHSLLTMPDTPRLFA 330
              : ::    |:|      | |: |        |:    | : :  |:  |: |
Db        299 HSSLGSMSPSNMEGYSKTQYNQVPSEDFERTPQSPTLPPAKVAAPNLSRMGA 350


RESULT 13
A33_HUMAN
ID   A33_HUMAN      STANDARD;      PRT;   319 AA.
AC   Q99795;
DT   01-NOV-1997 (Rel. 35, Created)
DT   01-NOV-1997 (Rel. 35, Last sequence update)
DT   15-MAR-2004 (Rel. 43, Last annotation update)
DE   Cell surface A33 antigen precursor (Glycoprotein A33).
GN   GPA33.
OS   Homo sapiens (Human).
OC   Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC   Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
OX   NCBI_TaxID=9606;
RN   [1]
RP   SEQUENCE FROM N.A., AND PARTIAL SEQUENCE.
RC   TISSUE=Colon carcinoma;
RX   MEDLINE=97165045; PubMed=9012807;
RA   Heath J.K., White S.J., Johnstone C.N., Catimel B., Simpson R.J.,
RA   Moritz R.L., Tu G.-F., Ji H., Whitehead R.H., Groenen L.C.,
RA   Scott A.M., Ritter G., Cohen L., Welt S., Old L.J., Nice E.C.,
RA   Burgess A.W.;
RT   "The human A33 antigen is a transmembrane glycoprotein and a novel
RT   member of the immunoglobulin superfamily.";
RL   Proc. Natl. Acad. Sci. U.S.A. 94:469-474(1997).
RN   [2]
RP   POST-TRANSLATIONAL MODIFICATIONS.
RX   MEDLINE=97396159; PubMed=9245713;
RA   Ritter G., Cohen L.S., Nice E.C., Catimel B., Burgess A.W.,
RA   Moritz R.L., Ji H., Heath J.K., White S.J., Welt S., Old L.J.,
RA   Simpson R.J.;
RT   "Characterization of posttranslational modifications of human A33
RT   antigen, a novel palmitoylated surface glycoprotein of human
RT   gastrointestinal epithelium.";
RL   Biochem. Biophys. Res. Commun. 236:682-686(1997).
CC   -!- FUNCTION: May play a role in cell-cell recognition and signaling.
CC   -!- SUBCELLULAR LOCATION: Type I membrane protein.
CC   -!- TISSUE SPECIFICITY: Expressed in normal gastrointestinal
CC       epithelium and in 95% of colon cancers.
CC   -!- PTM: N-GLYCOSYLATED, CONTAINS APPROXIMATELY 8 KDA OF N-LINKED
CC       CARBOHYDRATE.
CC   -!- PTM: Palmitoylated.
CC   -!- SIMILARITY: Contains 1 immunoglobulin-like V-type domain.
CC   -!- SIMILARITY: Contains 1 immunoglobulin-like C2-type domain.
CC   ---------------------------------------------------------------------
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CC   or send an email to license@isb-sib.ch).
CC   ---------------------------------------------------------------------
DR   EMBL; U79725; AAC50957.1; -.
DR   Genew; HGNC:4445; GPA33.
DR   MIM; 602171; -.
DR   GO; GO:0005888; C:proteoglycan integral to plasma membrane; TAS.
DR   GO; GO:0004872; F:receptor activity; TAS.
DR   InterPro; IPR007110; Ig-like.
DR   InterPro; IPR003596; Ig_v.
DR   Pfam; PF00047; ig; 2.
DR   SMART; SM00406; IGv; 1.
DR   PROSITE; PS50835; IG_LIKE; 2.
KW   Immunoglobulin domain; Lipoprotein; Palmitate; Glycoprotein;
KW   Transmembrane; Signal; Antigen.
FT   SIGNAL        1     21
FT   CHAIN        22    319       CELL SURFACE A33 ANTIGEN.
FT   DOMAIN       22    235       EXTRACELLULAR (POTENTIAL).
FT   TRANSMEM    236    256       POTENTIAL.
FT   DOMAIN      257    319       CYTOPLASMIC (POTENTIAL).
FT   DOMAIN       22    134       IG-LIKE V-TYPE.
FT   DOMAIN      140    227       IG-LIKE C2-TYPE.
FT   DOMAIN      258    261       POLY-CYS.
FT   DISULFID     43    117       POTENTIAL.
FT   DISULFID    146    222       POTENTIAL.
FT   DISULFID    162    211       POTENTIAL.
FT   CARBOHYD    112    112       N-LINKED (GLCNAC. . .).
FT   CARBOHYD    200    200       N-LINKED (GLCNAC. . .) (POTENTIAL).
FT   CARBOHYD    223    223       N-LINKED (GLCNAC. . .) (POTENTIAL).
SQ   SEQUENCE   319 AA;  35632 MW;  9BFC7AAF45C2408E CRC64;

  Query Match             6.6%;  Score 116.5;  DB 1;  Length 319;
  Best Local Similarity   22.6%;  Pred. No. 0.022;
  Matches   73;  Conservative   50;  Mismatches  123;  Indels   77;  Gaps   15;

Qy         13 ILWQL-----TGSAAS--GPVKELVGSVGGAVTFPL--------KSKVKQVDSIVWTFNT 57
              :|| |     |  | |   |   |  | | :|| |          :  : | | :: |
Db          8 VLWTLCAVRVTVDAISVETPQDVLRASQGKSVTLPCTYHTSTSSREGLIQWDKLLLTH-- 65

Qy         58 TPLVTIQPEGGTIIVTQNRNRERVDFPDGG----YSLKLSKLKKNDSGIYYVGIYSSSLQ 113
              |  | | |       :     : ||   :        |: : :|   |:| |   :   |
Db         66 TERVVIWPFSNKNYIHGELYKNRVSISNNAEQSDASITIDQLTMADNGTYECSVSLMSDL 125

Qy        114 QPSTQEYV-LHVYEHLSKPKVTMGLQSNKNGTCVTN---LTCCMEHGEEDVIYTWK---A 166
              : :|:  | | |    |||:   |::     | : |   |||  : |      :||
Db        126 EGNTKSRVRLLVLVPPSKPE--CGIEGE---TIIGNNIQLTCQSKEGSPTPQYSWKRYNI 180

Qy        167 LGQAANESHNGSILPISWRWGESDMT--FICVARNPVSRNFSSPILARKLCEGAADDPDS 224
              | |    :   |  |:| :   :| :  :|| : |     | :  :| :        |
Db        181 LNQEQPLAQPASGQPVSLKNISTDTSGYYICTSSNEEGTQFCNITVAVR-------SPSM 233

Qy        225 SMVLLCLLLVPLLLSLFVLGLFLWF--------------------------------LKR 252
              :: |   : | :: :| ::|: ::                                 | |
Db        234 NVALYVGIAVGVVAALIIIGIIIYCCCCRGKDDNTEDKEDARPNREAYEEPPEQLRELSR 293

Qy        253 ERQEE--YIEEKKRVDICRETPN 273
              ||:||  | :|::|    ||:|:
Db        294 EREEEDDYRQEEQR-STGRESPD 315


RESULT 14
CEA5_HUMAN
ID   CEA5_HUMAN     STANDARD;      PRT;   702 AA.
AC   P06731;
DT   01-JAN-1988 (Rel. 06, Created)
DT   01-DEC-1992 (Rel. 24, Last sequence update)
DT   15-MAR-2004 (Rel. 43, Last annotation update)
DE   Carcinoembryonic antigen-related cell adhesion molecule 5 precursor
DE   (Carcinoembryonic antigen) (CEA) (Meconium antigen 100) (CD66e
DE   antigen).
GN   CEACAM5 OR CEA.
OS   Homo sapiens (Human).
OC   Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
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OC   Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
OX   NCBI_TaxID=9606;
RN   [1]
RP   SEQUENCE FROM N.A.
RX   MEDLINE=90258861; PubMed=2342461;
RA   Schrewe H., Thompson J., Bona M., Hefta L.J.F., Maruya A.,
RA   Hassauer M., Shively J.E., von Kleist S., Zimmermann W.;
RT   "Cloning of the complete gene for carcinoembryonic antigen: analysis
RT   of its promoter indicates a region conveying cell type-specific
RT   expression.";
RL   Mol. Cell. Biol. 10:2738-2748(1990).
RN   [2]
RP   SEQUENCE FROM N.A.
RX   MEDLINE=88038876; PubMed=3670312;
RA   Beauchemin N., Benchimol S., Cournoyer D., Fuks A., Stanners C.P.;
RT   "Isolation and characterization of full-length functional cDNA clones
RT   for human carcinoembryonic antigen.";
RL   Mol. Cell. Biol. 7:3221-3230(1987).
RN   [3]
RP   SEQUENCE FROM N.A.
RX   MEDLINE=89122014; PubMed=3220478;
RA   Barnett T., Goebel S.J., Nothdurft M.A., Elting J.J.;
RT   "Carcinoembryonic antigen family: characterization of cDNAs coding
RT   for NCA and CEA and suggestion of nonrandom sequence variation in
RT   their conserved loop-domains.";
RL   Genomics 3:59-66(1988).
RN   [4]
RP   SEQUENCE OF 5-702 FROM N.A.
RX   MEDLINE=87128144; PubMed=3814146;
RA   Oikawa S., Nakazato H., Kosaki G.;
RT   "Primary structure of human carcinoembryonic antigen (CEA) deduced
RT   from cDNA sequence.";
RL   Biochem. Biophys. Res. Commun. 142:511-518(1987).
RN   [5]
RP   SEQUENCE OF 331-702 FROM N.A.
RX   MEDLINE=87204247; PubMed=3033671;
RA   Zimmermann W., Ortlieb B., Friedrich R.; von Kleist S.;
RT   "Isolation and characterization of cDNA clones encoding the human
RT   carcinoembryonic antigen reveal a highly conserved repeating
RT   structure.";
RL   Proc. Natl. Acad. Sci. U.S.A. 84:2960-2964(1987).
CC   -!- SUBCELLULAR LOCATION: Attached to the membrane by a GPI-anchor.
CC   -!- TISSUE SPECIFICITY: Found in adenocarcinomas of endodermally
CC       derived digestive system epithelium and fetal colon.
CC   -!- PTM: COMPLEX IMMUNOREACTIVE GLYCOPROTEIN WITH A MW OF 180 kDa
CC       COMPRISING 60% CARBOHYDRATE.
CC   -!- SIMILARITY: Belongs to the immunoglobulin superfamily. CEA family.
CC   -!- SIMILARITY: Contains 7 immunoglobulin-like domains.
CC   -!- DATABASE: NAME=PROW; NOTE=CD guide CD66e entry;
CC       WWW="http://www.ncbi.nlm.nih.gov/prow/cd/cd66e.htm".
CC   ---------------------------------------------------------------------
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CC   entities requires a license agreement (See http://www.isb-sib.ch/announce/
CC   or send an email to license@isb-sib.ch).
CC   ---------------------------------------------------------------------
DR   EMBL; M17303; AAB59513.1; -.
DR   EMBL; M59262; AAA62835.1; ALT_SEQ.
DR   EMBL; M59255; AAA62835.1; JOINED.
DR   EMBL; M59256; AAA62835.1; JOINED.
DR   EMBL; M59257; AAA62835.1; JOINED.
DR   EMBL; M59258; AAA62835.1; JOINED.
DR   EMBL; M59259; AAA62835.1; JOINED.
DR   EMBL; M59260; AAA62835.1; JOINED.
DR   EMBL; M59261; AAA62835.1; JOINED.
DR   EMBL; M59709; -; NOT_ANNOTATED_CDS.
DR   EMBL; M59710; -; NOT_ANNOTATED_CDS.
DR   EMBL; M29540; AAA51967.1; -.
DR   EMBL; X16455; CAA34474.1; -.
DR   EMBL; M15042; AAA51963.1; -.
DR   EMBL; M16234; AAA51972.1; -.
DR   PIR; A36319; A36319.
DR   PDB; 1E07; 04-JUL-00.
DR   Genew; HGNC:1817; CEACAM5.
DR   MIM; 114890; -.
DR   GO; GO:0005887; C:integral to plasma membrane; TAS.
DR   InterPro; IPR007110; Ig-like.
DR   Pfam; PF00047; ig; 6.
DR   PROSITE; PS50835; IG_LIKE; 6.
KW   Immunoglobulin domain; Glycoprotein; Lipoprotein; GPI-anchor;
KW   Membrane; Signal; Repeat; 3D-structure.
FT   SIGNAL       1    34
FT   CHAIN       35   685       CARCINOEMBRYONIC ANTIGEN-RELATED CELL
FT                               ADHESION MOLECULE 5.
FT   PROPEP     686   702       REMOVED IN MATURE FORM (POTENTIAL).
FT   DOMAIN      35   144       IG-LIKE 1.
FT   DOMAIN     146   237       IG-LIKE 2.
FT   DOMAIN     238   322       IG-LIKE 3.
FT   DOMAIN     324   415       IG-LIKE 4.
FT   DOMAIN     416   498       IG-LIKE 5.
FT   DOMAIN     502   593       IG-LIKE 6.
FT   DOMAIN     594   677       IG-LIKE 7.
FT   LIPID      685   685       GPI-anchor amidated alanine (Potential).
FT   CARBOHYD   104   104       N-LINKED (GLCNAC. . .) (POTENTIAL).
FT   CARBOHYD   115   115       N-LINKED (GLCNAC. . .) (POTENTIAL).
FT   CARBOHYD   152   152       N-LINKED (GLCNAC. . .) (POTENTIAL).
FT   CARBOHYD   182   182       N-LINKED (GLCNAC. . .) (POTENTIAL).
FT   CARBOHYD   197   197       N-LINKED (GLCNAC. . .) (POTENTIAL).
FT   CARBOHYD   204   204       N-LINKED (GLCNAC. . .) (POTENTIAL).
FT   CARBOHYD   208   208       N-LINKED (GLCNAC. . .) (POTENTIAL).
FT   CARBOHYD   246   246       N-LINKED (GLCNAC. . .) (POTENTIAL).
FT   CARBOHYD   256   256       N-LINKED (GLCNAC. . .) (POTENTIAL).
FT   CARBOHYD   274   274       N-LINKED (GLCNAC. . .) (POTENTIAL).
FT   CARBOHYD   288   288       N-LINKED (GLCNAC. . .) (POTENTIAL).
FT   CARBOHYD   292   292       N-LINKED (GLCNAC. . .) (POTENTIAL).
FT   CARBOHYD   309   309       N-LINKED (GLCNAC. . .) (POTENTIAL).
FT   CARBOHYD   330   330       N-LINKED (GLCNAC. . .) (POTENTIAL).
FT   CARBOHYD   351   351       N-LINKED (GLCNAC. . .) (POTENTIAL).
FT   CARBOHYD   360   360       N-LINKED (GLCNAC. . .) (POTENTIAL).
FT   CARBOHYD   375   375       N-LINKED (GLCNAC. . .) (POTENTIAL).
FT   CARBOHYD   432   432       N-LINKED (GLCNAC. . .) (POTENTIAL).
FT   CARBOHYD   466   466       N-LINKED (GLCNAC. . .) (POTENTIAL).
FT   CARBOHYD   480   480       N-LINKED (GLCNAC. . .) (POTENTIAL).
FT   CARBOHYD   508   508       N-LINKED (GLCNAC. . .) (POTENTIAL).
FT   CARBOHYD   529   529       N-LINKED (GLCNAC. . .) (POTENTIAL).
FT   CARBOHYD   553   553       N-LINKED (GLCNAC. . .) (POTENTIAL).
FT   CARBOHYD   560   560       N-LINKED (GLCNAC. . .) (POTENTIAL).
FT   CARBOHYD   580   580       N-LINKED (GLCNAC. . .) (POTENTIAL).
FT   CARBOHYD   612   612       N-LINKED (GLCNAC. . .) (POTENTIAL).
FT   CARBOHYD   650   650       N-LINKED (GLCNAC. . .) (POTENTIAL).
FT   CARBOHYD   665   665       N-LINKED (GLCNAC. . .) (POTENTIAL).
FT   CONFLICT   320   320       MISSING (IN REF. 4).
SQ   SEQUENCE   702 AA;  76795 MW;  6299AE26CDDBDB5C CRC64;

  Query Match             6.5%;  Score 114.5;  DB 1;  Length 702;
  Best Local Similarity   21.2%;  Pred. No. 0.084;
  Matches   66;  Conservative   36;  Mismatches  111;  Indels   99;  Gaps   14;

Qy         68 GTIIVTQNR------NRERVDFPDGGYSLKLSKLKKNDSGIYYVGIYSSSL-QQPSTQEY 120
              | :| ||        :   : :|:   || :  : :||:| | : :  | |  : :| ::
Db         81 GYVIGTQQATPGPAYSGREIIYPNA--SLLIQNIIQNDTGFYTLHVIKSDLVNEEATGQF 138

Qy        121 VLHVYEHLSKPKVTMGLQSNKNGTCVTNLTCCMEHGEEDVIYTWKALGQAANESHNGSIL 180
                ||  | || ::             .||  |  :|  | |           |   |
Db        139 --RVYPELPKPSISSNNSKPVEDKDAVAFTC--EPETQDATYLWWV---------NNQSL 185

Qy        181 PISWRW----GESDMT----------FICVARNPVSRNFSSPILARKL---------- 214
              |:| |     |   :|          : |  :||||   |  ::   |
Db        186 PVSPRLQLSNGNRTLTLFNVTRNDTASYKCETQNPVSARRSDSVILNVLYGPDAPTISPL 245

Qy        215 ------------CEGAADDPDSSMVLLCLLLVPLLLSLFVLGLFLWFLKRERQEEYIEE 261
                         |  || :|          |   | || | |    ::  || :|
Db        246 NTSYRSGENLNLSCH-AASNP----------PAQYSWFVNGTF----QQSTQELFI-- 286
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Qy        262 KKRVDICRETPNI---------CPHSGENTEYDTIPHTNRTILKEDPANTVYSTVEIPKK 312
                          |||         |     :|  :    |  |:  | |   : |    | :
Db        287 ----------PNITVNNSGSYTCQAHNSDTGLNRTTVTTITVYAEPPKPFITSNNSNPVE 336

Qy        313 MENPHSLLTMPD 324
                |:  :|   |:
Db        337 DEDAVALTCEPE 348


RESULT 15
CEA1_MOUSE
ID   CEA1_MOUSE     STANDARD;      PRT;   521 AA.
AC   P31809;
DT   01-JUL-1993 (Rel. 26, Created)
DT   01-JUL-1993 (Rel. 26, Last sequence update)
DT   10-OCT-2003 (Rel. 42, Last annotation update)
DE   Carcinoembryonic antigen-related cell adhesion molecule 1 precursor
DE   (Biliary glycoprotein 1) (BGP-1) (Murine hepatitis virus receptor)
DE   (MHV-R) (Biliary glycoprotein D).
GN   CEACAM1 OR BGP OR BGP1 OR BGPD.
OS   Mus musculus (Mouse).
OC   Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC   Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus.
OX   NCBI_TaxID=10090;
RN   [1]
RP   SEQUENCE FROM N.A.
RC   STRAIN=CD-1; TISSUE=Colon;
RX   MEDLINE=93100785; PubMed=8380065;
RA   Dveksler G.S., Dieffenback C.B., Cardellichio C.B., McCuaig K.,
RA   Pensiero M.N.;
RT   "Several members of the mouse carcinoembryonic antigen-related
RT   glycoprotein family are functional receptors for the coronavirus
RT   mouse hepatitis virus-A59.";
RL   J. Virol. 67:1-8(1993).
RN   [2]
RP   SEQUENCE FROM N.A.
RC   STRAIN=BALB/c; TISSUE=Liver;
RX   MEDLINE=92046352; PubMed=1719235;
RA   Dveksler G.S., Pensiero M.N., Cardellichio C.B., Williams R.K.,
RA   Jiang G.-S., Holmes K.V., Dieffenbach C.W.;
RT   "Cloning of the mouse hepatitis virus (MHV) receptor: expression in
RT   human and hamster cell lines confers susceptibility to MHV.";
RL   J. Virol. 65:6881-6891(1991).
RN   [3]
RP   SEQUENCE FROM N.A.
RX   MEDLINE=93273228; PubMed=8500759;
RA   McCuaig K., Rosenberg M., Nedellec P., Turbide C., Beauchemin N.;
RT   "Expression of the Bgp gene and characterization of mouse colon
RT   biliary glycoprotein isoforms.";
RL   Gene 127:173-183(1993).
RN   [4]
RP   SEQUENCE FROM N.A. (ISOFORM SHORT).
RC   STRAIN=CD-1; TISSUE=Colon;
RX   MEDLINE=89195121; PubMed=2702644;
RA   Beauchemin N., Turbide C., Afar D., Raymond M., Bell J.,
RA   Stanners C.P., Fuks A.;
RT   "A mouse analogue of the human carcinoembryonic antigen.";
RL   Cancer Res. 49:2017-2021(1989).
RN   [5]
RP   SEQUENCE OF 35-59.
RX   MEDLINE=91288498; PubMed=1648219;
RA   Williams R.K., Jiang G.-S., Holmes K.V.;
RT   "Receptor for mouse hepatitis virus is a member of the
RT   carcinoembryonic antigen family of glycoproteins.";
RL   Proc. Natl. Acad. Sci. U.S.A. 88:5533-5536(1991).
CC   -!- FUNCTION: Unknown; receptor for murine coronavirus MHV-A59.
CC   -!- SUBCELLULAR LOCATION: Type I membrane protein.
CC   -!- ALTERNATIVE PRODUCTS:
CC       Event=Alternative splicing; Named isoforms=2;
CC       Name=Long;
CC         IsoId=P31809-1; Sequence=Displayed;
CC       Name=Short;
CC         IsoId=P31809-2; Sequence=VSP_002484, VSP_002485;
CC   -!- SIMILARITY: Belongs to the immunoglobulin superfamily. CEA family.
CC   -!- SIMILARITY: Contains 1 immunoglobulin-like V-type domain.
CC   -!- SIMILARITY: Contains 3 immunoglobulin-like C2-type domains.
CC   ---------------------------------------------------------------------
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CC   or send an email to license@isb-sib.ch).
CC   ---------------------------------------------------------------------
DR   EMBL; X67279; CAA47696.1; -.
DR   EMBL; M77196; AAA37858.1; -.
DR   EMBL; X15351; CAA33409.1; -.
DR   PIR; JC1505; WMMSR1.
DR   PIR; JC1508; JC1508.
DR   MGD; MGI:1347245; Ceacam1.
DR   InterPro; IPR007110; Ig-like.
DR   Pfam; PF00047; ig; 3.
DR   PROSITE; PS50835; IG_LIKE; 3.
KW   Immunoglobulin domain; Glycoprotein; Transmembrane; Signal;
KW   Repeat; Alternative splicing; Receptor.
FT   SIGNAL        1     34
FT   CHAIN        35    521       CARCINOEMBRYONIC ANTIGEN-RELATED CELL
FT                                 ADHESION MOLECULE 1.
FT   DOMAIN        35    428       EXTRACELLULAR (POTENTIAL).
FT   TRANSMEM     429    447       POTENTIAL.
FT   DOMAIN       448    521       CYTOPLASMIC (POTENTIAL).
FT   DOMAIN        35    142       IG-LIKE V-TYPE.
FT   DOMAIN       147    234       IG-LIKE C2-TYPE 1.
FT   DOMAIN       239    319       IG-LIKE C2-TYPE 2.
FT   DOMAIN       323    411       IG-LIKE C2-TYPE 3.
FT   DISULFID     167    217       PROBABLE.
FT   DISULFID     261    301       PROBABLE.
FT   DISULFID     346    394       PROBABLE.
FT   CARBOHYD      71     71       N-LINKED (GLCNAC. . .) (POTENTIAL).
FT   CARBOHYD      89     89       N-LINKED (GLCNAC. . .) (POTENTIAL).
FT   CARBOHYD     104    104       N-LINKED (GLCNAC. . .) (POTENTIAL).
FT   CARBOHYD     148    148       N-LINKED (GLCNAC. . .) (POTENTIAL).
FT   CARBOHYD     152    152       N-LINKED (GLCNAC. . .) (POTENTIAL).
FT   CARBOHYD     199    199       N-LINKED (GLCNAC. . .) (POTENTIAL).
FT   CARBOHYD     206    206       N-LINKED (GLCNAC. . .) (POTENTIAL).
FT   CARBOHYD     210    210       N-LINKED (GLCNAC. . .) (POTENTIAL).
FT   CARBOHYD     226    226       N-LINKED (GLCNAC. . .) (POTENTIAL).
FT   CARBOHYD     258    258       N-LINKED (GLCNAC. . .) (POTENTIAL).
FT   CARBOHYD     290    290       N-LINKED (GLCNAC. . .) (POTENTIAL).
FT   CARBOHYD     294    294       N-LINKED (GLCNAC. . .) (POTENTIAL).
FT   CARBOHYD     304    304       N-LINKED (GLCNAC. . .) (POTENTIAL).
FT   CARBOHYD     317    317       N-LINKED (GLCNAC. . .) (POTENTIAL).
FT   CARBOHYD     333    333       N-LINKED (GLCNAC. . .) (POTENTIAL).
FT   CARBOHYD     375    375       N-LINKED (GLCNAC. . .) (POTENTIAL).
FT   VARSPLIC     455    458       GSDQ -> SGSF (in isoform Short).
FT                                 /FTId=VSP_002484.
FT   VARSPLIC     459    521       Missing (in isoform Short).
FT                                 /FTId=VSP_002485.
SQ   SEQUENCE   521 AA;  57015 MW;  1C8F71FAC47DD54E CRC64;

  Query Match             6.4%;  Score 113.5;  DB 1;  Length 521;
  Best Local Similarity   26.6%;  Pred. No. 0.071;
  Matches   46;  Conservative   25;  Mismatches   69;  Indels   33;  Gaps    9;

Qy         56 NTTPLVTIQPEGGTIIVTQNRN--------RERVDFPDGGYSLKLSKLKKNDSGIYYVGI 107
              |||   |  |    :  | |          || : : :|  ||    :   | |:| : :
Db         71 NTT---AIDKEIARFVPNSNMNFTGQAYSGRE-IIYSNG--SLLFQMITMKDMGVYTLDM 124

Qy        108 YSSSLQQPSTQEYV-LHVYEHLSKPKVTMGLQSNKNGTCVTNLTCCMEHGEEDVIYTWKA 166
               : ::  ||  |  ||:  | || :|    :   |    :|||      ::: | |
Db        125 TDENYRR--TQATVRFHVHPILLKPNITSNNSNPVEGDDSVSLTCDSYTDPDNINYLWSR 182

Qy        167 LGQAANESHNGSILPISWRWGESDMT----------FICVARNPVSRNFSSP 208
              |:: :|   |  | :|   |   :|          ::|  ||||| | | |
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Db 183 NGESLSE---GDRLKLS--EGNRTLTLLNVTRNDTGPYVCETRNPVSVNRSDP 230

Search completed: August 18, 2004, 15:51:35
Job time : 18 secs

GenCore version 5.1.6

OM protein - protein search, using sw model

Run on: August 18, 2004, 15:52:59 ; Search time 54 Seconds
(without alignments)
1752.841 Million cell updates/sec

Title: US-10-063-549-46
Perfect score: 335
Sequence: 1 MAGSPTCLTLIYILWQLTGS.....PHSLLTMPDTPRLFAYENVI 335

Scoring table: OLIGO
Gapop 60.0 , Gapext 60.0

Searched: 1586107 seqs, 282547505 residues

Word size : 0

Total number of hits satisfying chosen parameters: 1586107

Minimum DB seq length: 0
Maximum DB seq length: 2000000000

Post-processing: Listing first 700 summaries

Database : A_Geneseq_29Jan04:*
1: geneseqp1980s:*
2: geneseqp1990s:*
3: geneseqp2000s:*
4: geneseqp2001s:*
5: geneseqp2002s:*
6: geneseqp2003as:*
7: geneseqp2003bs:*
8: geneseqp2004s:*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	% Query Match	Length	DB	ID	Description
1	335	100.0	335	3	AAY66701	Aay66701 Membrane-
2	335	100.0	335	3	AAY70431	Aay70431 Human cel
3	335	100.0	335	3	AAY44609	Aay44609 Human myo
4	335	100.0	335	4	AAU29119	Aau29119 Human PRO
5	335	100.0	335	4	AAB87548	Aab87548 Human PRO
6	335	100.0	335	4	AAB47321	Aab47321 APEX-1. 8
7	335	100.0	335	4	AAB65224	Aab65224 Human PRO
8	335	100.0	335	5	ABG95873	Abg95873 Human sec
9	335	100.0	335	6	ABU58495	Abu58495 Human PRO
10	335	100.0	335	6	ABU88043	Abu88043 Novel hum
11	335	100.0	335	6	ABU84358	Abu84358 Human sec
12	335	100.0	335	6	ABR66232	Abr66232 Human sec
13	335	100.0	335	6	ABR65622	Abr65622 Human sec
14	335	100.0	335	6	ABU99562	Abu99562 Human sec
15	335	100.0	335	6	ABU58039	Abu58039 Human PRO
16	335	100.0	335	6	ABU59117	Abu59117 Novel hum
17	335	100.0	335	6	ABU82629	Abu82629 Human sec
18	335	100.0	335	6	ABU82801	Abu82801 Human PRO
19	335	100.0	335	6	ABU89922	Abu89922 Novel hum
20	335	100.0	335	6	ABR68171	Abr68171 Human sec
21	335	100.0	335	6	ABU60548	Abu60548 Human sec
22	335	100.0	335	6	ABU96224	Abu96224 Novel hum
23	335	100.0	335	6	ABU92655	Abu92655 Human sec
24	335	100.0	335	6	ABO08732	Abo08732 Human sec
25	335	100.0	335	6	ABO02784	Abo02784 Human sec
26	335	100.0	335	6	ABR74938	Abr74938 Human sec
27	335	100.0	335	6	ABR94700	Abr94700 Human sec
28	335	100.0	335	6	ABU13930	Abu13930 Human PRO
29	335	100.0	335	6	ABU85673	Abu85673 Human PRO
30	335	100.0	335	6	ABU98833	Abu98833 Novel hum
31	335	100.0	335	6	ABU98048	Abu98048 Novel hum
32	335	100.0	335	6	ABU91754	Abu91754 Novel hum
33	335	100.0	335	6	ABU89447	Abu89447 Human PRO
34	335	100.0	335	6	ABU86288	Abu86288 Human sec
35	335	100.0	335	6	ABU67501	Abu67501 Human sec
36	335	100.0	335	6	ABU80529	Abu80529 Human PRO
37	335	100.0	335	6	ABU72515	Abu72515 Novel hum
38	335	100.0	335	6	ABU90898	Abu90898 Novel hum
39	335	100.0	335	6	ABO33957	Abo33957 Human sec
40	335	100.0	335	6	ABR99447	Abr99447 Human sec
41	335	100.0	335	6	ABR98837	Abr98837 Human sec
42	335	100.0	335	6	ABO16360	Abo16360 Human sec
43	335	100.0	335	6	ABR92260	Abr92260 Human sec
44	335	100.0	335	6	ABO18901	Abo18901 Human sec
45	335	100.0	335	6	ABR78322	Abr78322 Human sec
46	335	100.0	335	6	ABU71974	Abu71974 Novel hum
47	335	100.0	335	6	ABU85058	Abu85058 Novel hum
48	335	100.0	335	6	ABO00197	Abo00197 Novel hum
49	335	100.0	335	6	ABO11529	Abo11529 Human sec
50	335	100.0	335	6	ABO02174	Abo02174 Human sec
51	335	100.0	335	6	ABU88748	Abu88748 Novel hum
52	335	100.0	335	6	ABU83443	Abu83443 Human sec
53	335	100.0	335	6	ABO06244	Abo06244 Novel hum
54	335	100.0	335	6	ABR59280	Abr59280 Human sec
55	335	100.0	335	6	ABO09342	Abo09342 Human sec
56	335	100.0	335	6	ABO19206	Abo19206 Novel hum
57	335	100.0	335	6	ABO11224	Abo11224 Human sec
58	335	100.0	335	6	ABR66842	Abr66842 Human sec
59	335	100.0	335	6	ABO16055	Abo16055 Human sec
60	335	100.0	335	6	ABO13761	Abo13761 Human sec
61	335	100.0	335	6	ABU71528	Abu71528 Human sec
62	335	100.0	335	6	ABU65664	Abu65664 Human sec
63	335	100.0	335	6	ABO07512	Abo07512 Human PRO
64	335	100.0	335	6	ABO03699	Abo03699 Human sec
65	335	100.0	335	6	ABR67147	Abr67147 Human sec
66	335	100.0	335	6	ABO15750	Abo15750 Human sec
67	335	100.0	335	6	ABU56031	Abu56031 Human sec
68	335	100.0	335	6	ABU72309	Abu72309 Human PRO
69	335	100.0	335	6	ABU65359	Abu65359 Human PRO
70	335	100.0	335	6	ABU95304	Abu95304 Novel hum
71	335	100.0	335	6	ABU71207	Abu71207 Human PRO
72	335	100.0	335	6	ABO07817	Abo07817 Human PRO
73	335	100.0	335	6	ABR70058	Abr70058 Human sec
74	335	100.0	335	6	ABR69391	Abr69391 Human sec
75	335	100.0	335	6	ABO01532	Abo01532 Human PRO
76	335	100.0	335	6	ABU81334	Abu81334 Human PRO
77	335	100.0	335	6	ABR60131	Abr60131 Human sec
78	335	100.0	335	6	ABU90982	Abu90982 Human PRO
79	335	100.0	335	6	ABR67866	Abr67866 Human sec
80	335	100.0	335	6	ABR65254	Abr65254 Human sec
81	335	100.0	335	6	ABR68476	Abr68476 Human sec
82	335	100.0	335	6	ABR71888	Abr71888 Human sec
83	335	100.0	335	6	ABU59264	Abu59264 Human sec
84	335	100.0	335	6	ABU85368	Abu85368 Human PRO
85	335	100.0	335	6	ABU89058	Abu89058 Human sec
86	335	100.0	335	6	ABU83138	Abu83138 Human sec
87	335	100.0	335	6	ABU94994	Abu94994 Novel hum
88	335	100.0	335	6	ABU90542	Abu90542 Novel hum
89	335	100.0	335	6	ABU84053	Abu84053 Human sec
90	335	100.0	335	6	ABU93704	Abu93704 Novel hum
91	335	100.0	335	6	ABO25961	Abo25961 Human PRO
92	335	100.0	335	6	ABR64949	Abr64949 Human sec
93	335	100.0	335	6	ABO27303	Abo27303 Human sec
94	335	100.0	335	6	ABR68781	Abr68781 Human sec
95	335	100.0	335	6	ABO06597	Abo06597 Human sec
96	335	100.0	335	6	ABR99142	Abr99142 Human sec
97	335	100.0	335	6	ABU57026	Abu57026 Human PRO
98	335	100.0	335	6	ABU85978	Abu85978 Novel hum

99	335	100.0	335	6	ABU82265	Abu82265 Novel hum	172	335	100.0	335	6	ABO44026	Abo44026 Human PRO
100	335	100.0	335	6	ABU87276	Abu87276 Human PRO	173	335	100.0	335	6	ADA77944	Ada77944 Human sec
101	335	100.0	335	6	ABU83748	Abu83748 Human sec	174	335	100.0	335	6	ABM24821	Abm24821 Human sec
102	335	100.0	335	6	ABO08122	Abo08122 Human PRO	175	335	100.0	335	6	ABO03089	Abo03089 Human sec
103	335	100.0	335	6	ABU92498	Abu92498 Human sec	176	335	100.0	335	6	ABR90345	Abr90345 Human sec
104	335	100.0	335	6	ABU81833	Abu81833 Novel hum	177	335	100.0	335	6	ABM17259	Abm17259 Human sec
105	335	100.0	335	6	ABU65997	Abu65997 Novel hum	178	335	100.0	335	6	ABR95005	Abr95005 Human sec
106	335	100.0	335	6	ABU81168	Abu81168 Human sec	179	335	100.0	335	6	ABR95310	Abr95310 Human sec
107	335	100.0	335	6	ABR59826	Abr59826 Human sec	180	335	100.0	335	6	ADB17103	Adb17103 Human tra
108	335	100.0	335	6	ABU94014	Abu94014 Novel hum	181	335	100.0	335	6	ABO21548	Abo21548 Human sec
109	335	100.0	335	6	ABU99867	Abu99867 Novel hum	182	335	100.0	335	6	ABR97812	Abr97812 Human sec
110	335	100.0	335	6	ABR66537	Abr66537 Human sec	183	335	100.0	335	6	ABR87600	Abr87600 Human sec
111	335	100.0	335	6	ABR90955	Abr90955 Human sec	184	335	100.0	335	6	ABM77641	Abm77641 Human sec
112	335	100.0	335	6	ABO53283	Abo53283 Novel hum	185	335	100.0	335	6	ABM27871	Abm27871 Human sec
113	335	100.0	335	6	ABU58970	Abu58970 Human sec	186	335	100.0	335	6	ABM06152	Abm06152 Human sec
114	335	100.0	335	6	ABU94382	Abu94382 Human PRO	187	335	100.0	335	6	ABM03658	Abm03658 Human sec
115	335	100.0	335	6	ABU79264	Abu79264 Human PRO	188	335	100.0	335	6	ABM35109	Abm35109 Human sec
116	335	100.0	335	6	ABU86593	Abu86593 Human sec	189	335	100.0	335	6	ABM26346	Abm26346 Human sec
117	335	100.0	335	6	ABU86898	Abu86898 Novel hum	190	335	100.0	335	6	ABO48128	Abo48128 Human sec
118	335	100.0	335	6	ABU94687	Abu94687 Human PRO	191	335	100.0	335	6	ABR92870	Abr92870 Human sec
119	335	100.0	335	6	ABO04614	Abo04614 Human PRO	192	335	100.0	335	6	ABO24631	Abo24631 Human sec
120	335	100.0	335	6	ABR70363	Abr70363 Human sec	193	335	100.0	335	6	ADA37764	Ada37764 Human sec
121	335	100.0	335	6	ABU92348	Abu92348 Novel hum	194	335	100.0	335	6	ABM11642	Abm11642 Human sec
122	335	100.0	335	6	ABU98528	Abu98528 Human PRO	195	335	100.0	335	6	ABM02743	Abm02743 Human sec
123	335	100.0	335	6	ABR65927	Abr65927 Human sec	196	335	100.0	335	6	ABM16039	Abm16039 Human sec
124	335	100.0	335	6	ABR64644	Abr64644 Human sec	197	335	100.0	335	6	ABO27600	Abo27600 Human sec
125	335	100.0	335	6	ABU59413	Abu59413 Novel hum	198	335	100.0	335	6	ABM29091	Abm29091 Human sec
126	335	100.0	335	6	ABU79569	Abu79569 Human PRO	199	335	100.0	335	6	ABM07067	Abm07067 Human sec
127	335	100.0	335	6	ABU92960	Abu92960 Human sec	200	335	100.0	335	6	ABM21161	Abm21161 Human sec
128	335	100.0	335	6	ABU95919	Abu95919 Human PRO	201	335	100.0	335	6	ABM09507	Abm09507 Human sec
129	335	100.0	335	6	ABU91139	Abu91139 Novel hum	202	335	100.0	335	6	ABO41377	Abo41377 Human sec
130	335	100.0	335	6	ABU90232	Abu90232 Novel hum	203	335	100.0	335	6	ABO36192	Abo36192 Human PRO
131	335	100.0	335	6	ABO09647	Abo09647 Human sec	204	335	100.0	335	6	ABO43721	Abo43721 Human PRO
132	335	100.0	335	6	ABR58417	Abr58417 Human NOV	205	335	100.0	335	6	ABM76421	Abm76421 Human sec
133	335	100.0	335	6	ABO10919	Abo10919 Human sec	206	335	100.0	335	6	ABM76117	Abm76117 Human sec
134	335	100.0	335	6	ABR70973	Abr70973 Human sec	207	335	100.0	335	6	ABM25736	Abm25736 Human sec
135	335	100.0	335	6	ABU98285	Abu98285 Novel hum	208	335	100.0	335	6	ABM26041	Abm26041 Human sec
136	335	100.0	335	6	ABU87581	Abu87581 Human PRO	209	335	100.0	335	6	ADA21450	Ada21450 Human sec
137	335	100.0	335	6	ABU91449	Abu91449 Human PRO	210	335	100.0	335	6	ABO03394	Abo03394 Human sec
138	335	100.0	335	6	ABU89290	Abu89290 Novel hum	211	335	100.0	335	6	ABO02479	Abo02479 Human sec
139	335	100.0	335	6	ABU84663	Abu84663 Human sec	212	335	100.0	335	6	ABO44261	Abo44261 Human sec
140	335	100.0	335	6	ABR69753	Abr69753 Human sec	213	335	100.0	335	6	ABR90650	Abr90650 Human sec
141	335	100.0	335	6	ABU80130	Abu80130 Human PRO	214	335	100.0	335	6	ABR73718	Abr73718 Human sec
142	335	100.0	335	6	ABU82497	Abu82497 Novel hum	215	335	100.0	335	6	ABO16970	Abo16970 Human sec
143	335	100.0	335	6	ABU92179	Abu92179 Novel hum	216	335	100.0	335	6	ABR94395	Abr94395 Human sec
144	335	100.0	335	6	ABU93399	Abu93399 Human PRO	217	335	100.0	335	6	ABR75902	Abr75902 Human sec
145	335	100.0	335	6	ABO09952	Abo09952 Human sec	218	335	100.0	335	6	ABR71278	Abr71278 Human sec
146	335	100.0	335	6	ABO09037	Abo09037 Human sec	219	335	100.0	335	6	ABR93175	Abr93175 Human sec
147	335	100.0	335	6	ABU96461	Abu96461 Human PRO	220	335	100.0	335	6	ABR93480	Abr93480 Human sec
148	335	100.0	335	6	ABU10885	Abu10885 Human PRO	221	335	100.0	335	6	ADA10237	Ada10237 Human sec
149	335	100.0	335	6	ABU10605	Abu10605 Human sec	222	335	100.0	335	6	ABR87905	Abr87905 Human sec
150	335	100.0	335	6	ABU81637	Abu81637 Novel hum	223	335	100.0	335	6	ABO27905	Abo27905 Human sec
151	335	100.0	335	6	ABU72131	Abu72131 Human PRO	224	335	100.0	335	6	ABO30040	Abo30040 Human sec
152	335	100.0	335	6	ABU95614	Abu95614 Human PRO	225	335	100.0	335	6	ABO33249	Abo33249 Human PRO
153	335	100.0	335	6	ABU96823	Abu96823 Novel hum	226	335	100.0	335	6	ABM04937	Abm04937 Human sec
154	335	100.0	335	6	ABR70668	Abr70668 Human sec	227	335	100.0	335	6	ABM08897	Abm08897 Human sec
155	335	100.0	335	6	ABO05019	Abo05019 Novel hum	228	335	100.0	335	6	ABO36497	Abo36497 Human sec
156	335	100.0	335	6	ABO08427	Abo08427 Human sec	229	335	100.0	335	6	ABO35582	Abo35582 Human PRO
157	335	100.0	335	6	ABU88576	Abu88576 Human sec	230	335	100.0	335	6	ABO39547	Abo39547 Human sec
158	335	100.0	335	6	ABO34090	Abo34090 Human PRO	231	335	100.0	335	6	ABM10422	Abm10422 Human sec
159	335	100.0	335	6	ABO05634	Abo05634 Human sec	232	335	100.0	335	6	ABM11947	Abm11947 Human sec
160	335	100.0	335	6	ABR74023	Abr74023 Human sec	233	335	100.0	335	6	ABO52093	Abo52093 Human PRO
161	335	100.0	335	6	ABR95615	Abr95615 Human sec	234	335	100.0	335	6	ABO52398	Abo52398 Human PRO
162	335	100.0	335	6	ABR80912	Abr80912 Human sec	235	335	100.0	335	6	ADA19908	Ada19908 Novel hum
163	335	100.0	335	6	ABR81217	Abr81217 Human sec	236	335	100.0	335	6	ABO23716	Abo23716 Human sec
164	335	100.0	335	6	ABM00913	Abm00913 Human sec	237	335	100.0	335	6	ADB17291	Adb17291 Human tra
165	335	100.0	335	6	ABR88515	Abr88515 Human sec	238	335	100.0	335	6	ADA17781	Ada17781 Human PRO
166	335	100.0	335	6	ABM77336	Abm77336 Human sec	239	335	100.0	335	6	ABR97202	Abr97202 Human sec
167	335	100.0	335	6	ABO28820	Abo28820 Human sec	240	335	100.0	335	6	ABR86990	Abr86990 Human sec
168	335	100.0	335	6	ABO31565	Abo31565 Human sec	241	335	100.0	335	6	ABM11032	Abm11032 Human sec
169	335	100.0	335	6	ABM07982	Abm07982 Human sec	242	335	100.0	335	6	ABM28176	Abm28176 Human sec
170	335	100.0	335	6	ABO40462	Abo40462 Human sec	243	335	100.0	335	6	ABO32175	Abo32175 Human sec
171	335	100.0	335	6	ABO35887	Abo35887 Human PRO	244	335	100.0	335	6	ABM15302	Abm15302 Human sec

245	335	100.0	335	6	ABM06457	Abm06457 Human sec	
246	335	100.0	335	6	ABM04268	Abm04268 Human sec	
247	335	100.0	335	6	ABM22381	Abm22381 Human sec	
248	335	100.0	335	6	ABM07677	Abm07677 Human sec	
249	335	100.0	335	6	ABO40767	Abo40767 Human sec	
250	335	100.0	335	6	ABM35414	Abm35414 Human sec	
251	335	100.0	335	6	ABM33177	Abm33177 Human sec	
252	335	100.0	335	6	ABO52703	Abo52703 Human PRO	
253	335	100.0	335	6	ABO50263	Abo50263 Human sec	
254	335	100.0	335	6	ABU99257	Abu99257 Human sec	
255	335	100.0	335	6	ABO04309	Abo04309 Human sec	
256	335	100.0	335	6	ABO05939	Abo05939 Human sec	
257	335	100.0	335	6	ABM18479	Abm18479 Human sec	
258	335	100.0	335	6	ADA27889	Ada27889 Human sec	
259	335	100.0	335	6	ABR97507	Abr97507 Human sec	
260	335	100.0	335	6	ABR80607	Abr80607 Human sec	
261	335	100.0	335	6	ABM01218	Abm01218 Human sec	
262	335	100.0	335	6	ABR88820	Abr88820 Human sec	
263	335	100.0	335	6	ABM13472	Abm13472 Human sec	
264	335	100.0	335	6	ABM20856	Abm20856 Human sec	
265	335	100.0	335	6	ABO41987	Abo41987 Human sec	
266	335	100.0	335	6	ABO42597	Abo42597 Human sec	
267	335	100.0	335	6	ABM10117	Abm10117 Human sec	
268	335	100.0	335	6	ABO38632	Abo38632 Human sec	
269	335	100.0	335	6	ABM32872	Abm32872 Human sec	
270	335	100.0	335	6	ABM22686	Abm22686 Human sec	
271	335	100.0	335	6	ABM74897	Abm74897 Human sec	
272	335	100.0	335	6	ADA79736	Ada79736 Human sec	
273	335	100.0	335	6	ABR96287	Abr96287 Human sec	
274	335	100.0	335	6	ABM02438	Abm02438 Human sec	
275	335	100.0	335	6	ABR86380	Abr86380 Human sec	
276	335	100.0	335	6	ABR86685	Abr86685 Human sec	
277	335	100.0	335	6	ABM16649	Abm16649 Human sec	
278	335	100.0	335	6	ABM29701	Abm29701 Human sec	
279	335	100.0	335	6	ABO29125	Abo29125 Human sec	
280	335	100.0	335	6	ABM23906	Abm23906 Human sec	
281	335	100.0	335	6	ABM23296	Abm23296 Human sec	
282	335	100.0	335	6	ABM22076	Abm22076 Human sec	
283	335	100.0	335	6	ABO37717	Abo37717 Human sec	
284	335	100.0	335	6	ABM28481	Abm28481 Human sec	
285	335	100.0	335	6	ABM28786	Abm28786 Human sec	
286	335	100.0	335	6	ABM66430	Abm66430 Human sec	
287	335	100.0	335	6	ABM75812	Abm75812 Human sec	
288	335	100.0	335	6	ABM34092	Abm34092 Human sec	
289	335	100.0	335	6	ABM34397	Abm34397 Human sec	
290	335	100.0	335	6	ABO20328	Abo20328 Human sec	
291	335	100.0	335	6	ABO21243	Abo21243 Human sec	
292	335	100.0	335	6	ABO22158	Abo22158 Human sec	
293	335	100.0	335	6	ADA20080	Ada20080 Novel hum	
294	335	100.0	335	6	ABO34189	Abo34189 Human sec	
295	335	100.0	335	6	ABR96592	Abr96592 Human sec	
296	335	100.0	335	6	ADA94469	Ada94469 Human sec	
297	335	100.0	335	6	ABR85770	Abr85770 Human sec	
298	335	100.0	335	6	ABR99752	Abr99752 Human sec	
299	335	100.0	335	6	ABM00608	Abm00608 Human sec	
300	335	100.0	335	6	ABM00303	Abm00303 Human sec	
301	335	100.0	335	6	ABO29735	Abo29735 Human sec	
302	335	100.0	335	6	ABM23601	Abm23601 Human sec	
303	335	100.0	335	6	ABM29396	Abm29396 Human sec	
304	335	100.0	335	6	ABO38327	Abo38327 Human sec	
305	335	100.0	335	6	ABO45627	Abo45627 Human PRO	
306	335	100.0	335	6	ABM20551	Abm20551 Human sec	
307	335	100.0	335	6	ADA81463	Ada81463 Human sec	
308	335	100.0	335	6	ABO16665	Abo16665 Human sec	
309	335	100.0	335	6	ABO18291	Abo18291 Human sec	
310	335	100.0	335	6	ABO22718	Abo22718 Human PRO	
311	335	100.0	335	6	ABO23023	Abo23023 Human PRO	
312	335	100.0	335	6	ABR92565	Abr92565 Human sec	
313	335	100.0	335	6	ABR81522	Abr81522 Human sec	
314	335	100.0	335	6	ABM77946	Abm77946 Human sec	
315	335	100.0	335	6	ABR89735	Abr89735 Human sec	
316	335	100.0	335	6	ABM26651	Abm26651 Human sec	
317	335	100.0	335	6	ABM13777	Abm13777 Human sec	
318	335	100.0	335	6	ABO28515	Abo28515 Human sec	
319	335	100.0	335	6	ABO30345	Abo30345 Human sec	
320	335	100.0	335	6	ABM07372	Abm07372 Human sec	
321	335	100.0	335	6	ABM03963	Abm03963 Human sec	
322	335	100.0	335	6	ABO37107	Abo37107 Human sec	
323	335	100.0	335	6	ABO41682	Abo41682 Human sec	
324	335	100.0	335	6	ABO35277	Abo35277 Human PRO	
325	335	100.0	335	6	ABM25126	Abm25126 Human sec	
326	335	100.0	335	6	ABO47518	Abo47518 Human sec	
327	335	100.0	335	6	ABO47823	Abo47823 Human sec	
328	335	100.0	335	6	ABO48433	Abo48433 Human sec	
329	335	100.0	335	6	ABO51483	Abo51483 Human PRO	
330	335	100.0	335	6	ABO51788	Abo51788 Human PRO	
331	335	100.0	335	6	ABO50568	Abo50568 Human sec	
332	335	100.0	335	6	ABR79692	Abr79692 Human sec	
333	335	100.0	335	6	ABM16954	Abm16954 Human sec	
334	335	100.0	335	6	ABO17986	Abo17986 Human sec	
335	335	100.0	335	6	ABO20938	Abo20938 Human sec	
336	335	100.0	335	6	ABR96897	Abr96897 Human sec	
337	335	100.0	335	6	ADA38694	Ada38694 Human sec	
338	335	100.0	335	6	ABM12252	Abm12252 Human sec	
339	335	100.0	335	6	ABM16344	Abm16344 Human sec	
340	335	100.0	335	6	ABM24211	Abm24211 Human sec	
341	335	100.0	335	6	ABM14692	Abm14692 Human sec	
342	335	100.0	335	6	ABM04573	Abm04573 Human sec	
343	335	100.0	335	6	ABM06762	Abm06762 Human sec	
344	335	100.0	335	6	ABM09202	Abm09202 Human sec	
345	335	100.0	335	6	ABO39242	Abo39242 Human sec	
346	335	100.0	335	6	ABM75507	Abm75507 Human sec	
347	335	100.0	335	6	ABM25431	Abm25431 Human sec	
348	335	100.0	335	6	ABM19941	Abm19941 Human sec	
349	335	100.0	335	6	ABO46847	Abo46847 Human PRO	
350	335	100.0	335	6	ABO47152	Abo47152 Human PRO	
351	335	100.0	335	6	ADA83261	Ada83261 Human sec	
352	335	100.0	335	6	ABR71583	Abr71583 Human sec	
353	335	100.0	335	6	ABR72193	Abr72193 Human sec	
354	335	100.0	335	6	ABR98532	Abr98532 Human sec	
355	335	100.0	335	6	ABO06902	Abo06902 Human sec	
356	335	100.0	335	6	ABR84855	Abr84855 Human sec	
357	335	100.0	335	6	ABR73413	Abr73413 Human sec	
358	335	100.0	335	6	ABR76507	Abr76507 Human sec	
359	335	100.0	335	6	ABR73108	Abr73108 Human sec	
360	335	100.0	335	6	ABM18174	Abm18174 Human sec	
361	335	100.0	335	6	ABO20633	Abo20633 Human sec	
362	335	100.0	335	6	ABO25376	Abo25376 Human PRO	
363	335	100.0	335	6	ABO25681	Abo25681 Human PRO	
364	335	100.0	335	6	ABR94090	Abr94090 Human sec	
365	335	100.0	335	6	ADA92815	Ada92815 Human sec	
366	335	100.0	335	6	ABR79997	Abr79997 Human sec	
367	335	100.0	335	6	ABM11337	Abm11337 Human sec	
368	335	100.0	335	6	ABO32944	Abo32944 Human PRO	
369	335	100.0	335	6	ABO30650	Abo30650 Human sec	
370	335	100.0	335	6	ABO30955	Abo30955 Human sec	
371	335	100.0	335	6	ABM27261	Abm27261 Human sec	
372	335	100.0	335	6	ABM30006	Abm30006 Human sec	
373	335	100.0	335	6	ABM05542	Abm05542 Human sec	
374	335	100.0	335	6	ABM15607	Abm15607 Human sec	
375	335	100.0	335	6	ABM08592	Abm08592 Human sec	
376	335	100.0	335	6	ABO42292	Abo42292 Human sec	
377	335	100.0	335	6	ABO38022	Abo38022 Human sec	
378	335	100.0	335	6	ABO45932	Abo45932 Human PRO	
379	335	100.0	335	6	ABM66735	Abm66735 Human sec	
380	335	100.0	335	6	ADB20304	Adb20304 Human sec	
381	335	100.0	335	6	ABM19636	Abm19636 Human sec	
382	335	100.0	335	6	ABO49348	Abo49348 Human sec	
383	335	100.0	335	6	ABO49653	Abo49653 Human sec	
384	335	100.0	335	6	ADA78556	Ada78556 Human sec	
385	335	100.0	335	6	ABR88210	Abr88210 Human sec	
386	335	100.0	335	6	ADA00377	Ada00377 Human sec	
387	335	100.0	335	6	ABM26956	Abm26956 Human sec	
388	335	100.0	335	6	ABM03353	Abm03353 Human sec	
389	335	100.0	335	6	ABO39852	Abo39852 Human sec	
390	335	100.0	335	7	ABO49958	Abo49958 Human sec	

391	335	100.0	335	7	ABO50873	Abo50873 Human sec
392	335	100.0	335	7	ABO05329	Abo05329 Human sec
393	335	100.0	335	7	ABR74633	Abr74633 Human sec
394	335	100.0	335	7	ABR77112	Abr77112 Human sec
395	335	100.0	335	7	ABM17869	Abm17869 Human sec
396	335	100.0	335	7	ABR95920	Abr95920 Human sec
397	335	100.0	335	7	ABO21853	Abo21853 Human sec
398	335	100.0	335	7	ABO20023	Abo20023 Human sec
399	335	100.0	335	7	ABO24326	Abo24326 Human sec
400	335	100.0	335	7	ABR86075	Abr86075 Human sec
401	335	100.0	335	7	ABM10727	Abm10727 Human sec
402	335	100.0	335	7	ABM76726	Abm76726 Human sec
403	335	100.0	335	7	ABR89430	Abr89430 Human sec
404	335	100.0	335	7	ABM12557	Abm12557 Human sec
405	335	100.0	335	7	ABM05847	Abm05847 Human sec
406	335	100.0	335	7	ABO34972	Abo34972 Human PRO
407	335	100.0	335	7	ABM03048	Abm03048 Human sec
408	335	100.0	335	7	ABM19026	Abm19026 Human sec
409	335	100.0	335	7	ABM19331	Abm19331 Human sec
410	335	100.0	335	7	ABO46542	Abo46542 Human PRO
411	335	100.0	335	7	ABO49043	Abo49043 Human sec
412	335	100.0	335	7	ABR69086	Abr69086 Human sec
413	335	100.0	335	7	ABR89125	Abr89125 Human sec
414	335	100.0	335	7	ABR72498	Abr72498 Human sec
415	335	100.0	335	7	ABR74328	Abr74328 Human sec
416	335	100.0	335	7	ABO18596	Abo18596 Human sec
417	335	100.0	335	7	ABR80302	Abr80302 Human sec
418	335	100.0	335	7	ABM01523	Abm01523 Human sec
419	335	100.0	335	7	ABM02133	Abm02133 Human sec
420	335	100.0	335	7	ABR87295	Abr87295 Human sec
421	335	100.0	335	7	ABM12862	Abm12862 Human sec
422	335	100.0	335	7	ABM30616	Abm30616 Human sec
423	335	100.0	335	7	ABM24516	Abm24516 Human sec
424	335	100.0	335	7	ABO29430	Abo29430 Human sec
425	335	100.0	335	7	ABO31260	Abo31260 Human sec
426	335	100.0	335	7	ABM14387	Abm14387 Human sec
427	335	100.0	335	7	ABM09812	Abm09812 Human sec
428	335	100.0	335	7	ABO38937	Abo38937 Human sec
429	335	100.0	335	7	ABM34702	Abm34702 Human sec
430	335	100.0	335	7	ABO51178	Abo51178 Human sec
431	335	100.0	335	7	ABO04004	Abo04004 Human sec
432	335	100.0	335	7	ABO10474	Abo10474 Human PRO
433	335	100.0	335	7	ABO53176	Abo53176 Human sec
434	335	100.0	335	7	ABR77717	Abr77717 Human sec
435	335	100.0	335	7	ABR78927	Abr78927 Human sec
436	335	100.0	335	7	ABO24021	Abo24021 Human sec
437	335	100.0	335	7	ABR93785	Abr93785 Human sec
438	335	100.0	335	7	ABM01828	Abm01828 Human sec
439	335	100.0	335	7	ABM78251	Abm78251 Human sec
440	335	100.0	335	7	ABR90040	Abr90040 Human sec
441	335	100.0	335	7	ADA22376	Ada22376 Human sec
442	335	100.0	335	7	ABM27566	Abm27566 Human sec
443	335	100.0	335	7	ABM13167	Abm13167 Human sec
444	335	100.0	335	7	ABO31870	Abo31870 Human sec
445	335	100.0	335	7	ABM14082	Abm14082 Human sec
446	335	100.0	335	7	ABM08287	Abm08287 Human sec
447	335	100.0	335	7	ABO40157	Abo40157 Human sec
448	335	100.0	335	7	ABM74592	Abm74592 Human sec
449	335	100.0	335	7	ABM33787	Abm33787 Human sec
450	335	100.0	335	7	ABM20246	Abm20246 Human sec
451	335	100.0	335	7	ABO48738	Abo48738 Human sec
452	335	100.0	335	7	ABO22546	Abo22546 Human sec
453	335	100.0	335	7	ABR72803	Abr72803 Human sec
454	335	100.0	335	7	ABO15445	Abo15445 Human sec
455	335	100.0	335	7	ABR85160	Abr85160 Human sec
456	335	100.0	335	7	ABO15140	Abo15140 Human sec
457	335	100.0	335	7	ABO17275	Abo17275 Human sec
458	335	100.0	335	7	ABM17564	Abm17564 Human sec
459	335	100.0	335	7	ADA06542	Ada06542 Human sec
460	335	100.0	335	7	ADA39235	Ada39235 Human sec
461	335	100.0	335	7	ABR85465	Abr85465 Human sec
462	335	100.0	335	7	ABM77031	Abm77031 Human sec
463	335	100.0	335	7	ABO28210	Abo28210 Human sec
464	335	100.0	335	7	ABM22991	Abm22991 Human sec
465	335	100.0	335	7	ABM30311	Abm30311 Human sec
466	335	100.0	335	7	ABM21771	Abm21771 Human sec
467	335	100.0	335	7	ABM21466	Abm21466 Human sec
468	335	100.0	335	7	ABM14997	Abm14997 Human sec
469	335	100.0	335	7	ABO41072	Abo41072 Human sec
470	335	100.0	335	7	ABO36802	Abo36802 Human sec
471	335	100.0	335	7	ABO37412	Abo37412 Human sec
472	335	100.0	335	7	ABM75202	Abm75202 Human sec
473	335	100.0	335	7	ABM33482	Abm33482 Human sec
474	335	100.0	335	7	ABO46237	Abo46237 Human PRO
475	335	100.0	335	7	ADA82627	Ada82627 Human sec
476	335	100.0	335	7	ADB85619	Adb85619 Novel hum
477	335	100.0	335	7	ADB96261	Adb96261 Human PRO
478	335	100.0	335	7	ABM31836	Abm31836 Human sec
479	335	100.0	335	7	ABM31226	Abm31226 Human sec
480	335	100.0	335	7	ADB85935	Adb85935 Human sec
481	335	100.0	335	7	ABM32141	Abm32141 Human sec
482	335	100.0	335	7	ABM32446	Abm32446 Human sec
483	335	100.0	335	7	ADB68298	Adb68298 Human PRO
484	335	100.0	335	7	ADB68105	Adb68105 Human PRO
485	335	100.0	335	7	ABM31531	Abm31531 Human sec
486	335	100.0	335	7	ABM30921	Abm30921 Human sec
487	335	100.0	335	7	ADB90922	Adb90922 Novel hum
488	335	100.0	335	7	ADC57733	Adc57733 Human PRO
489	335	100.0	335	7	ADC55097	Adc55097 Human PRO
490	335	100.0	335	7	ADC11964	Adc11964 Human sec
491	335	100.0	335	7	ADC07002	Adc07002 Human PRO
492	335	100.0	335	7	ADC56386	Adc56386 Human PRO
493	335	100.0	335	7	ADC17181	Adc17181 Mammalian
494	335	100.0	335	7	ADC07441	Adc07441 Human sec
495	335	100.0	335	7	ADC11431	Adc11431 Human sec
496	335	100.0	335	7	ADC14879	Adc14879 Novel hum
497	335	100.0	335	7	ADC52374	Adc52374 Novel hum
498	335	100.0	335	7	ADC14553	Adc14553 Novel hum
499	335	100.0	335	7	ADD08085	Add08085 Novel hum
500	335	100.0	335	7	ADC81910	Adc81910 Human PRO
501	335	100.0	335	7	ADD07552	Add07552 Novel hum
502	335	100.0	335	7	ADC82443	Adc82443 Human PRO
503	335	100.0	335	7	ADD05665	Add05665 Human sec
504	335	100.0	335	7	ADD08623	Add08623 Novel hum
505	335	100.0	335	7	ADD06872	Add06872 Novel hum
506	335	100.0	335	7	ADC89503	Adc89503 Human nat
507	335	100.0	335	7	ADC83119	Adc83119 Human PRO
508	335	100.0	335	7	ADD67525	Add67525 Human Ly1
509	335	100.0	335	7	ADD55226	Add55226 Human PRO
510	335	100.0	335	7	ADD36050	Add36050 Novel hum
511	335	100.0	335	7	ADD56184	Add56184 Human PRO
512	335	100.0	335	7	ADD54622	Add54622 Human PRO
513	335	100.0	335	7	ADE26776	Ade26776 Novel hum
514	335	100.0	335	7	ADE26243	Ade26243 Novel hum
515	335	100.0	335	8	ADC52184	Adc52184 Novel hum
516	335	100.0	335	8	ADE74329	Ade74329 Human sec
517	335	100.0	335	8	ADE74941	Ade74941 Human sec
518	335	100.0	336	3	AAB32373	Aab32373 Human sec
519	312	93.1	312	3	AAY44610	Aay44610 Mature hu
520	257	76.7	328	5	ABB97473	Abb97473 Novel hum
521	234	69.9	335	7	ADD18672	Add18672 Human dis
522	217	64.8	348	6	ABR58418	Abr58418 Human NOV
523	110	32.8	110	2	AAW67811	Aaw67811 Human sec
524	110	32.8	110	3	AAB32405	Aab32405 Human sec
525	110	32.8	110	6	ADA57321	Ada57321 Human sec
526	110	32.8	110	6	ADA56750	Ada56750 Human sec
527	110	32.8	110	6	ADA40601	Ada40601 Human sec
528	110	32.8	110	6	ADA41198	Ada41198 Human sec
529	97	29.0	97	3	AAG00391	Aag00391 Human sec
530	97	29.0	98	2	AAY11662	Aay11662 Human 5'
531	92	27.5	684	4	ABG11697	Abg11697 Novel hum
532	92	27.5	684	4	ABG12169	Abg12169 Novel hum
533	91	27.2	91	4	AAM21122	Aam21122 Peptide #
534	91	27.2	91	4	ABB43438	Abb43438 Peptide #
535	91	27.2	91	4	AAM37326	Aam37326 Peptide #
536	91	27.2	91	4	ABB26408	Abb26408 Protein #

537	91	27.2	91	4	AAM77190	Aam77190	Human bon
538	91	27.2	91	4	AAM64367	Aam64367	Human bra
539	91	27.2	91	4	ABG58815	Abg58815	Human liv
540	91	27.2	91	5	ABG46203	Abg46203	Human pep
541	86	25.7	90	3	AAB32404	Aab32404	Human sec
542	68	20.3	124	2	AAY12645	Aay12645	Human 5'
543	33	9.9	33	2	AAW67933	Aaw67933	Fragment
544	27	8.1	28	2	AAW67932	Aaw67932	Fragment
545	19	5.7	114	4	AAM87990	Aam87990	Human imm
546	11	3.3	11	7	ADC89505	Adc89505	Human nat
547	11	3.3	12	7	ADC89504	Adc89504	Human nat
548	11	3.3	16	7	ADC89506	Adc89506	Human nat
549	9	2.7	66	3	AAG25088	Aag25088	Arabidops
550	9	2.7	66	3	AAG35118	Aag35118	Arabidops
551	9	2.7	456	4	ABG25025	Abg25025	Novel hum
552	8	2.4	15	2	AAY13308	Aay13308	Naturally
553	8	2.4	26	4	AAB74404	Aab74404	Desmoglei
554	8	2.4	105	4	AAB80619	Aab80619	Environme
555	8	2.4	122	2	AAW37871	Aaw37871	Human pro
556	8	2.4	172	4	AAB27244	Aab27244	Human EXM
557	8	2.4	194	4	AAM40751	Aam40751	Human pol
558	8	2.4	289	3	AAY93912	Aay93912	A human h
559	8	2.4	306	6	ABU24508	Abu24508	Protein e
560	8	2.4	310	6	ADA55489	Ada55489	Human pro
561	8	2.4	360	2	AAY13381	Aay13381	Amino aci
562	8	2.4	360	3	ADC78533	Adc78533	Human PRO
563	8	2.4	360	4	AAB80249	Aab80249	Human PRO
564	8	2.4	360	4	AAU29037	Aau29037	Human PRO
565	8	2.4	360	4	AAM38965	Aam38965	Human pol
566	8	2.4	360	6	ABU58413	Abu58413	Human PRO
567	8	2.4	360	6	ABU71627	Abu71627	Human PRO
568	8	2.4	360	6	ABU87961	Abu87961	Novel hum
569	8	2.4	360	6	ABU84276	Abu84276	Human sec
570	8	2.4	360	6	ABR66150	Abr66150	Human sec
571	8	2.4	360	6	ABR65540	Abr65540	Human sec
572	8	2.4	360	6	ABU99480	Abu99480	Human sec
573	8	2.4	360	6	ABU82719	Abu82719	Human PRO
574	8	2.4	360	6	ABU89840	Abu89840	Novel hum
575	8	2.4	360	6	ABU71482	Abu71482	Human PRO
576	8	2.4	360	6	ABR68089	Abr68089	Human sec
577	8	2.4	360	6	ABU96142	Abu96142	Novel hum
578	8	2.4	360	6	ABU92573	Abu92573	Human sec
579	8	2.4	360	6	ABO08650	Abo08650	Human sec
580	8	2.4	360	6	ABO02702	Abo02702	Human sec
581	8	2.4	360	6	ABR74856	Abr74856	Human sec
582	8	2.4	360	6	ABR94618	Abr94618	Human sec
583	8	2.4	360	6	ABU85591	Abu85591	Human PRO
584	8	2.4	360	6	ABU98751	Abu98751	Novel hum
585	8	2.4	360	6	ABU97966	Abu97966	Novel hum
586	8	2.4	360	6	ABU91672	Abu91672	Novel hum
587	8	2.4	360	6	ABU71928	Abu71928	Human sec
588	8	2.4	360	6	ABU89365	Abu89365	Human PRO
589	8	2.4	360	6	ABU86206	Abu86206	Human sec
590	8	2.4	360	6	ABU67419	Abu67419	Human sec
591	8	2.4	360	6	ABU80447	Abu80447	Human PRO
592	8	2.4	360	6	ABO01811	Abo01811	Novel hum
593	8	2.4	360	6	ABR99365	Abr99365	Human sec
594	8	2.4	360	6	ABR98755	Abr98755	Human sec
595	8	2.4	360	6	ABO16278	Abo16278	Human sec
596	8	2.4	360	6	ABR92178	Abr92178	Human sec
597	8	2.4	360	6	ABO18819	Abo18819	Human sec
598	8	2.4	360	6	ABR78240	Abr78240	Human sec
599	8	2.4	360	6	ABU84976	Abu84976	Novel hum
600	8	2.4	360	6	ABO00115	Abo00115	Novel hum
601	8	2.4	360	6	ABO11447	Abo11447	Human sec
602	8	2.4	360	6	ABO02092	Abo02092	Human sec
603	8	2.4	360	6	ABU54384	Abu54384	Human sec
604	8	2.4	360	6	ABU88666	Abu88666	Novel hum
605	8	2.4	360	6	ABU83361	Abu83361	Human sec
606	8	2.4	360	6	ABO06162	Abo06162	Novel hum
607	8	2.4	360	6	ABR59198	Abr59198	Human sec
608	8	2.4	360	6	ABO09260	Abo09260	Human sec
609	8	2.4	360	6	ABO19124	Abo19124	Novel hum
610	8	2.4	360	6	ABO11142	Abo11142	Human sec
611	8	2.4	360	6	ABR66760	Abr66760	Human sec
612	8	2.4	360	6	ABO15973	Abo15973	Human sec
613	8	2.4	360	6	ABO13679	Abo13679	Human sec
614	8	2.4	360	6	ABO47399	Abo47399	Human sec
615	8	2.4	360	6	ABU65582	Abu65582	Human sec
616	8	2.4	360	6	ABO07430	Abo07430	Human PRO
617	8	2.4	360	6	ABO03617	Abo03617	Human sec
618	8	2.4	360	6	ABR67065	Abr67065	Human sec
619	8	2.4	360	6	ABO15668	Abo15668	Human sec
620	8	2.4	360	6	ABU55949	Abu55949	Human sec
621	8	2.4	360	6	ABU65277	Abu65277	Human PRO
622	8	2.4	360	6	ABU95222	Abu95222	Novel hum
623	8	2.4	360	6	ABU71125	Abu71125	Human PRO
624	8	2.4	360	6	ABO07735	Abo07735	Human PRO
625	8	2.4	360	6	ABR69976	Abr69976	Human sec
626	8	2.4	360	6	ABR69309	Abr69309	Human sec
627	8	2.4	360	6	ABO01450	Abo01450	Human PRO
628	8	2.4	360	6	ABU81252	Abu81252	Human PRO
629	8	2.4	360	6	ABR60049	Abr60049	Human sec
630	8	2.4	360	6	ABR67784	Abr67784	Human sec
631	8	2.4	360	6	ABR65172	Abr65172	Human sec
632	8	2.4	360	6	ABR68394	Abr68394	Human sec
633	8	2.4	360	6	ABR71806	Abr71806	Human sec
634	8	2.4	360	6	ABU85286	Abu85286	Human PRO
635	8	2.4	360	6	ABU88976	Abu88976	Human sec
636	8	2.4	360	6	ABU83056	Abu83056	Human sec
637	8	2.4	360	6	ABU94912	Abu94912	Novel hum
638	8	2.4	360	6	ABU90460	Abu90460	Novel hum
639	8	2.4	360	6	ABU83971	Abu83971	Human sec
640	8	2.4	360	6	ABU93622	Abu93622	Novel hum
641	8	2.4	360	6	ABR64867	Abr64867	Human sec
642	8	2.4	360	6	ABR68699	Abr68699	Human sec
643	8	2.4	360	6	ABO06515	Abo06515	Human sec
644	8	2.4	360	6	ABR99060	Abr99060	Human sec
645	8	2.4	360	6	ABU56944	Abu56944	Human PRO
646	8	2.4	360	6	ABU64536	Abu64536	Human sec
647	8	2.4	360	6	ABU85896	Abu85896	Novel hum
648	8	2.4	360	6	ABU67382	Abu67382	Human sec
649	8	2.4	360	6	ABU82183	Abu82183	Novel hum
650	8	2.4	360	6	ABU87194	Abu87194	Human PRO
651	8	2.4	360	6	ABU83666	Abu83666	Human sec
652	8	2.4	360	6	ABO08040	Abo08040	Human PRO
653	8	2.4	360	6	ABO14902	Abo14902	Human sec
654	8	2.4	360	6	ABU81751	Abu81751	Novel hum
655	8	2.4	360	6	ABU65915	Abu65915	Novel hum
656	8	2.4	360	6	ABR59744	Abr59744	Human sec
657	8	2.4	360	6	ABU93932	Abu93932	Novel hum
658	8	2.4	360	6	ABU99785	Abu99785	Novel hum
659	8	2.4	360	6	ABR66455	Abr66455	Human sec
660	8	2.4	360	6	ABR90873	Abr90873	Human sec
661	8	2.4	360	6	ABU94300	Abu94300	Human PRO
662	8	2.4	360	6	ABU79182	Abu79182	Human PRO
663	8	2.4	360	6	ABU86511	Abu86511	Human sec
664	8	2.4	360	6	ABU86816	Abu86816	Novel hum
665	8	2.4	360	6	ABU94605	Abu94605	Human PRO
666	8	2.4	360	6	ABO04532	Abo04532	Human PRO
667	8	2.4	360	6	ABR70281	Abr70281	Human sec
668	8	2.4	360	6	ABU98446	Abu98446	Human PRO
669	8	2.4	360	6	ABR65845	Abr65845	Human sec
670	8	2.4	360	6	ABR64562	Abr64562	Human sec
671	8	2.4	360	6	ABU79487	Abu79487	Human PRO
672	8	2.4	360	6	ABU92878	Abu92878	Human sec
673	8	2.4	360	6	ABU95837	Abu95837	Human PRO
674	8	2.4	360	6	ABU91057	Abu91057	Novel hum
675	8	2.4	360	6	ABU90150	Abu90150	Novel hum
676	8	2.4	360	6	ABO09565	Abo09565	Human sec
677	8	2.4	360	6	ABO10837	Abo10837	Human sec
678	8	2.4	360	6	ABR70891	Abr70891	Human sec
679	8	2.4	360	6	ABU87499	Abu87499	Human PRO
680	8	2.4	360	6	ABU91367	Abu91367	Human PRO
681	8	2.4	360	6	ABU84581	Abu84581	Human sec
682	8	2.4	360	6	ABR69671	Abr69671	Human sec

683	8	2.4	360	6	ABU80048	Abu80048 Human PRO
684	8	2.4	360	6	ABU69659	Abu69659 Novel hum
685	8	2.4	360	6	ABU93317	Abu93317 Human PRO
686	8	2.4	360	6	ABO09870	Abo09870 Human sec
687	8	2.4	360	6	ABO08955	Abo08955 Human sec
688	8	2.4	360	6	ABU10523	Abu10523 Human sec
689	8	2.4	360	6	ABU95532	Abu95532 Human PRO
690	8	2.4	360	6	ABU96741	Abu96741 Novel hum
691	8	2.4	360	6	ABR70586	Abr70586 Human sec
692	8	2.4	360	6	ABO04937	Abo04937 Novel hum
693	8	2.4	360	6	ABO08345	Abo08345 Human sec
694	8	2.4	360	6	ABO14841	Abo14841 Human sec
695	8	2.4	360	6	ABO05552	Abo05552 Human sec
696	8	2.4	360	6	ABR73941	Abr73941 Human sec
697	8	2.4	360	6	ABR95533	Abr95533 Human sec
698	8	2.4	360	6	ABR80830	Abr80830 Human sec
699	8	2.4	360	6	ABR81135	Abr81135 Human sec
700	8	2.4	360	6	ABM00831	Abm00831 Human sec

ALIGNMENTS

RESULT 1
AAY66701
ID AAY66701 standard; protein; 335 AA.
XX
AC AAY66701;
XX
DT 05-APR-2000 (first entry)
XX
DE Membrane-bound protein PRO1138.
XX
KW Membrane-bound polypeptide; PRO polypeptide; LDL receptor; TIE ligand;
KW pharmaceutical; receptor immunoadhesin; gene mapping.
XX
OS Homo sapiens.
XX
PN WO9963088-A2.
XX
PD 09-DEC-1999.
XX
PF 02-JUN-1999; 99WO-US012252.
XX
PR 02-JUN-1998; 98US-0087607P.
PR 02-JUN-1998; 98US-0087609P.
PR 02-JUN-1998; 98US-0087759P.
PR 03-JUN-1998; 98US-0087827P.
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PR   16-SEP-1998;   98US-0100634P.
PR   12-JAN-1999;   99US-0115565P.
XX
PA   (GETH ) GENENTECH INC.
XX
PI   Baker K,  Chen J,  Goddard A,  Gurney AL,  Smith V,  Watanabe CK;
PI   Wood WI,  Yuan J;
XX
DR   WPI; 2000-072883/06.
DR   N-PSDB; AAZ65040.
XX
PT   Membrane-bound proteins and related nucleotide sequences.
XX
PS   Claim 12; Fig 171; 822pp; English.
XX
CC   The invention provides membrane-bound PRO polypeptides and
CC   polynucleotides encoding them. The PRO sequences of the invention were
CC   identified based on extracellular domain homology screening. The PRO
CC   sequences have homology with proteins including LDL receptors, TIE
CC   ligands and various enzymes. The membrane-bound proteins and receptor
CC   molecules are useful as pharmaceutical and diagnostic agents. Receptor
CC   immunoadhesins, for instance, can be used as therapeutic agents to block
CC   receptor-ligand interactions. The membrane-bound proteins can also be
CC   employed for screening of potential peptide or small molecule inhibitors
CC   of the relevant receptor/ligand interaction. The PRO encoding sequences
CC   are useful as hybridization probes, in chromosome and gene mapping and in
CC   the generation of antisense RNA and DNA. PRO nucleic acid sequences will
CC   also be useful for the preparation of PRO polypeptides, especially by
CC   recombinant techniques
XX
SQ   Sequence 335 AA;

  Query Match             100.0%;  Score 335;  DB 3;  Length 335;
  Best Local Similarity   100.0%;  Pred. No. 1.6e-314;
  Matches  335;  Conservative    0;  Mismatches    0;  Indels    0;  Gaps    0;

Qy          1 MAGSPTCLTLIYILWQLTGSAASGPVKELVGSVGGAVTFPLKSKVKQVDSIVWTFNTTPL 60
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Db          1 MAGSPTCLTLIYILWQLTGSAASGPVKELVGSVGGAVTFPLKSKVKQVDSIVWTFNTTPL 60

Qy         61 VTIQPEGGTIIVTQNRNRERVDFPDGGYSLKLSKLKKNDSGIYYVGIYSSSLQQPSTQEY 120
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db         61 VTIQPEGGTIIVTQNRNRERVDFPDGGYSLKLSKLKKNDSGIYYVGIYSSSLQQPSTQEY 120

Qy        121 VLHVYEHLSKPKVTMGLQSNKNGTCVTNLTCCMEHGEEDVIYTWKALGQAANESHNGSIL 180
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        121 VLHVYEHLSKPKVTMGLQSNKNGTCVTNLTCCMEHGEEDVIYTWKALGQAANESHNGSIL 180

Qy        181 PISWRWGESDMTFICVARNPVSRNFSSPILARKLCEGAADDPDSSMVLLCLLLVPLLLSL 240
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        181 PISWRWGESDMTFICVARNPVSRNFSSPILARKLCEGAADDPDSSMVLLCLLLVPLLLSL 240

Qy        241 FVLGLFLWFLKRERQEEYIEEKKRVDICRETPNICPHSGENTEYDTIPHTNRTILKEDPA 300
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Db        241 FVLGLFLWFLKRERQEEYIEEKKRVDICRETPNICPHSGENTEYDTIPHTNRTILKEDPA 300

Qy        301 NTVYSTVEIPKKMENPHSLLTMPDTPRLFAYENVI 335
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Db        301 NTVYSTVEIPKKMENPHSLLTMPDTPRLFAYENVI 335


RESULT 2
AAY70431
ID   AAY70431 standard; protein; 335 AA.
XX
AC   AAY70431;
XX
DT   21-JUN-2000  (first entry)
XX
DE   Human cell surface immunomodulator-1 (CSIMM-1).
XX
KW   Cell surface immunomodulator-1; CSIMM-1; cell proliferation; CD84;
KW   differentiation; signal transduction; drug screening; prevention;
KW   treatment; cancer; leukaemia; melanoma; immune disorder; AIDS;
KW   rheumatoid arthritis; asthma; atherosclerosis; diabetes mellitus;
KW   emphysema; irritable bowel syndrome; multiple sclerosis; diagnosis;
KW   osteoporosis; psoriasis; microbial infections; cytostatic; antiarthritic;
KW   antiasthmatic; immunosuppressive; antiarteriosclerotic; anti-HIV;
KW   antidiabetic; antiinflammatory; neuroprotective; osteopathic;
KW   antipsoriatic; antimicrobial; human.
XX
OS   Homo sapiens.
XX
FH   Key             Location/Qualifiers
FT   Peptide         1. .22
FT                   /label= Signal_peptide
FT   Protein         23. .335
FT                   /label= Mature_CSIMM-1
FT   Region          34. .107
FT                   /note= "Homologous to immunoglobulin domain"
FT   Modified-site   89
FT                   /note= "Potential Protein kinase C phosphorylation site"
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FT                   /note= "Potential N-glycosylation site"
FT   Modified-site   103
FT                   /note= "Potential tyrosine kinase phosphorylation site"
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FT                   /note= "Potential Casein kinase II phosphorylation site"
FT   Modified-site   139
FT                   /note= "Potential Protein kinase C phosphorylation site"
FT   Modified-site   142
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FT                   /note= "Potential N-glycosylation site"
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FT   Modified-site   204
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FT   Domain          228. .248
FT                   /label= Transmembrane_domain
FT   Modified-site   282
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FT                   /label= SH2_domain_recognition_motif
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FT   Modified-site   291
FT                   /note= "Potential N-glycosylation site"
FT   Domain          304. .307
FT                   /label= SH2_domain_recognition_motif
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FT                   /note= "Potential Casein kinase II phosphorylation site"
FT   Modified-site   321
FT                   /note= "Potential Casein kinase II phosphorylation site"
FT   Modified-site   325
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XX
PN   WO200011150-A1.
XX
PD   02-MAR-2000.
XX
PF   24-AUG-1999;   99WO-US019386.
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PR   25-AUG-1998;   98US-00155261.
XX
PA   (INCY-) INCYTE PHARM INC.
XX
PI   Lal P,  Corley NC,  Gorgone GA,  Guegler KJ,  Patterson C,  Baughn MR;
XX
DR   WPI; 2000-246561/21.
DR   N-PSDB; AAZ51572.
XX
PT   New human cell surface immunomodulatory polypeptides and polynucleotides
PT   useful for diagnosis, prevention and treatment of cancer and immune
PT   disorders.
XX
PS   Claim 1; Page 61-62; 70pp; English.
XX
CC   The present sequence is the human cell surface immunomodulator-1 (CSIMM-
CC   1), which is a regulator of cell proliferation, differentiation, cell-
CC   cell communication and signal transduction. It is encoded by cDNA
CC   identified in Incyte clone 14448, derived from human promonocyte cell
CC   line (THP-1) cDNA library (THP1PLB01). It shows homology to cell surface
CC   antigen, CD84. CSIMM can be used for drug screening, prevention and
CC   treatment of cancers such as leukaemia and melanoma, immune disorders
CC   such as AIDS, rheumatoid arthritis, asthma, atherosclerosis, diabetes
CC   mellitus, emphysema, irritable bowel syndrome, multiple sclerosis,
CC   osteoporosis, psoriasis and microbial infections. CSIMM polynucleotide
CC   may be used for diagnosis of CSIMM-associated diseases and as source of
CC   probes useful in mapping naturally occurring genomic sequences
XX
SQ   Sequence 335 AA;

  Query Match             100.0%;  Score 335;  DB 3;  Length 335;
  Best Local Similarity   100.0%;  Pred. No. 1.6e-314;
  Matches  335;  Conservative    0;  Mismatches    0;  Indels    0;  Gaps    0;

Qy          1 MAGSPTCLTLIYILWQLTGSAASGPVKELVGSVGGAVTFPLKSKVKQVDSIVWTFNTTPL 60
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Qy         61 VTIQPEGGTIIVTQNRNRERVDFPDGGYSLKLSKLKKNDSGIYYVGIYSSSLQQPSTQEY 120
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db         61 VTIQPEGGTIIVTQNRNRERVDFPDGGYSLKLSKLKKNDSGIYYVGIYSSSLQQPSTQEY 120

Qy        121 VLHVYEHLSKPKVTMGLQSNKNGTCVTNLTCCMEHGEEDVIYTWKALGQAANESHNGSIL 180
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Db        121 VLHVYEHLSKPKVTMGLQSNKNGTCVTNLTCCMEHGEEDVIYTWKALGQAANESHNGSIL 180

Qy        181 PISWRWGESDMTFICVARNPVSRNFSSPILARKLCEGAADDPDSSMVLLCLLLVPLLLSL 240
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Db        181 PISWRWGESDMTFICVARNPVSRNFSSPILARKLCEGAADDPDSSMVLLCLLLVPLLLSL 240

Qy        241 FVLGLFLWFLKRERQEEYIEEKKRVDICRETPNICPHSGENTEYDTIPHTNRTILKEDPA 300
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        241 FVLGLFLWFLKRERQEEYIEEKKRVDICRETPNICPHSGENTEYDTIPHTNRTILKEDPA 300

Qy        301 NTVYSTVEIPKKMENPHSLLTMPDTPRLFAYENVI 335
              |||||||||||||||||||||||||||||||||||
Db        301 NTVYSTVEIPKKMENPHSLLTMPDTPRLFAYENVI 335


RESULT 3
AAY44609
ID   AAY44609 standard; protein; 335 AA.
XX
AC   AAY44609;
XX
DT   07-APR-2000  (first entry)
XX
DE   Human myocardium protein-7.
XX
KW   Human myocardium protein-7; MP-7; congestive heart failure;
KW   cardiovascular disorder; cardiomyopathy; hypertension; atherosclerosis;
KW   coronary artery spasm; coronary artery disease; cell-cell interaction;
KW   hypotensive; cardiant; screening assay.
XX
OS   Homo sapiens.
XX
FH   Key             Location/Qualifiers
FT   Peptide         1. .23
FT                   /label= Signal_peptide
FT   Protein         24. .335
FT                   /note= "mature protein"
FT   Domain          34. .107
FT                   /note= "First extracellular Ig-like domain"
FT   Domain          144. .197
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FT   Domain          250. .335
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XX
PN   WO9967387-A2.
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PD   29-DEC-1999.
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PF   24-JUN-1999;   99WO-US014307.
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PR   25-JUN-1998;   98US-0090579P.
PR   29-SEP-1998;   98US-00163284.
PR   02-MAR-1999;   99US-00261759.
XX
PA   (MILL-) MILLENNIUM PHARM INC.
XX
PI   Khodadoust M;
XX
DR   WPI; 2000-136984/12.
DR   N-PSDB; AAZ49571.
XX
PT   Novel myocardium protein-7 polynucleotides, used to modulate a variety of
PT   cellular processes.
XX
PS   Claim 2; Fig 2; 116pp; English.
XX
CC   The present sequence is myocardium protein-7 (MP-7). MP-7 is used to
CC   modulate a variety of cellular processes e.g. modulating the activity of
CC   proteins involved in cardiovascular disorders like congestive heart
CC   failure or cardiomyopathy. Diseases which can be treated include
CC   hypertension, atherosclerosis, coronary artery spasm, and coronary artery
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CC   disease. MP-7 proteins may also be used for cellular regulation of immune
CC   cell types, cell cycle, differentiation of multipotent cells, and
CC   modulation of cell-cell interactions. MP-7 may also be used in screening
CC   assays to identify agonists and antagonists and to raise antibodies
XX
SQ   Sequence 335 AA;

  Query Match             100.0%;  Score 335;  DB 3;  Length 335;
  Best Local Similarity   100.0%;  Pred. No. 1.6e-314;
  Matches  335;  Conservative    0;  Mismatches    0;  Indels    0;  Gaps    0;

Qy          1 MAGSPTCLTLIYILWQLTGSAASGPVKELVGSVGGAVTFPLKSKVKQVDSIVWTFNTTPL 60
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Db          1 MAGSPTCLTLIYILWQLTGSAASGPVKELVGSVGGAVTFPLKSKVKQVDSIVWTFNTTPL 60

Qy         61 VTIQPEGGTIIVTQNRNRERVDFPDGGYSLKLSKLKKNDSGIYYVGIYSSSLQQPSTQEY 120
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db         61 VTIQPEGGTIIVTQNRNRERVDFPDGGYSLKLSKLKKNDSGIYYVGIYSSSLQQPSTQEY 120

Qy        121 VLHVYEHLSKPKVTMGLQSNKNGTCVTNLTCCMEHGEEDVIYTWKALGQAANESHNGSIL 180
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        121 VLHVYEHLSKPKVTMGLQSNKNGTCVTNLTCCMEHGEEDVIYTWKALGQAANESHNGSIL 180

Qy        181 PISWRWGESDMTFICVARNPVSRNFSSPILARKLCEGAADDPDSSMVLLCLLLVPLLLSL 240
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Db        181 PISWRWGESDMTFICVARNPVSRNFSSPILARKLCEGAADDPDSSMVLLCLLLVPLLLSL 240

Qy        241 FVLGLFLWFLKRERQEEYIEEKKRVDICRETPNICPHSGENTEYDTIPHTNRTILKEDPA 300
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Db        241 FVLGLFLWFLKRERQEEYIEEKKRVDICRETPNICPHSGENTEYDTIPHTNRTILKEDPA 300

Qy        301 NTVYSTVEIPKKMENPHSLLTMPDTPRLFAYENVI 335
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Db        301 NTVYSTVEIPKKMENPHSLLTMPDTPRLFAYENVI 335


RESULT 4
AAU29119
ID   AAU29119 standard; protein; 335 AA.
XX
AC   AAU29119;
XX
DT   18-DEC-2001  (first entry)
XX
DE   Human PRO polypeptide sequence #96.
XX
KW   PRO polypeptide; mammal; tumour; cancer; human; cattle; horse; sheep;
KW   dog; cat; pig; goat; rabbit; tumour necrosis factor alpha; TNF-alpha;
KW   blood; chondrocyte cell; cell proliferation; cell differentiation; colon;
KW   adrenal; lung; breast; prostate; rectum; cervix; liver; genetic disorder.
XX
OS   Homo sapiens.
XX
PN   WO200168848-A2.
XX
PD   20-SEP-2001.
XX
PF   28-FEB-2001; 2001WO-US006520.
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PR   01-MAR-2000; 2000WO-US005601.
PR   02-MAR-2000; 2000WO-US005841.
PR   03-MAR-2000; 2000US-0187202P.
PR   06-MAR-2000; 2000US-0186968P.
PR   14-MAR-2000; 2000US-0189320P.
PR   14-MAR-2000; 2000US-0189328P.
PR   15-MAR-2000; 2000WO-US006884.
PR   21-MAR-2000; 2000US-0190828P.
PR   21-MAR-2000; 2000US-0191007P.
PR   21-MAR-2000; 2000US-0191048P.
PR   21-MAR-2000; 2000US-0191314P.
PR   28-MAR-2000; 2000US-0192655P.
PR   29-MAR-2000; 2000US-0193032P.
PR   29-MAR-2000; 2000US-0193053P.
PR   30-MAR-2000; 2000WO-US008439.
PR   04-APR-2000; 2000US-0194449P.
PR   04-APR-2000; 2000US-0194647P.
PR   11-APR-2000; 2000US-0195975P.
PR   11-APR-2000; 2000US-0196000P.
PR   11-APR-2000; 2000US-0196187P.
PR   11-APR-2000; 2000US-0196690P.
PR   11-APR-2000; 2000US-0196820P.
PR   18-APR-2000; 2000US-0198121P.
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PR   25-APR-2000; 2000US-0199397P.
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PR   03-MAY-2000; 2000US-0201516P.
PR   17-MAY-2000; 2000WO-US013705.
PR   22-MAY-2000; 2000WO-US014042.
PR   30-MAY-2000; 2000WO-US014941.
PR   02-JUN-2000; 2000WO-US015264.
PR   05-JUN-2000; 2000US-0209832P.
PR   28-JUL-2000; 2000WO-US020710.
PR   22-AUG-2000; 2000US-00644848.
PR   24-AUG-2000; 2000WO-US023328.
PR   08-NOV-2000; 2000WO-US030952.
PR   01-DEC-2000; 2000WO-US032678.
PR   20-DEC-2000; 2000WO-US034956.
XX
PA   (GETH ) GENENTECH INC.
XX
PI   Baker KP,  Chen J,  Desnoyers L,  Goddard A,  Godowski PJ,  Gurney AL;
PI   Pan J,  Smith V,  Watanabe CK,  Wood WI,  Zhang Z;
XX
DR   WPI; 2001-602746/68.
DR   N-PSDB; AAS46020.
XX
PT   Novel nucleic acids encoding PRO polypeptides, used to diagnose the
PT   presence of tumors, such as prostate and breast tumors, in mammals and to
PT   screen for modulators of the compounds.
XX
PS   Claim 11; Fig 192; 774pp; English.
XX
CC   Sequences AAU29024-AAU29328 represent PRO polypeptides of the invention.
CC   The PRO polypeptides and their associated nucleic acids can be used to
CC   detect the presence of a tumour in a mammal by comparing the level of
CC   expression of a PRO polypeptide in a test sample of cells from the animal
CC   and a control sample of normal cells, whereby a higher level of
CC   expression in the test sample indicates the presence of a tumour in the
CC   mammal. Mammals include dogs, cats, cattle, horses, sheep, pigs, goats
CC   and rabbits but are preferably human. The polypeptides can be used to
CC   stimulate tumour necrosis factor (TNF) alpha release from human blood,
CC   when contacted with it. A specific polypeptide can be used to stimulate
CC   the proliferation or differentiation of chondrocyte cells. The PRO
CC   proteins can be used to determine the presence of tumours and also
CC   susceptibility to tumour development, particularly adrenal, lung, colon,
CC   breast, prostate, rectal, cervical, or liver tumours, in mammalian
CC   subjects. The oligonucleotide probes specific for the PRO nucleic acids
CC   can be used for genetic analysis of individuals with genetic disorders
XX
SQ   Sequence 335 AA;

  Query Match             100.0%;  Score 335;  DB 4;  Length 335;
  Best Local Similarity   100.0%;  Pred. No. 1.6e-314;
  Matches  335;  Conservative    0;  Mismatches    0;  Indels    0;  Gaps    0;

Qy          1 MAGSPTCLTLIYILWQLTGSAASGPVKELVGSVGGAVTFPLKSKVKQVDSIVWTFNTTPL 60
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db          1 MAGSPTCLTLIYILWQLTGSAASGPVKELVGSVGGAVTFPLKSKVKQVDSIVWTFNTTPL 60

Qy         61 VTIQPEGGTIIVTQNRNRERVDFPDGGYSLKLSKLKKNDSGIYYVGIYSSSLQQPSTQEY 120
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db         61 VTIQPEGGTIIVTQNRNRERVDFPDGGYSLKLSKLKKNDSGIYYVGIYSSSLQQPSTQEY 120

Qy        121 VLHVYEHLSKPKVTMGLQSNKNGTCVTNLTCCMEHGEEDVIYTWKALGQAANESHNGSIL 180
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
```

```
Db        121 VLHVYEHLSKPKVTMGLQSNKNGTCVTNLTCCMEHGEEDVIYTWKALGQAANESHNGSIL 180

Qy        181 PISWRWGESDMTFICVARNPVSRNFSSPILARKLCEGAADDPDSSMVLLCLLLVPLLLSL 240
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        181 PISWRWGESDMTFICVARNPVSRNFSSPILARKLCEGAADDPDSSMVLLCLLLVPLLLSL 240

Qy        241 FVLGLFLWFLKRERQEEYIEEKKRVDICRETPNICPHSGENTEYDTIPHTNRTILKEDPA 300
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        241 FVLGLFLWFLKRERQEEYIEEKKRVDICRETPNICPHSGENTEYDTIPHTNRTILKEDPA 300

Qy        301 NTVYSTVEIPKKMENPHSLLTMPDTPRLFAYENVI 335
              |||||||||||||||||||||||||||||||||||
Db        301 NTVYSTVEIPKKMENPHSLLTMPDTPRLFAYENVI 335


RESULT 5
AAB87548
ID   AAB87548 standard; protein; 335 AA.
XX
AC   AAB87548;
XX
DT   15-MAY-2001  (first entry)
XX
DE   Human PRO1138.
XX
KW   Human; PRO protein; mapping.
XX
OS   Homo sapiens.
XX
PN   WO200116318-A2.
XX
PD   08-MAR-2001.
XX
PF   24-AUG-2000; 2000WO-US023328.
XX
PR   01-SEP-1999;   99WO-US020111.
PR   15-SEP-1999;   99WO-US021090.
PR   07-DEC-1999;   99US-0169495P.
PR   09-DEC-1999;   99US-0170262P.
PR   11-JAN-2000; 2000US-0175481P.
PR   18-FEB-2000; 2000WO-US004341.
PR   18-FEB-2000; 2000WO-US004342.
PR   22-FEB-2000; 2000WO-US004414.
PR   01-MAR-2000; 2000WO-US005601.
PR   03-MAR-2000; 2000US-0187202P.
PR   21-MAR-2000; 2000US-0191007P.
PR   30-MAR-2000; 2000WO-US008439.
PR   25-APR-2000; 2000US-0199397P.
PR   22-MAY-2000; 2000WO-US014042.
PR   05-JUN-2000; 2000US-0209832P.
XX
PA   (GETH ) GENENTECH INC.
XX
PI   Eaton DL,  Filvaroff E,  Gerritsen ME,  Goddard A,  Godowski PJ;
PI   Grimaldi CJ,  Gurney AL,  Watanabe CK,  Wood WI;
XX
DR   WPI; 2001-183260/18.
DR   N-PSDB; AAF92080.
XX
PT   Eighty four nucleic acids encoding PRO polypeptides, useful in molecular
PT   biology, including use as hybridization probes, and in chromosome and
PT   gene mapping.
XX
PS   Claim 12; Fig 46; 278pp; English.
XX
CC   The present sequence is a human PRO polypeptide (secreted and
CC   transmembrane). The PRO protein, and PRO agonists, PRO antagonists or
CC   anti-PRO antibodies are useful for preparation of a medicament useful in
CC   the treatment of a condition which is responsive to the PRO protein,
CC   agonists, antagonists or anti-PRO antibodies. The PRO protein may also be
CC   employed as molecular weight markers for protein electrophoresis. The PRO
CC   coding sequence has applications in molecular biology, including use as
CC   hybridisation probes, and in chromosome and gene mapping
XX
SQ   Sequence 335 AA;

  Query Match             100.0%;  Score 335;  DB 4;  Length 335;
  Best Local Similarity   100.0%;  Pred. No. 1.6e-314;
  Matches  335;  Conservative    0;  Mismatches    0;  Indels    0;  Gaps    0;

Qy          1 MAGSPTCLTLIYILWQLTGSAASGPVKELVGSVGGAVTFPLKSKVKQVDSIVWTFNTTPL 60
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db          1 MAGSPTCLTLIYILWQLTGSAASGPVKELVGSVGGAVTFPLKSKVKQVDSIVWTFNTTPL 60

Qy         61 VTIQPEGGTIIVTQNRNRERVDFPDGGYSLKLSKLKKNDSGIYYVGIYSSSLQQPSTQEY 120
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db         61 VTIQPEGGTIIVTQNRNRERVDFPDGGYSLKLSKLKKNDSGIYYVGIYSSSLQQPSTQEY 120

Qy        121 VLHVYEHLSKPKVTMGLQSNKNGTCVTNLTCCMEHGEEDVIYTWKALGQAANESHNGSIL 180
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        121 VLHVYEHLSKPKVTMGLQSNKNGTCVTNLTCCMEHGEEDVIYTWKALGQAANESHNGSIL 180

Qy        181 PISWRWGESDMTFICVARNPVSRNFSSPILARKLCEGAADDPDSSMVLLCLLLVPLLLSL 240
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        181 PISWRWGESDMTFICVARNPVSRNFSSPILARKLCEGAADDPDSSMVLLCLLLVPLLLSL 240

Qy        241 FVLGLFLWFLKRERQEEYIEEKKRVDICRETPNICPHSGENTEYDTIPHTNRTILKEDPA 300
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        241 FVLGLFLWFLKRERQEEYIEEKKRVDICRETPNICPHSGENTEYDTIPHTNRTILKEDPA 300

Qy        301 NTVYSTVEIPKKMENPHSLLTMPDTPRLFAYENVI 335
              |||||||||||||||||||||||||||||||||||
Db        301 NTVYSTVEIPKKMENPHSLLTMPDTPRLFAYENVI 335


RESULT 6
AAB47321
ID   AAB47321 standard; protein; 335 AA.
XX
AC   AAB47321;
XX
DT   29-AUG-2001  (first entry)
XX
DE   APEX-1.
XX
KW   Antigen presenting cell expression protein; APEX-1; APEX-2; APEX-3;
KW   extracellular domain; immunoglobulin-like domain; Ig-like structure;
KW   N-glycosylation site; transmembrane domain; cytoplasmic domain;
KW   SH2-binding motif; asthma; arteriosclerosis; AIDS; cirrhosis;
KW   Crohn's disease; atopic dermatitis; autoimmune anaemia; bursitis;
KW   cholecystitis; diabetes mellitus; emphysema; atrophic gastritis;
KW   inflammatory bowel disease; multiple sclerosis; myasthenia gravis;
KW   myocardial inflammation; pericardial inflammation; osteoarthritis;
KW   osteoporosis; psoriasis; Reiter's syndrome; rheumatoid arthritis;
KW   inflammation; cancer; autoimmune disease; graft rejection;
KW   graft versus host disease; systemic lupus erythematosus.
XX
OS   Homo sapiens.
XX
FH   Key             Location/Qualifiers
FT   Peptide         1. .22
FT                   /label= Signal peptide
FT   Protein         23. .335
FT                   /label= Mature APEX-1
FT   Domain          226. .250
FT                   /label= Transmembrane domain
XX
PN   WO200146260-A2.
XX
PD   28-JUN-2001.
XX
PF   22-DEC-2000; 2000WO-US034963.
XX
PR   23-DEC-1999;   99US-0172025P.
XX
PA   (BRIM ) BRISTOL-MYERS SQUIBB CO.
```

XX
PI Starling GC, Finger J;
XX
DR WPI; 2001-418044/44.
DR N-PSDB; AAC86114.
XX
PT Novel Antigen presenting cell expression protein useful for treating
PT asthma, arteriosclerosis, autoimmune diseases, AIDS, cirrhosis, Crohn's
PT disease and atopic dermatitis.
XX
PS Claim 3; Fig 2; 112pp; English.
XX
CC The sequences given in AAB47321-23 represent antigen presenting cell
CC expression (APEX)-1, APEX-2 and APEX-3 proteins. APEX-1 and APEX-2
CC comprise an extracellular domain having one immunoglobulin (Ig)-like
CC structure and N-glycosylation site, a transmembrane domain, and a
CC cytoplasmic domain having at least one SH2-binding motif. APEX proteins
CC and antibodies are useful in the study, diagnosis, prevention and
CC treatment of disease associated with the presence of an APEX protein
CC e.g., asthma, arteriosclerosis, AIDS, cirrhosis, Crohn's disease, atopic
CC dermatitis, autoimmune anaemia, bursitis, cholecystitis, diabetes
CC mellitus, emphysema, atrophic gastritis, inflammatory bowel disease,
CC multiple sclerosis, myasthenia gravis, myocardial or pericardial
CC inflammation, osteoarthritis, osteoporosis, psoriasis, Reiter's syndrome,
CC rheumatoid arthritis, inflammation, cancer, immune disorders, autoimmune
CC diseases, graft rejections, graft versus host reaction and systemic lupus
CC erythematosus. APEX proteins are useful as diagnostic and/or prognostic
CC markers on APCs or APEX expressing cells, the ability to elicit the
CC generation of antibodies and as targets for various therapeutic
CC modalities. APEX proteins are also useful for identifying and isolating
CC ligand that bind APEX
XX
SQ Sequence 335 AA;

Query Match 100.0%; Score 335; DB 4; Length 335;
Best Local Similarity 100.0%; Pred. No. 1.6e-314;
Matches 335; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

```
Qy          1 MAGSPTCLTLIYILWQLTGSAASGPVKELVGSVGGAVTFPLKSKVKQVDSIVWTFNTTPL 60
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db          1 MAGSPTCLTLIYILWQLTGSAASGPVKELVGSVGGAVTFPLKSKVKQVDSIVWTFNTTPL 60

Qy         61 VTIQPEGGTIIVTQNRNRERVDFPDGGYSLKLSKLKKNDSGIYYVGIYSSSLQQPSTQEY 120
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db         61 VTIQPEGGTIIVTQNRNRERVDFPDGGYSLKLSKLKKNDSGIYYVGIYSSSLQQPSTQEY 120

Qy        121 VLHVYEHLSKPKVTMGLQSNKNGTCVTNLTCCMEHGEEDVIYTWKALGQAANESHNGSIL 180
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        121 VLHVYEHLSKPKVTMGLQSNKNGTCVTNLTCCMEHGEEDVIYTWKALGQAANESHNGSIL 180

Qy        181 PISWRWGESDMTFICVARNPVSRNFSSPILARKLCEGAADDPDSSMVLLCLLLVPLLLSL 240
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        181 PISWRWGESDMTFICVARNPVSRNFSSPILARKLCEGAADDPDSSMVLLCLLLVPLLLSL 240

Qy        241 FVLGLFLWFLKRERQEEYIEEKKRVDICRETPNICPHSGENTEYDTIPHTNRTILKEDPA 300
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        241 FVLGLFLWFLKRERQEEYIEEKKRVDICRETPNICPHSGENTEYDTIPHTNRTILKEDPA 300

Qy        301 NTVYSTVEIPKKMENPHSLLTMPDTPRLFAYENVI 335
              |||||||||||||||||||||||||||||||||||
Db        301 NTVYSTVEIPKKMENPHSLLTMPDTPRLFAYENVI 335
```

RESULT 7
AAB65224
ID AAB65224 standard; protein; 335 AA.
XX
AC AAB65224;
XX
DT 02-APR-2001 (first entry)
XX
DE Human PRO1138 (UNQ576) protein sequence SEQ ID NO:253.
XX
KW Human; secreted and transmembrane protein; PRO; cytostatic; cell death;
KW cancer; chromosomal mapping; gene mapping; tissue typing;
KW diagnostic assay.
XX
OS Homo sapiens.
XX
PN WO200073454-A1.
XX
PD 07-DEC-2000.
XX
PF 30-MAR-2000; 2000WO-US008439.
XX
PR 02-JUN-1999; 99WO-US012252.
PR 23-JUN-1999; 99US-0141037P.
PR 07-JUL-1999; 99US-0143048P.
PR 20-JUL-1999; 99US-0144758P.
PR 26-JUL-1999; 99US-0145698P.
PR 28-JUL-1999; 99US-0146222P.
PR 17-AUG-1999; 99US-0149396P.
PR 15-SEP-1999; 99WO-US021090.
PR 15-SEP-1999; 99WO-US021547.
PR 08-OCT-1999; 99US-0158663P.
PR 30-NOV-1999; 99WO-US028313.
PR 01-DEC-1999; 99WO-US028301.
PR 16-DEC-1999; 99WO-US030095.
PR 20-DEC-1999; 99WO-US030911.
PR 05-JAN-2000; 2000WO-US000219.
PR 06-JAN-2000; 2000WO-US000376.
PR 11-FEB-2000; 2000WO-US003565.
PR 18-FEB-2000; 2000WO-US004341.
PR 22-FEB-2000; 2000WO-US004414.
PR 24-FEB-2000; 2000WO-US004914.
PR 24-FEB-2000; 2000WO-US005004.
PR 02-MAR-2000; 2000WO-US005841.
PR 15-MAR-2000; 2000WO-US006884.
PR 20-MAR-2000; 2000WO-US007377.
XX
PA (GETH) GENENTECH INC.
XX
PI Ashkenazi AJ, Baker KP, Botstein D, Desnoyers L, Eaton DL;
PI Ferrara N, Fong S, Gerber H, Gerritsen ME, Goddard A, Godowski PJ;
PI Grimaldi CJ, Gurney AL, Kljavin IJ, Napier MA, Pan J, Paoni NF;
PI Roy MA, Stewart TA, Tumas D, Watanabe CK, Williams PM, Wood WI;
PI Zhang Z;
XX
DR WPI; 2001-032160/04.
DR N-PSDB; AAF44186.
XX
PT PRO polynucleotides used to produce polypeptides used to target bioactive
PT molecules such as toxins, radiolabels or antibodies, to specific cells,
PT to cause targeted cell death.
XX
PS Claim 12; Fig 171; 935pp; English.
XX
CC The present invention describes human secreted and transmembrane PRO
CC proteins. The PRO proteins have cytostatic activity. The PRO proteins can
CC be used for targeted delivery of bioactive molecules, such as toxins,
CC radiolabels or antibodies, that cause cell death. PRO nucleotide
CC sequences, and their fragments, can be used as hybridisation probes, in
CC chromosomal and gene mapping, and in the generation of anti-sense RNA and
CC DNA. They may also be used to produce transgenic animals which are used
CC to develop and screen therapeutically useful reagents. The PRO nucleotide
CC and protein sequence can be used for tissue typing and in treating
CC cancer. Anti-PRO antibodies can be used in diagnostic assays. AAF44270 to
CC AAF44470 represent PCR primers and hybridisation probes used in the
CC isolation of human PRO sequences. AAF44087 to AAF44269 and AAB65154 to
CC AAB65300 represent human PRO polynucleotide and protein sequences given
CC in the exemplification of the present invention
XX
SQ Sequence 335 AA;

Query Match 100.0%; Score 335; DB 4; Length 335;
Best Local Similarity 100.0%; Pred. No. 1.6e-314;

```
  Matches  335;  Conservative    0;  Mismatches    0;  Indels    0;  Gaps    0;

Qy          1 MAGSPTCLTLIYILWQLTGSAASGPVKELVGSVGGAVTFPLKSKVKQVDSIVWTFNTTPL 60
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db          1 MAGSPTCLTLIYILWQLTGSAASGPVKELVGSVGGAVTFPLKSKVKQVDSIVWTFNTTPL 60

Qy         61 VTIQPEGGTIIVTQNRNRERVDFPDGGYSLKLSKLKKNDSGIYYVGIYSSSLQQPSTQEY 120
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db         61 VTIQPEGGTIIVTQNRNRERVDFPDGGYSLKLSKLKKNDSGIYYVGIYSSSLQQPSTQEY 120

Qy        121 VLHVYEHLSKPKVTMGLQSNKNGTCVTNLTCCMEHGEEDVIYTWKALGQAANESHNGSIL 180
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        121 VLHVYEHLSKPKVTMGLQSNKNGTCVTNLTCCMEHGEEDVIYTWKALGQAANESHNGSIL 180

Qy        181 PISWRWGESDMTFICVARNPVSRNFSSPILARKLCEGAADDPDSSMVLLCLLLVPLLLSL 240
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        181 PISWRWGESDMTFICVARNPVSRNFSSPILARKLCEGAADDPDSSMVLLCLLLVPLLLSL 240

Qy        241 FVLGLFLWFLKRERQEEYIEEKKRVDICRETPNICPHSGENTEYDTIPHTNRTILKEDPA 300
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        241 FVLGLFLWFLKRERQEEYIEEKKRVDICRETPNICPHSGENTEYDTIPHTNRTILKEDPA 300

Qy        301 NTVYSTVEIPKKMENPHSLLTMPDTPRLFAYENVI 335
              |||||||||||||||||||||||||||||||||||
Db        301 NTVYSTVEIPKKMENPHSLLTMPDTPRLFAYENVI 335


RESULT 8
ABG95873
ID   ABG95873 standard; protein; 335 AA.
XX
AC   ABG95873;
XX
DT   10-DEC-2002  (first entry)
XX
DE   Human secreted/transmembrane protein PRO1138.
XX
KW   Human; secreted protein; transmembrane protein; antirheumatic;
KW   antiarthritic; osteopathic; sports-related joint problem;
KW   articular cartilage defect; osteoarthritis; rheumatoid arthritis.
XX
OS   Homo sapiens.
XX
PN   US2002119130-A1.
XX
PD   29-AUG-2002.
XX
PF   06-DEC-2001; 2001US-00006867.
XX
PR   29-OCT-1997;   97US-0063435P.
PR   29-OCT-1997;   97US-0064215P.
PR   22-APR-1998;   98US-0082797P.
PR   29-APR-1998;   98US-0083495P.
PR   15-MAY-1998;   98US-0085579P.
PR   02-JUN-1998;   98US-0087759P.
PR   04-JUN-1998;   98US-0088021P.
PR   04-JUN-1998;   98US-0088029P.
PR   04-JUN-1998;   98US-0088030P.
PR   10-JUN-1998;   98US-0088734P.
PR   10-JUN-1998;   98US-0088740P.
PR   10-JUN-1998;   98US-0088811P.
PR   10-JUN-1998;   98US-0088824P.
PR   10-JUN-1998;   98US-0088825P.
PR   11-JUN-1998;   98US-0088863P.
PR   12-JUN-1998;   98US-0089105P.
PR   16-JUN-1998;   98US-0089514P.
PR   17-JUN-1998;   98US-0089653P.
PR   19-JUN-1998;   98US-0089952P.
PR   22-JUN-1998;   98US-0090246P.
PR   24-JUN-1998;   98US-0090444P.
PR   25-JUN-1998;   98US-0090688P.
PR   25-JUN-1998;   98US-0090696P.
PR   26-JUN-1998;   98US-0090862P.
PR   02-JUL-1998;   98US-0091628P.
PR   10-AUG-1998;   98US-0096012P.
PR   17-AUG-1998;   98US-0096757P.
PR   18-AUG-1998;   98US-0096949P.
PR   18-AUG-1998;   98US-0096959P.
PR   26-AUG-1998;   98US-0097954P.
PR   26-AUG-1998;   98US-0097971P.
PR   26-AUG-1998;   98US-0097979P.
PR   01-SEP-1998;   98US-0098749P.
PR   10-SEP-1998;   98US-0099741P.
PR   10-SEP-1998;   98US-0099763P.
PR   10-SEP-1998;   98US-0099792P.
PR   10-SEP-1998;   98US-0099812P.
PR   10-SEP-1998;   98US-0099815P.
PR   16-SEP-1998;   98US-0100627P.
PR   16-SEP-1998;   98US-0100662P.
PR   16-SEP-1998;   98WO-US019330.
PR   17-SEP-1998;   98US-0100683P.
PR   17-SEP-1998;   98US-0100684P.
PR   17-SEP-1998;   98US-0100930P.
PR   22-SEP-1998;   98US-0101279P.
PR   23-SEP-1998;   98US-0101475P.
PR   24-SEP-1998;   98US-0101738P.
PR   24-SEP-1998;   98US-0101743P.
PR   24-SEP-1998;   98US-0101916P.
PR   30-SEP-1998;   98US-0102570P.
PR   06-OCT-1998;   98US-0103449P.
PR   08-MAR-1999;   99WO-US005028.
PR   14-MAY-1999;   99WO-US010733.
PR   02-JUN-1999;   99WO-US012252.
PR   01-SEP-1999;   99WO-US020111.
PR   15-SEP-1999;   99WO-US021090.
PR   15-SEP-1999;   99WO-US021194.
PR   22-DEC-1999;   99WO-US030720.
PR   18-FEB-2000; 2000WO-US004341.
PR   18-FEB-2000; 2000WO-US004342.
PR   22-FEB-2000; 2000WO-US004414.
PR   01-MAR-2000; 2000WO-US005601.
PR   30-MAR-2000; 2000WO-US008439.
PR   22-MAY-2000; 2000WO-US014042.
PR   02-JUN-2000; 2000WO-US015264.
PR   23-AUG-2000; 2000WO-US023522.
PR   24-AUG-2000; 2000WO-US023328.
PR   10-NOV-2000; 2000WO-US030873.
PR   01-DEC-2000; 2000WO-US032378.
PR   20-DEC-2000; 2000WO-US034956.
PR   28-FEB-2001; 2001WO-US006520.
PR   01-MAR-2001; 2001WO-US006666.
PR   30-MAY-2001; 2001WO-US017443.
PR   01-JUN-2001; 2001WO-US017800.
PR   20-JUN-2001; 2001WO-US019692.
PR   29-JUN-2001; 2001WO-US021066.
PR   09-JUL-2001; 2001WO-US021735.
XX
PA   (GETH ) GENENTECH INC.
XX
PI   Eaton DL,  Filvaroff E,  Gerritsen ME,  Goddard A,  Godowski PJ;
PI   Grimaldi JC,  Gurney AL,  Watanabe CK,  Wood WI;
XX
DR   WPI; 2002-731348/79.
DR   N-PSDB; ABS74400.
XX
PT   New isolated secreted and transmembrane PRO polypeptide useful for
PT   modulating biological activity of a cell, or for treating sports-related
PT   joint problems, osteoarthritis or rheumatoid arthritis.
XX
PS   Claim 20; Fig 46; 399pp; English.
XX
CC   The invention relates to an isolated secreted and transmembrane PRO
CC   polypeptide having 80 % sequence identity to a sequence appearing as
CC   ABG95851-ABG95934 or their associated signal peptide, or a sequence of an
CC   extracellular domain of the proteins with their associated signal peptide
CC   or lacking its associated signal peptide. Also included are the nucleic
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CC   acids encoding the proteins, vectors, host cells, fusion proteins and
CC   antibodies which specifically bind to the proteins. The proteins are
CC   useful for detecting a polypeptide designated as A, B, C or D in a sample
CC   suspected of containing an A, B, C or D polypeptide, by contacting the
CC   sample with a polypeptide designated as E, F, G, H or I (or vice versa)
CC   and determining the formation of a A/E, B/F, B/G, C/H or D/I polypeptide
CC   conjugate in the sample, where the formation of the conjugate is
CC   indicative of the presence of an A, B, C or D polypeptide in the sample,
CC   where A is a PRO10272 polypeptide, B is a PRO20110 polypeptide, C is a
CC   PRO10096 polypeptide, D is a PRO19760 polypeptide, E is a PRO5801
CC   polypeptide, F is a PRO1 polypeptide, G is a PRO20040 polypeptide, H is a
CC   PRO20233 polypeptide and I is a PRO1890 polypeptide. The sample comprises
CC   a cell suspected of expressing the A, B, C or D polypeptide. The E, F, G,
CC   H or I polypeptide is labeled with a detectable label or is attached to a
CC   solid support. The proteins are useful for linking a bioactive molecule
CC   to a cell expressing a polypeptide designated as A, B, C or D or E, F, G,
CC   H or I. The bioactive molecule is a toxin, a radiolabel or an antibody.
CC   The bioactive molecule causes death of the cell. A, B, C, D, E, F, G, H,
CC   or I, or antibodies against them are useful for modulating a biological
CC   activity of a cell expressing a polypeptide designated as A, B, C or D or
CC   E, F, G, H, or I. The cell is killed. The proteins are useful for
CC   identifying agonists or antagonists, for the preparation of a medicament
CC   useful in the treatment of a condition which is responsive to the
CC   proteins, as molecular weight markers for protein electrophoresis
CC   purposes, and as therapeutic agents for treating sports-related joint
CC   problems, articular cartilage defects, osteoarthritis or rheumatoid
CC   arthritis. Nucleic acids encoding the proteins are useful as
CC   hybridisation probes, in chromosome and gene mapping, in the generation
CC   of anti-sense RNA and DNA, for the preparation of the proteins, to
CC   generate transgenic or knockout animals which are useful in the
CC   development and screening of therapeutic useful reagents, for chromosome
CC   identification, and in gene therapy. The antibody is useful as a
CC   therapeutic agent, in a diagnostic assay and for affinity purification of
CC   the protein from recombinant cell culture natural sources. The present
CC   sequence represents a novel secreted or transmembrane protein of the
CC   invention
XX
SQ   Sequence 335 AA;

  Query Match             100.0%;  Score 335;  DB 5;  Length 335;
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Qy        181 PISWRWGESDMTFICVARNPVSRNFSSPILARKLCEGAADDPDSSMVLLCLLLVPLLLSL 240
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Qy        241 FVLGLFLWFLKRERQEEYIEEKKRVDICRETPNICPHSGENTEYDTIPHTNRTILKEDPA 300
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Qy        301 NTVYSTVEIPKKMENPHSLLTMPDTPRLFAYENVI 335
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RESULT 9
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ID   ABU58495 standard; protein; 335 AA.
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AC   ABU58495;
XX
DT   15-APR-2003  (first entry)
XX
DE   Human PRO polypeptide #96.
XX
KW   Human; PRO; cytostatic; tumour; cancer; breast; lung; stomach; liver;
KW   dog; cat; cow; horse; sheep; pig; goat; rabbit; ADEPT;
KW   antibody-dependent enzyme mediated prodrug therapy.
XX
OS   Homo sapiens.
XX
PN   US2003027272-A1.
XX
PD   06-FEB-2003.
XX
PF   21-JUN-2002; 2002US-00176492.
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PR 07-OCT-1998; 98US-00168978.

Query Match 100.0%; Score 335; DB 6; Length 335;
Best Local Similarity 100.0%; Pred. No. 1.6e-314;
Matches 335; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

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RESULT 10
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ID   ABU88043 standard; protein; 335 AA.
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AC   ABU88043;
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DT   07-JUL-2003  (first entry)
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DE   Novel human secreted and transmembrane protein PRO1138.
XX
KW   Human; secreted and transmembrane protein: PRO; gene therapy;
KW   tumour necrosis factor-alpha release; TNF-alpha release;
KW   chondrocyte proliferation; chondrocyte differentiation; tumour;
KW   adrenal tumour; lung tumour; colon tumour; breast tumour;
KW   prostate tumour; rectal tumour; cervical tumour; liver tumour.
XX
OS   Homo sapiens.
XX
PN   US2003032127-A1.
XX
PD   13-FEB-2003.
XX
PF   26-JUN-2002; 2002US-00183012.
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PR   18-SEP-1997;   97US-0059263P.
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Qy        181 PISWRWGESDMTFICVARNPVSRNFSSPILARKLCEGAADDPDSSMVLLCLLLVPLLLSL 240
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RESULT 11
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AC ABU84358;
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DT 02-AUG-2003 (first entry)
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DE Human secreted/transmembrane protein (PRO) #96.
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KW tumour necrosis factor alpha; chondrocyte cell; tumour; gene therapy;
KW tissue typing.
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OS Homo sapiens.
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PN US2003032112-A1.
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PD 13-FEB-2003.
XX
PF 21-JUN-2002; 2002US-00176756.
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Qy        181 PISWRWGESDMTFICVARNPVSRNFSSPILARKLCEGAADDPDSSMVLLCLLLVPLLLSL 240
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RESULT 12
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AC   ABR66232;
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DT   05-AUG-2003  (first entry)
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DE   Human secreted polypeptide PRO1138, SEQ ID NO:192.
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KW   Human; PRO; secreted protein; transmembrane protein;
KW   extracellular domain; tumour necrosis factor-alpha; TNF-alpha;
KW   chondrocyte; proliferation; differentiation; cartilage disorder;
KW   bone disorder; arthritis; sports injury; cancer; tumour; diagnosis;
KW   adrenal tumour; lung; colon; breast; prostate; kidney; rectum; cervix;
KW   liver; drug screening; transgenic animal; genetic analysis;
KW   antiarthritic; vulnerary; gene therapy.
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OS   Homo sapiens.
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PN   US2003027278-A1.
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PD   06-FEB-2003.
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PF   21-JUN-2002; 2002US-00176987.
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DT 05-AUG-2003 (first entry)
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KW extracellular domain; tumour necrosis factor-alpha; TNF-alpha;
KW chondrocyte; proliferation; differentiation; cartilage disorder;
KW bone disorder; arthritis; sports injury; cancer; tumour; diagnosis;
KW adrenal tumour; lung; colon; breast; prostate; kidney; rectum; cervix;
KW liver; drug screening; transgenic animal; genetic analysis;
KW antiarthritic; vulnerary; gene therapy.
XX
OS Homo sapiens.
XX
PN US2003036159-A1.
XX
PD 20-FEB-2003.
XX
PF 02-JUL-2002; 2002US-00188773.
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ID   ABU99562 standard; protein; 335 AA.
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AC   ABU99562;
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DT   09-AUG-2003  (first entry)
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DE   Human secreted/transmembrane protein (PRO) #96.
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KW   Human; secreted and transmembrane protein; PRO; TNF-alpha;
KW   tumour necrosis factor alpha; chondrocyte cell; tumour; gene therapy;
KW   tissue typing.
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XX
PN   US2003040070-A1.
XX
PD   27-FEB-2003.
XX
PF   27-JUN-2002; 2002US-00184627.
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GenCore version 5.1.6

OM protein - protein search, using sw model

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Listing first 700 summaries

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43	1772	100.0	335	6	ABR92260	Abr92260 Human sec
44	1772	100.0	335	6	ABO18901	Abo18901 Human sec
45	1772	100.0	335	6	ABR78322	Abr78322 Human sec
46	1772	100.0	335	6	ABU71974	Abu71974 Novel hum
47	1772	100.0	335	6	ABU85058	Abu85058 Novel hum
48	1772	100.0	335	6	ABO00197	Abo00197 Novel hum
49	1772	100.0	335	6	ABO11529	Abo11529 Human sec
50	1772	100.0	335	6	ABO02174	Abo02174 Human sec
51	1772	100.0	335	6	ABU88748	Abu88748 Novel hum
52	1772	100.0	335	6	ABU83443	Abu83443 Human sec
53	1772	100.0	335	6	ABO06244	Abo06244 Novel hum
54	1772	100.0	335	6	ABR59280	Abr59280 Human sec
55	1772	100.0	335	6	ABO09342	Abo09342 Human sec
56	1772	100.0	335	6	ABO19206	Abo19206 Novel hum
57	1772	100.0	335	6	ABO11224	Abo11224 Human sec
58	1772	100.0	335	6	ABR66842	Abr66842 Human sec
59	1772	100.0	335	6	ABO16055	Abo16055 Human sec
60	1772	100.0	335	6	ABO13761	Abo13761 Human sec
61	1772	100.0	335	6	ABU71528	Abu71528 Human sec
62	1772	100.0	335	6	ABU65664	Abu65664 Human sec
63	1772	100.0	335	6	ABO07512	Abo07512 Human PRO
64	1772	100.0	335	6	ABO03699	Abo03699 Human sec
65	1772	100.0	335	6	ABR67147	Abr67147 Human sec
66	1772	100.0	335	6	ABO15750	Abo15750 Human sec
67	1772	100.0	335	6	ABU56031	Abu56031 Human sec
68	1772	100.0	335	6	ABU72309	Abu72309 Human PRO
69	1772	100.0	335	6	ABU65359	Abu65359 Human PRO
70	1772	100.0	335	6	ABU95304	Abu95304 Novel hum
71	1772	100.0	335	6	ABU71207	Abu71207 Human PRO
72	1772	100.0	335	6	ABO07817	Abo07817 Human PRO
73	1772	100.0	335	6	ABR70058	Abr70058 Human sec
74	1772	100.0	335	6	ABR69391	Abr69391 Human sec
75	1772	100.0	335	6	ABO01532	Abo01532 Human PRO
76	1772	100.0	335	6	ABU81334	Abu81334 Human PRO
77	1772	100.0	335	6	ABR60131	Abr60131 Human sec
78	1772	100.0	335	6	ABU90982	Abu90982 Human PRO
79	1772	100.0	335	6	ABR67866	Abr67866 Human sec
80	1772	100.0	335	6	ABR65254	Abr65254 Human sec
81	1772	100.0	335	6	ABR68476	Abr68476 Human sec
82	1772	100.0	335	6	ABR71888	Abr71888 Human sec
83	1772	100.0	335	6	ABU59264	Abu59264 Human sec
84	1772	100.0	335	6	ABU85368	Abu85368 Human PRO
85	1772	100.0	335	6	ABU89058	Abu89058 Human sec
86	1772	100.0	335	6	ABU83138	Abu83138 Human sec
87	1772	100.0	335	6	ABU94994	Abu94994 Novel hum
88	1772	100.0	335	6	ABU90542	Abu90542 Novel hum
89	1772	100.0	335	6	ABU84053	Abu84053 Human sec
90	1772	100.0	335	6	ABU93704	Abu93704 Novel hum
91	1772	100.0	335	6	ABO25961	Abo25961 Human PRO
92	1772	100.0	335	6	ABR64949	Abr64949 Human sec
93	1772	100.0	335	6	ABO27303	Abo27303 Human sec
94	1772	100.0	335	6	ABR68781	Abr68781 Human sec
95	1772	100.0	335	6	ABO06597	Abo06597 Human sec
96	1772	100.0	335	6	ABR99142	Abr99142 Human sec
97	1772	100.0	335	6	ABU57026	Abu57026 Human PRO
98	1772	100.0	335	6	ABU85978	Abu85978 Novel hum

99	1772	100.0	335	6	ABU82265	Abu82265 Novel hum		172	1772	100.0	335	6	ABO44026	Abo44026 Human PRO
100	1772	100.0	335	6	ABU87276	Abu87276 Human PRO		173	1772	100.0	335	6	ADA77944	Ada77944 Human sec
101	1772	100.0	335	6	ABU83748	Abu83748 Human sec		174	1772	100.0	335	6	ABM24821	Abm24821 Human sec
102	1772	100.0	335	6	ABO08122	Abo08122 Human PRO		175	1772	100.0	335	6	ABO03089	Abo03089 Human sec
103	1772	100.0	335	6	ABU92498	Abu92498 Human sec		176	1772	100.0	335	6	ABR90345	Abr90345 Human sec
104	1772	100.0	335	6	ABU81833	Abu81833 Novel hum		177	1772	100.0	335	6	ABM17259	Abm17259 Human sec
105	1772	100.0	335	6	ABU65997	Abu65997 Novel hum		178	1772	100.0	335	6	ABR95005	Abr95005 Human sec
106	1772	100.0	335	6	ABU81168	Abu81168 Human sec		179	1772	100.0	335	6	ABR95310	Abr95310 Human sec
107	1772	100.0	335	6	ABR59826	Abr59826 Human sec		180	1772	100.0	335	6	ADB17103	Adb17103 Human tra
108	1772	100.0	335	6	ABU94014	Abu94014 Novel hum		181	1772	100.0	335	6	ABO21548	Abo21548 Human sec
109	1772	100.0	335	6	ABU99867	Abu99867 Novel hum		182	1772	100.0	335	6	ABR97812	Abr97812 Human sec
110	1772	100.0	335	6	ABR66537	Abr66537 Human sec		183	1772	100.0	335	6	ABR87600	Abr87600 Human sec
111	1772	100.0	335	6	ABR90955	Abr90955 Human sec		184	1772	100.0	335	6	ABM77641	Abm77641 Human sec
112	1772	100.0	335	6	ABO53283	Abo53283 Novel hum		185	1772	100.0	335	6	ABM27871	Abm27871 Human sec
113	1772	100.0	335	6	ABU58970	Abu58970 Human sec		186	1772	100.0	335	6	ABM06152	Abm06152 Human sec
114	1772	100.0	335	6	ABU94382	Abu94382 Human PRO		187	1772	100.0	335	6	ABM03658	Abm03658 Human sec
115	1772	100.0	335	6	ABU79264	Abu79264 Human PRO		188	1772	100.0	335	6	ABM35109	Abm35109 Human sec
116	1772	100.0	335	6	ABU86593	Abu86593 Human sec		189	1772	100.0	335	6	ABM26346	Abm26346 Human sec
117	1772	100.0	335	6	ABU86898	Abu86898 Novel hum		190	1772	100.0	335	6	ABO48128	Abo48128 Human sec
118	1772	100.0	335	6	ABU94687	Abu94687 Human PRO		191	1772	100.0	335	6	ABR92870	Abr92870 Human sec
119	1772	100.0	335	6	ABO04614	Abo04614 Human PRO		192	1772	100.0	335	6	ABO24631	Abo24631 Human sec
120	1772	100.0	335	6	ABR70363	Abr70363 Human sec		193	1772	100.0	335	6	ADA37764	Ada37764 Human sec
121	1772	100.0	335	6	ABU92348	Abu92348 Novel hum		194	1772	100.0	335	6	ABM11642	Abm11642 Human sec
122	1772	100.0	335	6	ABU98528	Abu98528 Human PRO		195	1772	100.0	335	6	ABM02743	Abm02743 Human sec
123	1772	100.0	335	6	ABR65927	Abr65927 Human sec		196	1772	100.0	335	6	ABM16039	Abm16039 Human sec
124	1772	100.0	335	6	ABR64644	Abr64644 Human sec		197	1772	100.0	335	6	ABO27600	Abo27600 Human sec
125	1772	100.0	335	6	ABU59413	Abu59413 Novel hum		198	1772	100.0	335	6	ABM29091	Abm29091 Human sec
126	1772	100.0	335	6	ABU79569	Abu79569 Human PRO		199	1772	100.0	335	6	ABM07067	Abm07067 Human sec
127	1772	100.0	335	6	ABU92960	Abu92960 Human sec		200	1772	100.0	335	6	ABM21161	Abm21161 Human sec
128	1772	100.0	335	6	ABU95919	Abu95919 Human PRO		201	1772	100.0	335	6	ABM09507	Abm09507 Human sec
129	1772	100.0	335	6	ABU91139	Abu91139 Novel hum		202	1772	100.0	335	6	ABO41377	Abo41377 Human sec
130	1772	100.0	335	6	ABU90232	Abu90232 Novel hum		203	1772	100.0	335	6	ABO36192	Abo36192 Human PRO
131	1772	100.0	335	6	ABO09647	Abo09647 Human sec		204	1772	100.0	335	6	ABO43721	Abo43721 Human PRO
132	1772	100.0	335	6	ABR58417	Abr58417 Human NOV		205	1772	100.0	335	6	ABM76421	Abm76421 Human sec
133	1772	100.0	335	6	ABO10919	Abo10919 Human sec		206	1772	100.0	335	6	ABM76117	Abm76117 Human sec
134	1772	100.0	335	6	ABR70973	Abr70973 Human sec		207	1772	100.0	335	6	ABM25736	Abm25736 Human sec
135	1772	100.0	335	6	ABU98285	Abu98285 Novel hum		208	1772	100.0	335	6	ABM26041	Abm26041 Human sec
136	1772	100.0	335	6	ABU87581	Abu87581 Human PRO		209	1772	100.0	335	6	ADA21450	Ada21450 Human sec
137	1772	100.0	335	6	ABU91449	Abu91449 Human PRO		210	1772	100.0	335	6	ABO03394	Abo03394 Human sec
138	1772	100.0	335	6	ABU89290	Abu89290 Novel hum		211	1772	100.0	335	6	ABO02479	Abo02479 Human sec
139	1772	100.0	335	6	ABU84663	Abu84663 Human sec		212	1772	100.0	335	6	ABO44261	Abo44261 Human sec
140	1772	100.0	335	6	ABR69753	Abr69753 Human sec		213	1772	100.0	335	6	ABR90650	Abr90650 Human sec
141	1772	100.0	335	6	ABU80130	Abu80130 Human PRO		214	1772	100.0	335	6	ABR73718	Abr73718 Human sec
142	1772	100.0	335	6	ABU82497	Abu82497 Novel hum		215	1772	100.0	335	6	ABO16970	Abo16970 Human sec
143	1772	100.0	335	6	ABU92179	Abu92179 Novel hum		216	1772	100.0	335	6	ABR94395	Abr94395 Human sec
144	1772	100.0	335	6	ABU93399	Abu93399 Human PRO		217	1772	100.0	335	6	ABR75902	Abr75902 Human sec
145	1772	100.0	335	6	ABO09952	Abo09952 Human sec		218	1772	100.0	335	6	ABR71278	Abr71278 Human sec
146	1772	100.0	335	6	ABO09037	Abo09037 Human sec		219	1772	100.0	335	6	ABR93175	Abr93175 Human sec
147	1772	100.0	335	6	ABU96461	Abu96461 Human PRO		220	1772	100.0	335	6	ABR93480	Abr93480 Human sec
148	1772	100.0	335	6	ABU10885	Abu10885 Human PRO		221	1772	100.0	335	6	ADA10237	Ada10237 Human sec
149	1772	100.0	335	6	ABU10605	Abu10605 Human sec		222	1772	100.0	335	6	ABR87905	Abr87905 Human sec
150	1772	100.0	335	6	ABU81637	Abu81637 Novel hum		223	1772	100.0	335	6	ABO27905	Abo27905 Human sec
151	1772	100.0	335	6	ABU72131	Abu72131 Human PRO		224	1772	100.0	335	6	ABO30040	Abo30040 Human sec
152	1772	100.0	335	6	ABU95614	Abu95614 Human PRO		225	1772	100.0	335	6	ABO33249	Abo33249 Human PRO
153	1772	100.0	335	6	ABU96823	Abu96823 Novel hum		226	1772	100.0	335	6	ABM04937	Abm04937 Human sec
154	1772	100.0	335	6	ABR70668	Abr70668 Human sec		227	1772	100.0	335	6	ABM08897	Abm08897 Human sec
155	1772	100.0	335	6	ABO05019	Abo05019 Novel hum		228	1772	100.0	335	6	ABO36497	Abo36497 Human sec
156	1772	100.0	335	6	ABO08427	Abo08427 Human sec		229	1772	100.0	335	6	ABO35582	Abo35582 Human PRO
157	1772	100.0	335	6	ABU88576	Abu88576 Human sec		230	1772	100.0	335	6	ABO39547	Abo39547 Human sec
158	1772	100.0	335	6	ABO34090	Abo34090 Human PRO		231	1772	100.0	335	6	ABM10422	Abm10422 Human sec
159	1772	100.0	335	6	ABO05634	Abo05634 Human sec		232	1772	100.0	335	6	ABM11947	Abm11947 Human sec
160	1772	100.0	335	6	ABR74023	Abr74023 Human sec		233	1772	100.0	335	6	ABO52093	Abo52093 Human PRO
161	1772	100.0	335	6	ABR95615	Abr95615 Human sec		234	1772	100.0	335	6	ABO52398	Abo52398 Human PRO
162	1772	100.0	335	6	ABR80912	Abr80912 Human sec		235	1772	100.0	335	6	ADA19908	Ada19908 Novel hum
163	1772	100.0	335	6	ABR81217	Abr81217 Human sec		236	1772	100.0	335	6	ABO23716	Abo23716 Human sec
164	1772	100.0	335	6	ABM00913	Abm00913 Human sec		237	1772	100.0	335	6	ADB17291	Adb17291 Human tra
165	1772	100.0	335	6	ABR88515	Abr88515 Human sec		238	1772	100.0	335	6	ADA17781	Ada17781 Human PRO
166	1772	100.0	335	6	ABM77336	Abm77336 Human sec		239	1772	100.0	335	6	ABR97202	Abr97202 Human sec
167	1772	100.0	335	6	ABO28820	Abo28820 Human sec		240	1772	100.0	335	6	ABR86990	Abr86990 Human sec
168	1772	100.0	335	6	ABO31565	Abo31565 Human sec		241	1772	100.0	335	6	ABM11032	Abm11032 Human sec
169	1772	100.0	335	6	ABM07982	Abm07982 Human sec		242	1772	100.0	335	6	ABM28176	Abm28176 Human sec
170	1772	100.0	335	6	ABO40462	Abo40462 Human sec		243	1772	100.0	335	6	ABO32175	Abo32175 Human sec
171	1772	100.0	335	6	ABO35887	Abo35887 Human PRO		244	1772	100.0	335	6	ABM15302	Abm15302 Human sec

245	1772	100.0	335	6	ABM06457	Abm06457 Human sec	
246	1772	100.0	335	6	ABM04268	Abm04268 Human sec	
247	1772	100.0	335	6	ABM22381	Abm22381 Human sec	
248	1772	100.0	335	6	ABM07677	Abm07677 Human sec	
249	1772	100.0	335	6	ABO40767	Abo40767 Human sec	
250	1772	100.0	335	6	ABM35414	Abm35414 Human sec	
251	1772	100.0	335	6	ABM33177	Abm33177 Human sec	
252	1772	100.0	335	6	ABO52703	Abo52703 Human PRO	
253	1772	100.0	335	6	ABO50263	Abo50263 Human sec	
254	1772	100.0	335	6	ABU99257	Abu99257 Human sec	
255	1772	100.0	335	6	ABO04309	Abo04309 Human sec	
256	1772	100.0	335	6	ABO05939	Abo05939 Human sec	
257	1772	100.0	335	6	ABM18479	Abm18479 Human sec	
258	1772	100.0	335	6	ADA27889	Ada27889 Human sec	
259	1772	100.0	335	6	ABR97507	Abr97507 Human sec	
260	1772	100.0	335	6	ABR80607	Abr80607 Human sec	
261	1772	100.0	335	6	ABM01218	Abm01218 Human sec	
262	1772	100.0	335	6	ABR88820	Abr88820 Human sec	
263	1772	100.0	335	6	ABM13472	Abm13472 Human sec	
264	1772	100.0	335	6	ABM20856	Abm20856 Human sec	
265	1772	100.0	335	6	ABO41987	Abo41987 Human sec	
266	1772	100.0	335	6	ABO42597	Abo42597 Human sec	
267	1772	100.0	335	6	ABM10117	Abm10117 Human sec	
268	1772	100.0	335	6	ABO38632	Abo38632 Human sec	
269	1772	100.0	335	6	ABM32872	Abm32872 Human sec	
270	1772	100.0	335	6	ABM22686	Abm22686 Human sec	
271	1772	100.0	335	6	ABM74897	Abm74897 Human sec	
272	1772	100.0	335	6	ADA79736	Ada79736 Human sec	
273	1772	100.0	335	6	ABR96287	Abr96287 Human sec	
274	1772	100.0	335	6	ABM02438	Abm02438 Human sec	
275	1772	100.0	335	6	ABR86380	Abr86380 Human sec	
276	1772	100.0	335	6	ABR86685	Abr86685 Human sec	
277	1772	100.0	335	6	ABM16649	Abm16649 Human sec	
278	1772	100.0	335	6	ABM29701	Abm29701 Human sec	
279	1772	100.0	335	6	ABO29125	Abo29125 Human sec	
280	1772	100.0	335	6	ABM23906	Abm23906 Human sec	
281	1772	100.0	335	6	ABM23296	Abm23296 Human sec	
282	1772	100.0	335	6	ABM22076	Abm22076 Human sec	
283	1772	100.0	335	6	ABO37717	Abo37717 Human sec	
284	1772	100.0	335	6	ABM28481	Abm28481 Human sec	
285	1772	100.0	335	6	ABM28786	Abm28786 Human sec	
286	1772	100.0	335	6	ABM66430	Abm66430 Human sec	
287	1772	100.0	335	6	ABM75812	Abm75812 Human sec	
288	1772	100.0	335	6	ABM34092	Abm34092 Human sec	
289	1772	100.0	335	6	ABM34397	Abm34397 Human sec	
290	1772	100.0	335	6	ABO20328	Abo20328 Human sec	
291	1772	100.0	335	6	ABO21243	Abo21243 Human sec	
292	1772	100.0	335	6	ABO22158	Abo22158 Human sec	
293	1772	100.0	335	6	ADA20080	Ada20080 Novel hum	
294	1772	100.0	335	6	ABO34189	Abo34189 Human sec	
295	1772	100.0	335	6	ABR96592	Abr96592 Human sec	
296	1772	100.0	335	6	ADA94469	Ada94469 Human sec	
297	1772	100.0	335	6	ABR85770	Abr85770 Human sec	
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303	1772	100.0	335	6	ABM29396	Abm29396 Human sec	
304	1772	100.0	335	6	ABO38327	Abo38327 Human sec	
305	1772	100.0	335	6	ABO45627	Abo45627 Human PRO	
306	1772	100.0	335	6	ABM20551	Abm20551 Human sec	
307	1772	100.0	335	6	ADA81463	Ada81463 Human sec	
308	1772	100.0	335	6	ABO16665	Abo16665 Human sec	
309	1772	100.0	335	6	ABO18291	Abo18291 Human sec	
310	1772	100.0	335	6	ABO22718	Abo22718 Human PRO	
311	1772	100.0	335	6	ABO23023	Abo23023 Human PRO	
312	1772	100.0	335	6	ABR92565	Abr92565 Human sec	
313	1772	100.0	335	6	ABR81522	Abr81522 Human sec	
314	1772	100.0	335	6	ABM77946	Abm77946 Human sec	
315	1772	100.0	335	6	ABR89735	Abr89735 Human sec	
316	1772	100.0	335	6	ABM26651	Abm26651 Human sec	
317	1772	100.0	335	6	ABM13777	Abm13777 Human sec	
318	1772	100.0	335	6	ABO28515	Abo28515 Human sec	
319	1772	100.0	335	6	ABO30345	Abo30345 Human sec	
320	1772	100.0	335	6	ABM07372	Abm07372 Human sec	
321	1772	100.0	335	6	ABM03963	Abm03963 Human sec	
322	1772	100.0	335	6	ABO37107	Abo37107 Human sec	
323	1772	100.0	335	6	ABO41682	Abo41682 Human sec	
324	1772	100.0	335	6	ABO35277	Abo35277 Human PRO	
325	1772	100.0	335	6	ABM25126	Abm25126 Human sec	
326	1772	100.0	335	6	ABO47518	Abo47518 Human sec	
327	1772	100.0	335	6	ABO47823	Abo47823 Human sec	
328	1772	100.0	335	6	ABO48433	Abo48433 Human sec	
329	1772	100.0	335	6	ABO51483	Abo51483 Human PRO	
330	1772	100.0	335	6	ABO51788	Abo51788 Human PRO	
331	1772	100.0	335	6	ABO50568	Abo50568 Human sec	
332	1772	100.0	335	6	ABR79692	Abr79692 Human sec	
333	1772	100.0	335	6	ABM16954	Abm16954 Human sec	
334	1772	100.0	335	6	ABO17986	Abo17986 Human sec	
335	1772	100.0	335	6	ABO20938	Abo20938 Human sec	
336	1772	100.0	335	6	ABR96897	Abr96897 Human sec	
337	1772	100.0	335	6	ADA38694	Ada38694 Human sec	
338	1772	100.0	335	6	ABM12252	Abm12252 Human sec	
339	1772	100.0	335	6	ABM16344	Abm16344 Human sec	
340	1772	100.0	335	6	ABM24211	Abm24211 Human sec	
341	1772	100.0	335	6	ABM14692	Abm14692 Human sec	
342	1772	100.0	335	6	ABM04573	Abm04573 Human sec	
343	1772	100.0	335	6	ABM06762	Abm06762 Human sec	
344	1772	100.0	335	6	ABM09202	Abm09202 Human sec	
345	1772	100.0	335	6	ABO39242	Abo39242 Human sec	
346	1772	100.0	335	6	ABM75507	Abm75507 Human sec	
347	1772	100.0	335	6	ABM25431	Abm25431 Human sec	
348	1772	100.0	335	6	ABM19941	Abm19941 Human sec	
349	1772	100.0	335	6	ABO46847	Abo46847 Human PRO	
350	1772	100.0	335	6	ABO47152	Abo47152 Human PRO	
351	1772	100.0	335	6	ADA83261	Ada83261 Human sec	
352	1772	100.0	335	6	ABR71583	Abr71583 Human sec	
353	1772	100.0	335	6	ABR72193	Abr72193 Human sec	
354	1772	100.0	335	6	ABR98532	Abr98532 Human sec	
355	1772	100.0	335	6	ABO06902	Abo06902 Human sec	
356	1772	100.0	335	6	ABR84855	Abr84855 Human sec	
357	1772	100.0	335	6	ABR73413	Abr73413 Human sec	
358	1772	100.0	335	6	ABR76507	Abr76507 Human sec	
359	1772	100.0	335	6	ABR73108	Abr73108 Human sec	
360	1772	100.0	335	6	ABM18174	Abm18174 Human sec	
361	1772	100.0	335	6	ABO20633	Abo20633 Human sec	
362	1772	100.0	335	6	ABO25376	Abo25376 Human PRO	
363	1772	100.0	335	6	ABO25681	Abo25681 Human PRO	
364	1772	100.0	335	6	ABR94090	Abr94090 Human sec	
365	1772	100.0	335	6	ADA92815	Ada92815 Human sec	
366	1772	100.0	335	6	ABR79997	Abr79997 Human sec	
367	1772	100.0	335	6	ABM11337	Abm11337 Human sec	
368	1772	100.0	335	6	ABO32944	Abo32944 Human PRO	
369	1772	100.0	335	6	ABO30650	Abo30650 Human sec	
370	1772	100.0	335	6	ABO30955	Abo30955 Human sec	
371	1772	100.0	335	6	ABM27261	Abm27261 Human sec	
372	1772	100.0	335	6	ABM30006	Abm30006 Human sec	
373	1772	100.0	335	6	ABM05542	Abm05542 Human sec	
374	1772	100.0	335	6	ABM15607	Abm15607 Human sec	
375	1772	100.0	335	6	ABM08592	Abm08592 Human sec	
376	1772	100.0	335	6	ABO42292	Abo42292 Human sec	
377	1772	100.0	335	6	ABO38022	Abo38022 Human sec	
378	1772	100.0	335	6	ABO45932	Abo45932 Human PRO	
379	1772	100.0	335	6	ABM66735	Abm66735 Human sec	
380	1772	100.0	335	6	ADB20304	Adb20304 Human sec	
381	1772	100.0	335	6	ABM19636	Abm19636 Human sec	
382	1772	100.0	335	6	ABO49348	Abo49348 Human sec	
383	1772	100.0	335	6	ABO49653	Abo49653 Human sec	
384	1772	100.0	335	6	ADA78556	Ada78556 Human sec	
385	1772	100.0	335	6	ABR88210	Abr88210 Human sec	
386	1772	100.0	335	6	ADA00377	Ada00377 Human sec	
387	1772	100.0	335	6	ABM26956	Abm26956 Human sec	
388	1772	100.0	335	6	ABM03353	Abm03353 Human sec	
389	1772	100.0	335	6	ABO39852	Abo39852 Human sec	
390	1772	100.0	335	7	ABO49958	Abo49958 Human sec	

391	1772	100.0	335	7	ABO50873	Abo50873 Human sec
392	1772	100.0	335	7	ABO05329	Abo05329 Human sec
393	1772	100.0	335	7	ABR74633	Abr74633 Human sec
394	1772	100.0	335	7	ABR77112	Abr77112 Human sec
395	1772	100.0	335	7	ABM17869	Abm17869 Human sec
396	1772	100.0	335	7	ABR95920	Abr95920 Human sec
397	1772	100.0	335	7	ABO21853	Abo21853 Human sec
398	1772	100.0	335	7	ABO20023	Abo20023 Human sec
399	1772	100.0	335	7	ABO24326	Abo24326 Human sec
400	1772	100.0	335	7	ABR86075	Abr86075 Human sec
401	1772	100.0	335	7	ABM10727	Abm10727 Human sec
402	1772	100.0	335	7	ABM76726	Abm76726 Human sec
403	1772	100.0	335	7	ABR89430	Abr89430 Human sec
404	1772	100.0	335	7	ABM12557	Abm12557 Human sec
405	1772	100.0	335	7	ABM05847	Abm05847 Human sec
406	1772	100.0	335	7	ABO34972	Abo34972 Human PRO
407	1772	100.0	335	7	ABM03048	Abm03048 Human sec
408	1772	100.0	335	7	ABM19026	Abm19026 Human sec
409	1772	100.0	335	7	ABM19331	Abm19331 Human sec
410	1772	100.0	335	7	ABO46542	Abo46542 Human PRO
411	1772	100.0	335	7	ABO49043	Abo49043 Human sec
412	1772	100.0	335	7	ABR69086	Abr69086 Human sec
413	1772	100.0	335	7	ABR89125	Abr89125 Human sec
414	1772	100.0	335	7	ABR72498	Abr72498 Human sec
415	1772	100.0	335	7	ABR74328	Abr74328 Human sec
416	1772	100.0	335	7	ABO18596	Abo18596 Human sec
417	1772	100.0	335	7	ABR80302	Abr80302 Human sec
418	1772	100.0	335	7	ABM01523	Abm01523 Human sec
419	1772	100.0	335	7	ABM02133	Abm02133 Human sec
420	1772	100.0	335	7	ABR87295	Abr87295 Human sec
421	1772	100.0	335	7	ABM12862	Abm12862 Human sec
422	1772	100.0	335	7	ABM30616	Abm30616 Human sec
423	1772	100.0	335	7	ABM24516	Abm24516 Human sec
424	1772	100.0	335	7	ABO29430	Abo29430 Human sec
425	1772	100.0	335	7	ABO31260	Abo31260 Human sec
426	1772	100.0	335	7	ABM14387	Abm14387 Human sec
427	1772	100.0	335	7	ABM09812	Abm09812 Human sec
428	1772	100.0	335	7	ABO38937	Abo38937 Human sec
429	1772	100.0	335	7	ABM34702	Abm34702 Human sec
430	1772	100.0	335	7	ABO51178	Abo51178 Human sec
431	1772	100.0	335	7	ABO04004	Abo04004 Human sec
432	1772	100.0	335	7	ABO10474	Abo10474 Human PRO
433	1772	100.0	335	7	ABO53176	Abo53176 Human sec
434	1772	100.0	335	7	ABR77717	Abr77717 Human sec
435	1772	100.0	335	7	ABR78927	Abr78927 Human sec
436	1772	100.0	335	7	ABO24021	Abo24021 Human sec
437	1772	100.0	335	7	ABR93785	Abr93785 Human sec
438	1772	100.0	335	7	ABM01828	Abm01828 Human sec
439	1772	100.0	335	7	ABM78251	Abm78251 Human sec
440	1772	100.0	335	7	ABR90040	Abr90040 Human sec
441	1772	100.0	335	7	ADA22376	Ada22376 Human sec
442	1772	100.0	335	7	ABM27566	Abm27566 Human sec
443	1772	100.0	335	7	ABM13167	Abm13167 Human sec
444	1772	100.0	335	7	ABO31870	Abo31870 Human sec
445	1772	100.0	335	7	ABM14082	Abm14082 Human sec
446	1772	100.0	335	7	ABM08287	Abm08287 Human sec
447	1772	100.0	335	7	ABO40157	Abo40157 Human sec
448	1772	100.0	335	7	ABM74592	Abm74592 Human sec
449	1772	100.0	335	7	ABM33787	Abm33787 Human sec
450	1772	100.0	335	7	ABM20246	Abm20246 Human sec
451	1772	100.0	335	7	ABO48738	Abo48738 Human sec
452	1772	100.0	335	7	ABO22546	Abo22546 Human sec
453	1772	100.0	335	7	ABR72803	Abr72803 Human sec
454	1772	100.0	335	7	ABO15445	Abo15445 Human sec
455	1772	100.0	335	7	ABR85160	Abr85160 Human sec
456	1772	100.0	335	7	ABO15140	Abo15140 Human sec
457	1772	100.0	335	7	ABO17275	Abo17275 Human sec
458	1772	100.0	335	7	ABM17564	Abm17564 Human sec
459	1772	100.0	335	7	ADA06542	Ada06542 Human sec
460	1772	100.0	335	7	ADA39235	Ada39235 Human sec
461	1772	100.0	335	7	ABR85465	Abr85465 Human sec
462	1772	100.0	335	7	ABM77031	Abm77031 Human sec
463	1772	100.0	335	7	ABO28210	Abo28210 Human sec
464	1772	100.0	335	7	ABM22991	Abm22991 Human sec
465	1772	100.0	335	7	ABM30311	Abm30311 Human sec
466	1772	100.0	335	7	ABM21771	Abm21771 Human sec
467	1772	100.0	335	7	ABM21466	Abm21466 Human sec
468	1772	100.0	335	7	ABM14997	Abm14997 Human sec
469	1772	100.0	335	7	ABO41072	Abo41072 Human sec
470	1772	100.0	335	7	ABO36802	Abo36802 Human sec
471	1772	100.0	335	7	ABO37412	Abo37412 Human sec
472	1772	100.0	335	7	ABM75202	Abm75202 Human sec
473	1772	100.0	335	7	ABM33482	Abm33482 Human sec
474	1772	100.0	335	7	ABO46237	Abo46237 Human PRO
475	1772	100.0	335	7	ADA82627	Ada82627 Human sec
476	1772	100.0	335	7	ADB85619	Adb85619 Novel hum
477	1772	100.0	335	7	ADB96261	Adb96261 Human PRO
478	1772	100.0	335	7	ABM31836	Abm31836 Human sec
479	1772	100.0	335	7	ABM31226	Abm31226 Human sec
480	1772	100.0	335	7	ADB85935	Adb85935 Human sec
481	1772	100.0	335	7	ABM32141	Abm32141 Human sec
482	1772	100.0	335	7	ABM32446	Abm32446 Human sec
483	1772	100.0	335	7	ADB68298	Adb68298 Human PRO
484	1772	100.0	335	7	ADB68105	Adb68105 Human PRO
485	1772	100.0	335	7	ABM31531	Abm31531 Human sec
486	1772	100.0	335	7	ABM30921	Abm30921 Human sec
487	1772	100.0	335	7	ADB90922	Adb90922 Novel hum
488	1772	100.0	335	7	ADC57733	Adc57733 Human PRO
489	1772	100.0	335	7	ADC55097	Adc55097 Human PRO
490	1772	100.0	335	7	ADC11964	Adc11964 Human sec
491	1772	100.0	335	7	ADC07002	Adc07002 Human PRO
492	1772	100.0	335	7	ADC56386	Adc56386 Human PRO
493	1772	100.0	335	7	ADC17181	Adc17181 Mammalian
494	1772	100.0	335	7	ADC07441	Adc07441 Human sec
495	1772	100.0	335	7	ADC11431	Adc11431 Human sec
496	1772	100.0	335	7	ADC14879	Adc14879 Novel hum
497	1772	100.0	335	7	ADC52374	Adc52374 Novel hum
498	1772	100.0	335	7	ADC14553	Adc14553 Novel hum
499	1772	100.0	335	7	ADD08085	Add08085 Novel hum
500	1772	100.0	335	7	ADC81910	Adc81910 Human PRO
501	1772	100.0	335	7	ADD07552	Add07552 Novel hum
502	1772	100.0	335	7	ADC82443	Adc82443 Human PRO
503	1772	100.0	335	7	ADD05665	Add05665 Human sec
504	1772	100.0	335	7	ADD08623	Add08623 Novel hum
505	1772	100.0	335	7	ADD06872	Add06872 Novel hum
506	1772	100.0	335	7	ADC89503	Adc89503 Human nat
507	1772	100.0	335	7	ADC83119	Adc83119 Human PRO
508	1772	100.0	335	7	ADD67525	Add67525 Human Lyl
509	1772	100.0	335	7	ADD55226	Add55226 Human PRO
510	1772	100.0	335	7	ADD36050	Add36050 Novel hum
511	1772	100.0	335	7	ADD56184	Add56184 Human PRO
512	1772	100.0	335	7	ADD54622	Add54622 Human PRO
513	1772	100.0	335	7	ADE26776	Ade26776 Novel hum
514	1772	100.0	335	7	ADE26243	Ade26243 Novel hum
515	1772	100.0	335	8	ADC52184	Adc52184 Novel hum
516	1772	100.0	335	8	ADE74329	Ade74329 Human sec
517	1772	100.0	335	8	ADE74941	Ade74941 Human sec
518	1772	100.0	336	3	AAB32373	Aab32373 Human sec
519	1769	99.8	335	7	ADD18672	Add18672 Human dis
520	1755.5	99.1	348	6	ABR58418	Abr58418 Human NOV
521	1653	93.3	312	3	AAY44610	Aay44610 Mature hu
522	1392.5	78.6	328	5	ABB97473	Abb97473 Novel hum
523	933.5	52.7	684	4	ABG11697	Abg11697 Novel hum
524	933.5	52.7	684	4	ABG12169	Abg12169 Novel hum
525	622	35.1	124	2	AAY12645	Aay12645 Human 5'
526	582	32.8	110	2	AAW67811	Aaw67811 Human sec
527	582	32.8	110	3	AAB32405	Aab32405 Human sec
528	582	32.8	110	6	ADA57321	Ada57321 Human sec
529	582	32.8	110	6	ADA56750	Ada56750 Human sec
530	582	32.8	110	6	ADA40601	Ada40601 Human sec
531	582	32.8	110	6	ADA41198	Ada41198 Human sec
532	498	28.1	97	3	AAG00391	Aag00391 Human sec
533	498	28.1	98	2	AAY11662	Aay11662 Human 5'
534	471	26.6	91	4	AAM21122	Aam21122 Peptide #
535	471	26.6	91	4	ABB43438	Abb43438 Peptide #
536	471	26.6	91	4	AAM37326	Aam37326 Peptide #

537	471	26.6	91	4	ABB26408	Abb26408 Protein #
538	471	26.6	91	4	AAM77190	Aam77190 Human bon
539	471	26.6	91	4	AAM64367	Aam64367 Human bra
540	471	26.6	91	4	ABG58815	Abg58815 Human liv
541	471	26.6	91	5	ABG46203	Abg46203 Human pep
542	445	25.1	90	3	AAB32404	Aab32404 Human sec
543	362.5	20.5	328	5	AAB47878	Aab47878 SCZ/CD84.
544	362.5	20.5	328	5	AAE26238	Aae26238 Human CD8
545	362.5	20.5	329	2	AAW74891	Aaw74891 Human sec
546	362.5	20.5	329	5	ABG95343	Abg95343 Human nov
547	362.5	20.5	329	6	ABO34537	Abo34537 Region of
548	343	19.4	629	5	AAU74424	Aau74424 Mouse pro
549	333.5	18.8	289	5	AAE26250	Aae26250 Human CD2
550	330.5	18.7	289	4	AAE12078	Aae12078 Dendritic
551	330.5	18.7	289	5	AAE26243	Aae26243 Human CD2
552	330.5	18.7	289	5	AAE26253	Aae26253 Human CD2
553	330.5	18.7	289	5	ABP65110	Abp65110 Hypoxia-i
554	327.5	18.5	289	5	AAE26251	Aae26251 Human CD2
555	327.5	18.5	289	5	AAE26252	Aae26252 Human CD2
556	327	18.5	270	5	AAE26244	Aae26244 Human CD2
557	319.5	18.0	331	5	AAE26239	Aae26239 Human CD2
558	315.5	17.8	309	5	AAE26222	Aae26222 Human CD2
559	315.5	17.8	331	5	ABB90183	Abb90183 Human pol
560	315.5	17.8	331	5	AAE26220	Aae26220 Human CD2
561	315.5	17.8	331	6	ABR39107	Abr39107 Human NTB
562	315.5	17.8	331	6	ABU03145	Abu03145 Human imm
563	315.5	17.8	331	7	ADC52556	Adc52556 human den
564	315.5	17.8	346	5	AAU09868	Aau09868 Novel hum
565	314.5	17.7	331	5	AAE26241	Aae26241 Human CD2
566	313.5	17.7	331	5	AAE26240	Aae26240 Human CD2
567	312.5	17.6	610	5	AAU74425	Aau74425 Human pro
568	311.5	17.6	331	5	AAE26242	Aae26242 Human CD2
569	311	17.6	332	4	AAG63166	Aag63166 Amino aci
570	311	17.6	332	5	ABG96267	Abg96267 Human imm
571	311	17.6	332	5	ABG34067	Abg34067 Human Pro
572	311	17.6	332	6	ABU03170	Abu03170 Human imm
573	311	17.6	332	6	ADA37159	Ada37159 Human PRO
574	311	17.6	332	6	ADA01344	Ada01344 Human PRO
575	311	17.6	332	6	ADA43773	Ada43773 Human sec
576	311	17.6	332	6	ADA43541	Ada43541 Human sec
577	311	17.6	332	6	ADA01216	Ada01216 Human PRO
578	311	17.6	332	7	ADA01100	Ada01100 Human sec
579	311	17.6	332	7	ADA43657	Ada43657 Human sec
580	311	17.6	332	7	ADA06919	Ada06919 Human PRO
581	311	17.6	332	7	ADA08407	Ada08407 Novel hum
582	311	17.6	332	7	ADB99700	Adb99700 Human PRO
583	311	17.6	332	7	ADB86983	Adb86983 Human PRO
584	311	17.6	332	7	ADB66138	Adb66138 Human sec
585	311	17.6	332	7	ADB99816	Adb99816 Human PRO
586	311	17.6	332	7	ADB99471	Adb99471 Novel hum
587	311	17.6	332	7	ADB66022	Adb66022 Human sec
588	311	17.6	332	7	ADC23420	Adc23420 Human tra
589	311	17.6	332	7	ADC26113	Adc26113 Human PRO
590	311	17.6	332	7	ADE04940	Ade04940 Human PRO
591	311	17.6	332	7	ADE11246	Ade11246 Human PRO
592	311	17.6	332	7	ADD88177	Add88177 Human PRO
593	311	17.6	332	7	ADD95472	Add95472 Human sec
594	311	17.6	332	7	ADE06402	Ade06402 Human PRO
595	311	17.6	332	7	ADE38177	Ade38177 Human PRO
596	311	17.6	332	7	ADD88293	Add88293 Human PRO
597	311	17.6	332	7	ADD90874	Add90874 Human sec
598	311	17.6	332	8	ADE51727	Ade51727 Human sec
599	311	17.6	332	8	ADE51843	Ade51843 Human sec
600	311	17.6	332	8	ADE37701	Ade37701 Human sec
601	311	17.6	332	8	ADE37585	Ade37585 Human sec
602	311	17.6	332	8	ADD95356	Add95356 Human sec
603	311	17.6	332	8	ADE52379	Ade52379 Human PRO
604	311	17.6	332	8	ADE38056	Ade38056 Human PRO
605	311	17.6	332	8	ADE76145	Ade76145 Human PRO
606	311	17.6	332	8	ADE39468	Ade39468 Human PRO
607	311	17.6	332	8	ADE04272	Ade04272 Human PRO
608	311	17.6	332	8	ADE39869	Ade39869 Human PRO
609	311	17.6	332	8	ADE19734	Ade19734 Human PRO
610	311	17.6	332	8	ADE77312	Ade77312 Human sec
611	311	17.6	332	8	ADE65420	Ade65420 Human PRO
612	311	17.6	332	8	ADE76029	Ade76029 Human PRO
613	311	17.6	332	8	ADE37940	Ade37940 Human PRO
614	311	17.6	332	8	ADE64550	Ade64550 Human PRO
615	311	17.6	332	8	ADE38885	Ade38885 Human PRO
616	311	17.6	332	8	ADE51959	Ade51959 Human sec
617	311	17.6	332	8	ADD90990	Add90990 Human sec
618	311	17.6	332	8	ADE38769	Ade38769 Human PRO
619	311	17.6	332	8	ADE37469	Ade37469 Human sec
620	311	17.6	332	8	ADE06286	Ade06286 Human PRO
621	311	17.6	332	8	ADD90145	Add90145 Human sec
622	311	17.6	332	8	ADE38653	Ade38653 Human PRO
623	311	17.6	332	8	ADE39584	Ade39584 Human PRO
624	311	17.6	332	8	ADD89189	Add89189 Human PRO
625	311	17.6	332	8	ADD88956	Add88956 Human PRO
626	311	17.6	332	8	ADE19850	Ade19850 Human PRO
627	311	17.6	332	8	ADE77428	Ade77428 Human sec
628	311	17.6	332	8	ADE65304	Ade65304 Human PRO
629	311	17.6	332	8	ADE39352	Ade39352 Human PRO
630	311	17.6	332	8	ADE38537	Ade38537 Human sec
631	301.5	17.0	236	5	AAE26249	Aae26249 Human CD2
632	298	16.8	217	5	AAE26246	Aae26246 Human CD2
633	294.5	16.6	551	5	ABG96270	Abg96270 Human imm
634	251	14.2	220	5	AAU09867	Aau09867 Novel hum
635	247	13.9	310	5	ABB53269	Abb53269 Human pol
636	245	13.8	195	5	AAE26231	Aae26231 Human CD2
637	245	13.8	203	5	AAE26232	Aae26232 Human CD2
638	236.5	13.3	229	5	ABB53268	Abb53268 Human pol
639	225.5	12.7	351	4	AAB47322	Aab47322 APEX-2. 8
640	219	12.4	168	5	ABB89245	Abb89245 Human pol
641	206	11.6	220	6	ABU03171	Abu03171 Human imm
642	200.5	11.3	159	5	AAE26225	Aae26225 Human CD2
643	199.5	11.3	221	5	ABG96266	Abg96266 Human imm
644	186	10.5	343	2	AAR97632	Aar97632 Mouse SLA
645	182.5	10.3	335	2	AAR97628	Aar97628 Human SLA
646	182.5	10.3	335	4	AAB71853	Aab71853 Human SLA
647	182.5	10.3	335	5	AAU11927	Aau11927 Human pro
648	182.5	10.3	335	5	ABB90776	Abb90776 Human Tum
649	182.5	10.3	335	6	ABU54483	Abu54483 Human nor
650	181.5	10.2	334	5	AAG77978	Aag77978 Human sig
651	180	10.2	307	2	AAR97631	Aar97631 Human SLA
652	179	10.1	278	3	AAY92181	Aay92181 Murine TA
653	179	10.1	278	6	ABG74266	Abg74266 Human tra
654	179	10.1	278	7	ABW01426	Abw01426 Murine TA
655	177.5	10.0	258	7	ABW01428	Abw01428 Murine TA
656	175	9.9	33	2	AAW67933	Aaw67933 Fragment
657	170	9.6	365	2	AAY43138	Aay43138 Human NAI
658	170	9.6	365	4	AAM23942	Aam23942 Human EST
659	170	9.6	365	5	AAU11929	Aau11929 Human pro
660	170	9.6	391	5	ABP41447	Abp41447 Human ova
661	164.5	9.3	305	2	AAR97630	Aar97630 Human SLA
662	164.5	9.3	305	5	ABB90777	Abb90777 Human Tum
663	164.5	9.3	305	6	ABU54484	Abu54484 Human nor
664	158.5	8.9	329	2	AAR97633	Aar97633 Mouse SLA
665	158.5	8.9	329	5	AAU11928	Aau11928 Mouse pro
666	152	8.6	298	2	AAR97629	Aar97629 Human SLA
667	152	8.6	298	5	ABB90778	Abb90778 Human Tum
668	152	8.6	298	6	ABU54485	Abu54485 Human nor
669	150.5	8.5	285	3	AAY52479	Aay52479 Human D-S
670	150.5	8.5	285	4	AAM93287	Aam93287 Human pol
671	150.5	8.5	285	4	AAB71852	Aab71852 Human D-S
672	150.5	8.5	285	4	AAB47323	Aab47323 APEX-3. 8
673	150.5	8.5	285	4	AAE12075	Aae12075 Dendritic
674	150.5	8.5	285	5	ABG32412	Abg32412 Dendritic
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676	150.5	8.5	285	7	ADD18914	Add18914 Human dis
677	146.5	8.3	211	7	ABW01429	Abw01429 Murine TA
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679	146	8.2	312	6	ABG74265	Abg74265 Human tra
680	146	8.2	312	7	ABW01412	Abw01412 Human TAN
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683	146	8.2	320	6	ABG74267	Abg74267 Human tra
684	146	8.2	320	7	ABW01436	Abw01436 Human TAN
685	144.5	8.2	285	3	AAY92183	Aay92183 Full-leng
686	144.5	8.2	285	6	ABG74268	Abg74268 Mouse tra
687	144.5	8.2	285	7	ABW01442	Abw01442 Human TAN
688	141	8.0	149	7	ADA07622	Ada07622 Human sec
689	140.5	7.9	142	6	ADA57556	Ada57556 Human sec
690	140.5	7.9	142	6	ADA41448	Ada41448 Human sec
691	140.5	7.9	142	7	ADC74567	Adc74567 Human sec
692	140.5	7.9	142	7	ADD38086	Add38086 Human sec
693	140.5	7.9	143	2	AAY02692	Aay02692 Human sec
694	140.5	7.9	143	7	ADA07371	Ada07371 Human sec
695	140.5	7.9	290	7	ABW01419	Abw01419 Human TAN
696	140.5	7.9	298	7	ABW01438	Abw01438 Human TAN
697	139	7.8	28	2	AAW67932	Aaw67932 Fragment
698	139	7.8	263	7	ABW01444	Abw01444 Human TAN
699	138	7.8	70	5	AAE26255	Aae26255 Human CD2
700	136.5	7.7	351	3	AAY83135	Aay83135 Human CD2

ALIGNMENTS

RESULT 1
AAY66701
ID AAY66701 standard; protein; 335 AA.
XX
AC AAY66701;
XX
DT 05-APR-2000 (first entry)
XX
DE Membrane-bound protein PRO1138.
XX
KW Membrane-bound polypeptide; PRO polypeptide; LDL receptor; TIE ligand;
KW pharmaceutical; receptor immunoadhesin; gene mapping.
XX
OS Homo sapiens.
XX
PN WO9963088-A2.
XX
PD 09-DEC-1999.
XX
PF 02-JUN-1999; 99WO-US012252.
XX
PR 02-JUN-1998; 98US-0087607P.
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PR 03-JUN-1998; 98US-0087827P.
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PR   16-SEP-1998;   98US-0100634P.
PR   12-JAN-1999;   99US-0115565P.
XX
PA   (GETH ) GENENTECH INC.
XX
PI   Baker K,  Chen J,  Goddard A,  Gurney AL,  Smith V,  Watanabe CK;
PI   Wood WI,  Yuan J;
XX
DR   WPI; 2000-072883/06.
DR   N-PSDB; AAZ65040.
XX
PT   Membrane-bound proteins and related nucleotide sequences.
XX
PS   Claim 12; Fig 171; 822pp; English.
XX
CC   The invention provides membrane-bound PRO polypeptides and
CC   polynucleotides encoding them. The PRO sequences of the invention were
CC   identified based on extracellular domain homology screening. The PRO
CC   sequences have homology with proteins including LDL receptors, TIE
CC   ligands and various enzymes. The membrane-bound proteins and receptor
CC   molecules are useful as pharmaceutical and diagnostic agents. Receptor
CC   immunoadhesins, for instance, can be used as therapeutic agents to block
CC   receptor-ligand interactions. The membrane-bound proteins can also be
CC   employed for screening of potential peptide or small molecule inhibitors
CC   of the relevant receptor/ligand interaction. The PRO encoding sequences
CC   are useful as hybridization probes, in chromosome and gene mapping and in
CC   the generation of antisense RNA and DNA. PRO nucleic acid sequences will
CC   also be useful for the preparation of PRO polypeptides, especially by
CC   recombinant techniques
XX
SQ   Sequence 335 AA;

  Query Match             100.0%;  Score 1772;  DB 3;  Length 335;
  Best Local Similarity   100.0%;  Pred. No. 6.9e-163;
  Matches  335;  Conservative    0;  Mismatches    0;  Indels    0;  Gaps    0;

Qy          1 MAGSPTCLTLIYILWQLTGSAASGPVKELVGSVGGAVTFPLKSKVKQVDSIVWTFNTTPL 60
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Qy        121 VLHVYEHLSKPKVTMGLQSNKNGTCVTNLTCCMEHGEEDVIYTWKALGQAANESHNGSIL 180
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Db        121 VLHVYEHLSKPKVTMGLQSNKNGTCVTNLTCCMEHGEEDVIYTWKALGQAANESHNGSIL 180

Qy        181 PISWRWGESDMTFICVARNPVSRNFSSPILARKLCEGAADDPDSSMVLLCLLLVPLLLSL 240
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Db        181 PISWRWGESDMTFICVARNPVSRNFSSPILARKLCEGAADDPDSSMVLLCLLLVPLLLSL 240

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Qy        301 NTVYSTVEIPKKMENPHSLLTMPDTPRLFAYENVI 335
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Db        301 NTVYSTVEIPKKMENPHSLLTMPDTPRLFAYENVI 335


RESULT 2
AAY70431
ID   AAY70431 standard; protein; 335 AA.
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AC   AAY70431;
XX
DT   21-JUN-2000  (first entry)
XX
DE   Human cell surface immunomodulator-1 (CSIMM-1).
XX
KW   Cell surface immunomodulator-1; CSIMM-1; cell proliferation; CD84;
KW   differentiation; signal transduction; drug screening; prevention;
KW   treatment; cancer; leukaemia; melanoma; immune disorder; AIDS;
KW   rheumatoid arthritis; asthma; atherosclerosis; diabetes mellitus;
KW   emphysema; irritable bowel syndrome; multiple sclerosis; diagnosis;
KW   osteoporosis; psoriasis; microbial infections; cytostatic; antiarthritic;
KW   antiasthmatic; immunosuppressive; antiarteriosclerotic; anti-HIV;
KW   antidiabetic; antiinflammatory; neuroprotective; osteopathic;
KW   antipsoriatic; antimicrobial; human.
XX
OS   Homo sapiens.
XX
FH   Key             Location/Qualifiers
FT   Peptide         1. .22
FT                   /label= Signal_peptide
FT   Protein         23. .335
FT                   /label= Mature_CSIMM-1
FT   Region          34. .107
FT                   /note= "Homologous to immunoglobulin domain"
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PN   WO200011150-A1.
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PD   02-MAR-2000.
XX
PF   24-AUG-1999;   99WO-US019386.
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PR   25-AUG-1998;   98US-00155261.
XX
PA   (INCY-) INCYTE PHARM INC.
XX
PI   Lal P,  Corley NC,  Gorgone GA,  Guegler KJ,  Patterson C,  Baughn MR;
XX
DR   WPI; 2000-246561/21.
DR   N-PSDB; AAZ51572.
XX
PT   New human cell surface immunomodulatory polypeptides and polynucleotides
PT   useful for diagnosis, prevention and treatment of cancer and immune
PT   disorders.
XX
PS   Claim 1; Page 61-62; 70pp; English.
XX
CC   The present sequence is the human cell surface immunomodulator-1 (CSIMM-
CC   1), which is a regulator of cell proliferation, differentiation, cell-
CC   cell communication and signal transduction. It is encoded by cDNA
CC   identified in Incyte clone 14448, derived from human promonocyte cell
CC   line (THP-1) cDNA library (THP1PLB01). It shows homology to cell surface
CC   antigen, CD84. CSIMM can be used for drug screening, prevention and
CC   treatment of cancers such as leukaemia and melanoma, immune disorders
CC   such as AIDS, rheumatoid arthritis, asthma, atherosclerosis, diabetes
CC   mellitus, emphysema, irritable bowel syndrome, multiple sclerosis,
CC   osteoporosis, psoriasis and microbial infections. CSIMM polynucleotide
CC   may be used for diagnosis of CSIMM-associated diseases and as source of
CC   probes useful in mapping naturally occurring genomic sequences
XX
SQ   Sequence 335 AA;

  Query Match            100.0%;  Score 1772;  DB 3;  Length 335;
  Best Local Similarity  100.0%;  Pred. No. 6.9e-163;
  Matches  335;  Conservative    0;  Mismatches    0;  Indels    0;  Gaps    0;

Qy          1 MAGSPTCLTLIYILWQLTGSAASGPVKELVGSVGGAVTFPLKSKVKQVDSIVWTFNTTPL 60
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Qy         61 VTIQPEGGTIIVTQNRNRERVDFPDGGYSLKLSKLKKNDSGIYYVGIYSSSLQQPSTQEY 120
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Qy        121 VLHVYEHLSKPKVTMGLQSNKNGTCVTNLTCCMEHGEEDVIYTWKALGQAANESHNGSIL 180
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Db        121 VLHVYEHLSKPKVTMGLQSNKNGTCVTNLTCCMEHGEEDVIYTWKALGQAANESHNGSIL 180

Qy        181 PISWRWGESDMTFICVARNPVSRNFSSPILARKLCEGAADDPDSSMVLLCLLLVPLLLSL 240
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Db        181 PISWRWGESDMTFICVARNPVSRNFSSPILARKLCEGAADDPDSSMVLLCLLLVPLLLSL 240

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Db        241 FVLGLFLWFLKRERQEEYIEEKKRVDICRETPNICPHSGENTEYDTIPHTNRTILKEDPA 300

Qy        301 NTVYSTVEIPKKMENPHSLLTMPDTPRLFAYENVI 335
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Db        301 NTVYSTVEIPKKMENPHSLLTMPDTPRLFAYENVI 335


RESULT 3
AAY44609
ID   AAY44609 standard; protein; 335 AA.
XX
AC   AAY44609;
XX
DT   07-APR-2000  (first entry)
XX
DE   Human myocardium protein-7.
XX
KW   Human myocardium protein-7; MP-7; congestive heart failure;
KW   cardiovascular disorder; cardiomyopathy; hypertension; atherosclerosis;
KW   coronary artery spasm; coronary artery disease; cell-cell interaction;
KW   hypotensive; cardiant; screening assay.
XX
OS   Homo sapiens.
XX
FH   Key             Location/Qualifiers
FT   Peptide         1. .23
FT                   /label= Signal_peptide
FT   Protein         24. .335
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PN   WO9967387-A2.
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PD   29-DEC-1999.
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PF   24-JUN-1999;   99WO-US014307.
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PR   25-JUN-1998;   98US-0090579P.
PR   29-SEP-1998;   98US-00163284.
PR   02-MAR-1999;   99US-00261759.
XX
PA   (MILL-) MILLENNIUM PHARM INC.
XX
PI   Khodadoust M;
XX
DR   WPI; 2000-136984/12.
DR   N-PSDB; AAZ49571.
XX
PT   Novel myocardium protein-7 polynucleotides, used to modulate a variety of
PT   cellular processes.
XX
PS   Claim 2; Fig 2; 116pp; English.
XX
CC   The present sequence is myocardium protein-7 (MP-7). MP-7 is used to
CC   modulate a variety of cellular processes e.g. modulating the activity of
CC   proteins involved in cardiovascular disorders like congestive heart
CC   failure or cardiomyopathy. Diseases which can be treated include
CC   hypertension, atherosclerosis, coronary artery spasm, and coronary artery
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CC   disease. MP-7 proteins may also be used for cellular regulation of immune
CC   cell types, cell cycle, differentiation of multipotent cells, and
CC   modulation of cell-cell interactions. MP-7 may also be used in screening
CC   assays to identify agonists and antagonists and to raise antibodies
XX
SQ   Sequence 335 AA;

  Query Match           100.0%;  Score 1772;  DB 3;  Length 335;
  Best Local Similarity  100.0%;  Pred. No. 6.9e-163;
  Matches  335; Conservative    0;  Mismatches    0;  Indels    0;  Gaps    0;

Qy          1 MAGSPTCLTLIYILWQLTGSAASGPVKELVGSVGGAVTFPLKSKVKQVDSIVWTFNTTPL 60
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Db         61 VTIQPEGGTIIVTQNRNRERVDFPDGGYSLKLSKLKKNDSGIYYVGIYSSSLQQPSTQEY 120

Qy        121 VLHVYEHLSKPKVTMGLQSNKNGTCVTNLTCCMEHGEEDVIYTWKALGQAANESHNGSIL 180
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Db        121 VLHVYEHLSKPKVTMGLQSNKNGTCVTNLTCCMEHGEEDVIYTWKALGQAANESHNGSIL 180

Qy        181 PISWRWGESDMTFICVARNPVSRNFSSPILARKLCEGAADDPDSSMVLLCLLLVPLLLSL 240
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        181 PISWRWGESDMTFICVARNPVSRNFSSPILARKLCEGAADDPDSSMVLLCLLLVPLLLSL 240

Qy        241 FVLGLFLWFLKRERQEEYIEEKKRVDICRETPNICPHSGENTEYDTIPHTNRTILKEDPA 300
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        241 FVLGLFLWFLKRERQEEYIEEKKRVDICRETPNICPHSGENTEYDTIPHTNRTILKEDPA 300

Qy        301 NTVYSTVEIPKKMENPHSLLTMPDTPRLFAYENVI 335
              |||||||||||||||||||||||||||||||||||
Db        301 NTVYSTVEIPKKMENPHSLLTMPDTPRLFAYENVI 335


RESULT 4
AAU29119
ID   AAU29119 standard; protein; 335 AA.
XX
AC   AAU29119;
XX
DT   18-DEC-2001  (first entry)
XX
DE   Human PRO polypeptide sequence #96.
XX
KW   PRO polypeptide; mammal; tumour; cancer; human; cattle; horse; sheep;
KW   dog; cat; pig; goat; rabbit; tumour necrosis factor alpha; TNF-alpha;
KW   blood; chondrocyte cell; cell proliferation; cell differentiation; colon;
KW   adrenal; lung; breast; prostate; rectum; cervix; liver; genetic disorder.
XX
OS   Homo sapiens.
XX
PN   WO200168848-A2.
XX
PD   20-SEP-2001.
XX
PF   28-FEB-2001; 2001WO-US006520.
XX
PR   01-MAR-2000; 2000WO-US005601.
PR   02-MAR-2000; 2000WO-US005841.
PR   03-MAR-2000; 2000US-0187202P.
PR   06-MAR-2000; 2000US-0186968P.
PR   14-MAR-2000; 2000US-0189320P.
PR   14-MAR-2000; 2000US-0189328P.
PR   15-MAR-2000; 2000WO-US006884.
PR   21-MAR-2000; 2000US-0190828P.
PR   21-MAR-2000; 2000US-0191007P.
PR   21-MAR-2000; 2000US-0191048P.
PR   21-MAR-2000; 2000US-0191314P.
PR   28-MAR-2000; 2000US-0192655P.
PR   29-MAR-2000; 2000US-0193032P.
PR   29-MAR-2000; 2000US-0193053P.
PR   30-MAR-2000; 2000WO-US008439.
PR   04-APR-2000; 2000US-0194449P.
PR   04-APR-2000; 2000US-0194647P.
PR   11-APR-2000; 2000US-0195975P.
PR   11-APR-2000; 2000US-0196000P.
PR   11-APR-2000; 2000US-0196187P.
PR   11-APR-2000; 2000US-0196690P.
PR   11-APR-2000; 2000US-0196820P.
PR   18-APR-2000; 2000US-0198121P.
PR   18-APR-2000; 2000US-0198585P.
PR   25-APR-2000; 2000US-0199397P.
PR   25-APR-2000; 2000US-0199550P.
PR   25-APR-2000; 2000US-0199654P.
PR   03-MAY-2000; 2000US-0201516P.
PR   17-MAY-2000; 2000WO-US013705.
PR   22-MAY-2000; 2000WO-US014042.
PR   30-MAY-2000; 2000WO-US014941.
PR   02-JUN-2000; 2000WO-US015264.
PR   05-JUN-2000; 2000US-0209832P.
PR   28-JUL-2000; 2000WO-US020710.
PR   22-AUG-2000; 2000US-00644848.
PR   24-AUG-2000; 2000WO-US023328.
PR   08-NOV-2000; 2000WO-US030952.
PR   01-DEC-2000; 2000WO-US032678.
PR   20-DEC-2000; 2000WO-US034956.
XX
PA   (GETH ) GENENTECH INC.
XX
PI   Baker KP,  Chen J,  Desnoyers L,  Goddard A,  Godowski PJ,  Gurney AL;
PI   Pan J,  Smith V,  Watanabe CK,  Wood WI,  Zhang Z;
XX
DR   WPI; 2001-602746/68.
DR   N-PSDB; AAS46020.
XX
PT   Novel nucleic acids encoding PRO polypeptides, used to diagnose the
PT   presence of tumors, such as prostate and breast tumors, in mammals and to
PT   screen for modulators of the compounds.
XX
PS   Claim 11; Fig 192; 774pp; English.
XX
CC   Sequences AAU29024-AAU29328 represent PRO polypeptides of the invention.
CC   The PRO polypeptides and their associated nucleic acids can be used to
CC   detect the presence of a tumour in a mammal by comparing the level of
CC   expression of a PRO polypeptide in a test sample of cells from the animal
CC   and a control sample of normal cells, whereby a higher level of
CC   expression in the test sample indicates the presence of a tumour in the
CC   mammal. Mammals include dogs, cats, cattle, horses, sheep, pigs, goats
CC   and rabbits but are preferably human. The polypeptides can be used to
CC   stimulate tumour necrosis factor (TNF) alpha release from human blood,
CC   when contacted with it. A specific polypeptide can be used to stimulate
CC   the proliferation or differentiation of chondrocyte cells. The PRO
CC   proteins can be used to determine the presence of tumours and also
CC   susceptibility to tumour development, particularly adrenal, lung, colon,
CC   breast, prostate, rectal, cervical, or liver tumours, in mammalian
CC   subjects. The oligonucleotide probes specific for the PRO nucleic acids
CC   can be used for genetic analysis of individuals with genetic disorders
XX
SQ   Sequence 335 AA;

  Query Match           100.0%;  Score 1772;  DB 4;  Length 335;
  Best Local Similarity  100.0%;  Pred. No. 6.9e-163;
  Matches  335; Conservative    0;  Mismatches    0;  Indels    0;  Gaps    0;

Qy          1 MAGSPTCLTLIYILWQLTGSAASGPVKELVGSVGGAVTFPLKSKVKQVDSIVWTFNTTPL 60
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db          1 MAGSPTCLTLIYILWQLTGSAASGPVKELVGSVGGAVTFPLKSKVKQVDSIVWTFNTTPL 60

Qy         61 VTIQPEGGTIIVTQNRNRERVDFPDGGYSLKLSKLKKNDSGIYYVGIYSSSLQQPSTQEY 120
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db         61 VTIQPEGGTIIVTQNRNRERVDFPDGGYSLKLSKLKKNDSGIYYVGIYSSSLQQPSTQEY 120

Qy        121 VLHVYEHLSKPKVTMGLQSNKNGTCVTNLTCCMEHGEEDVIYTWKALGQAANESHNGSIL 180
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
```

```
Db        121 VLHVYEHLSKPKVTMGLQSNKNGTCVTNLTCCMEHGEEDVIYTWKALGQAANESHNGSIL 180

Qy        181 PISWRWGESDMTFICVARNPVSRNFSSPILARKLCEGAADDPDSSMVLLCLLLVPLLLSL 240
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        181 PISWRWGESDMTFICVARNPVSRNFSSPILARKLCEGAADDPDSSMVLLCLLLVPLLLSL 240

Qy        241 FVLGLFLWFLKRERQEEYIEEKKRVDICRETPNICPHSGENTEYDTIPHTNRTILKEDPA 300
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        241 FVLGLFLWFLKRERQEEYIEEKKRVDICRETPNICPHSGENTEYDTIPHTNRTILKEDPA 300

Qy        301 NTVYSTVEIPKKMENPHSLLTMPDTPRLFAYENVI 335
              |||||||||||||||||||||||||||||||||||
Db        301 NTVYSTVEIPKKMENPHSLLTMPDTPRLFAYENVI 335


RESULT 5
AAB87548
ID   AAB87548 standard; protein; 335 AA.
XX
AC   AAB87548;
XX
DT   15-MAY-2001  (first entry)
XX
DE   Human PRO1138.
XX
KW   Human; PRO protein; mapping.
XX
OS   Homo sapiens.
XX
PN   WO200116318-A2.
XX
PD   08-MAR-2001.
XX
PF   24-AUG-2000; 2000WO-US023328.
XX
PR   01-SEP-1999;   99WO-US020111.
PR   15-SEP-1999;   99WO-US021090.
PR   07-DEC-1999;   99US-0169495P.
PR   09-DEC-1999;   99US-0170262P.
PR   11-JAN-2000; 2000US-0175481P.
PR   18-FEB-2000; 2000WO-US004341.
PR   18-FEB-2000; 2000WO-US004342.
PR   22-FEB-2000; 2000WO-US004414.
PR   01-MAR-2000; 2000WO-US005601.
PR   03-MAR-2000; 2000US-0187202P.
PR   21-MAR-2000; 2000US-0191007P.
PR   30-MAR-2000; 2000WO-US008439.
PR   25-APR-2000; 2000US-0199397P.
PR   22-MAY-2000; 2000WO-US014042.
PR   05-JUN-2000; 2000US-0209832P.
XX
PA   (GETH ) GENENTECH INC.
XX
PI   Eaton DL,  Filvaroff E,  Gerritsen ME,  Goddard A,  Godowski PJ;
PI   Grimaldi CJ,  Gurney AL,  Watanabe CK,  Wood WI;
XX
DR   WPI; 2001-183260/18.
DR   N-PSDB; AAF92080.
XX
PT   Eighty four nucleic acids encoding PRO polypeptides, useful in molecular
PT   biology, including use as hybridization probes, and in chromosome and
PT   gene mapping.
XX
PS   Claim 12; Fig 46; 278pp; English.
XX
CC   The present sequence is a human PRO polypeptide (secreted and
CC   transmembrane). The PRO protein, and PRO agonists, PRO antagonists or
CC   anti-PRO antibodies are useful for preparation of a medicament useful in
CC   the treatment of a condition which is responsive to the PRO protein,
CC   agonists, antagonists or anti-PRO antibodies. The PRO protein may also be
CC   employed as molecular weight markers for protein electrophoresis. The PRO
CC   coding sequence has applications in molecular biology, including use as
CC   hybridisation probes, and in chromosome and gene mapping
XX
SQ   Sequence 335 AA;

  Query Match            100.0%;  Score 1772;  DB 4;  Length 335;
  Best Local Similarity  100.0%;  Pred. No. 6.9e-163;
  Matches  335;  Conservative    0;  Mismatches    0;  Indels    0;  Gaps    0;

Qy          1 MAGSPTCLTLIYILWQLTGSAASGPVKELVGSVGGAVTFPLKSKVKQVDSIVWTFNTTPL 60
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db          1 MAGSPTCLTLIYILWQLTGSAASGPVKELVGSVGGAVTFPLKSKVKQVDSIVWTFNTTPL 60

Qy         61 VTIQPEGGTIIVTQNRNRERVDFPDGGYSLKLSKLKKNDSGIYYVGIYSSSLQQPSTQEY 120
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db         61 VTIQPEGGTIIVTQNRNRERVDFPDGGYSLKLSKLKKNDSGIYYVGIYSSSLQQPSTQEY 120

Qy        121 VLHVYEHLSKPKVTMGLQSNKNGTCVTNLTCCMEHGEEDVIYTWKALGQAANESHNGSIL 180
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        121 VLHVYEHLSKPKVTMGLQSNKNGTCVTNLTCCMEHGEEDVIYTWKALGQAANESHNGSIL 180

Qy        181 PISWRWGESDMTFICVARNPVSRNFSSPILARKLCEGAADDPDSSMVLLCLLLVPLLLSL 240
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        181 PISWRWGESDMTFICVARNPVSRNFSSPILARKLCEGAADDPDSSMVLLCLLLVPLLLSL 240

Qy        241 FVLGLFLWFLKRERQEEYIEEKKRVDICRETPNICPHSGENTEYDTIPHTNRTILKEDPA 300
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        241 FVLGLFLWFLKRERQEEYIEEKKRVDICRETPNICPHSGENTEYDTIPHTNRTILKEDPA 300

Qy        301 NTVYSTVEIPKKMENPHSLLTMPDTPRLFAYENVI 335
              |||||||||||||||||||||||||||||||||||
Db        301 NTVYSTVEIPKKMENPHSLLTMPDTPRLFAYENVI 335


RESULT 6
AAB47321
ID   AAB47321 standard; protein; 335 AA.
XX
AC   AAB47321;
XX
DT   29-AUG-2001  (first entry)
XX
DE   APEX-1.
XX
KW   Antigen presenting cell expression protein; APEX-1; APEX-2; APEX-3;
KW   extracellular domain; immunoglobulin-like domain; Ig-like structure;
KW   N-glycosylation site; transmembrane domain; cytoplasmic domain;
KW   SH2-binding motif; asthma; arteriosclerosis; AIDS; cirrhosis;
KW   Crohn's disease; atopic dermatitis; autoimmune anaemia; bursitis;
KW   cholecystitis; diabetes mellitus; emphysema; atrophic gastritis;
KW   inflammatory bowel disease; multiple sclerosis; myasthenia gravis;
KW   myocardial inflammation; pericardial inflammation; osteoarthritis;
KW   osteoporosis; psoriasis; Reiter's syndrome; rheumatoid arthritis;
KW   inflammation; cancer; autoimmune disease; graft rejection;
KW   graft versus host disease; systemic lupus erythematosus.
XX
OS   Homo sapiens.
XX
FH   Key             Location/Qualifiers
FT   Peptide         1. .22
FT                   /label= Signal peptide
FT   Protein         23. .335
FT                   /label= Mature APEX-1
FT   Domain          226. .250
FT                   /label= Transmembrane domain
XX
PN   WO200146260-A2.
XX
PD   28-JUN-2001.
XX
PF   22-DEC-2000; 2000WO-US034963.
XX
PR   23-DEC-1999;   99US-0172025P.
XX
PA   (BRIM ) BRISTOL-MYERS SQUIBB CO.
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```
XX
PI   Starling GC,  Finger J;
XX
DR   WPI; 2001-418044/44.
DR   N-PSDB; AAC86114.
XX
PT   Novel Antigen presenting cell expression protein useful for treating
PT   asthma, arteriosclerosis, autoimmune diseases, AIDS, cirrhosis, Crohn's
PT   disease and atopic dermatitis.
XX
PS   Claim 3; Fig 2; 112pp; English.
XX
CC   The sequences given in AAB47321-23 represent antigen presenting cell
CC   expression (APEX)-1, APEX-2 and APEX-3 proteins. APEX-1 and APEX-2
CC   comprise an extracellular domain having one immunoglobulin (Ig)-like
CC   structure and N-glycosylation site, a transmembrane domain, and a
CC   cytoplasmic domain having at least one SH2-binding motif. APEX proteins
CC   and antibodies are useful in the study, diagnosis, prevention and
CC   treatment of disease associated with the presence of an APEX protein
CC   e.g., asthma, arteriosclerosis, AIDS, cirrhosis, Crohn's disease, atopic
CC   dermatitis, autoimmune anaemia, bursitis, cholecystitis, diabetes
CC   mellitus, emphysema, atrophic gastritis, inflammatory bowel disease,
CC   multiple sclerosis, myasthenia gravis, myocardial or pericardial
CC   inflammation, osteoarthritis, osteoporosis, psoriasis, Reiter's syndrome,
CC   rheumatoid arthritis, inflammation, cancer, immune disorders, autoimmune
CC   diseases, graft rejections, graft versus host reaction and systemic lupus
CC   erythematosus. APEX proteins are useful as diagnostic and/or prognostic
CC   markers on APCs or APEX expressing cells, the ability to elicit the
CC   generation of antibodies and as targets for various therapeutic
CC   modalities. APEX proteins are also useful for identifying and isolating
CC   ligand that bind APEX
XX
SQ   Sequence 335 AA;

  Query Match             100.0%;  Score 1772;  DB 4;  Length 335;
  Best Local Similarity   100.0%;  Pred. No. 6.9e-163;
  Matches  335;  Conservative    0;  Mismatches    0;  Indels    0;  Gaps    0;

Qy          1 MAGSPTCLTLIYILWQLTGSAASGPVKELVGSVGGAVTFPLKSKVKQVDSIVWTFNTTPL 60
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db          1 MAGSPTCLTLIYILWQLTGSAASGPVKELVGSVGGAVTFPLKSKVKQVDSIVWTFNTTPL 60

Qy         61 VTIQPEGGTIIVTQNRNRERVDFPDGGYSLKLSKLKKNDSGIYYVGIYSSSLQQPSTQEY 120
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db         61 VTIQPEGGTIIVTQNRNRERVDFPDGGYSLKLSKLKKNDSGIYYVGIYSSSLQQPSTQEY 120

Qy        121 VLHVYEHLSKPKVTMGLQSNKNGTCVTNLTCCMEHGEEDVIYTWKALGQAANESHNGSIL 180
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        121 VLHVYEHLSKPKVTMGLQSNKNGTCVTNLTCCMEHGEEDVIYTWKALGQAANESHNGSIL 180

Qy        181 PISWRWGESDMTFICVARNPVSRNFSSPILARKLCEGAADDPDSSMVLLCLLLVPLLLSL 240
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        181 PISWRWGESDMTFICVARNPVSRNFSSPILARKLCEGAADDPDSSMVLLCLLLVPLLLSL 240

Qy        241 FVLGLFLWFLKRERQEEYIEEKKRVDICRETPNICPHSGENTEYDTIPHTNRTILKEDPA 300
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        241 FVLGLFLWFLKRERQEEYIEEKKRVDICRETPNICPHSGENTEYDTIPHTNRTILKEDPA 300

Qy        301 NTVYSTVEIPKKMENPHSLLTMPDTPRLFAYENVI 335
              ||||||||||||||||||||||||||||||||||||
Db        301 NTVYSTVEIPKKMENPHSLLTMPDTPRLFAYENVI 335


RESULT 7
AAB65224
ID   AAB65224 standard; protein; 335 AA.
XX
AC   AAB65224;
XX
DT   02-APR-2001  (first entry)
XX
DE   Human PRO1138 (UNQ576) protein sequence SEQ ID NO:253.
XX
KW   Human; secreted and transmembrane protein; PRO; cytostatic; cell death;
KW   cancer; chromosomal mapping; gene mapping; tissue typing;
KW   diagnostic assay.
XX
OS   Homo sapiens.
XX
PN   WO200073454-A1.
XX
PD   07-DEC-2000.
XX
PF   30-MAR-2000; 2000WO-US008439.
XX
PR   02-JUN-1999;   99WO-US012252.
PR   23-JUN-1999;   99US-0141037P.
PR   07-JUL-1999;   99US-0143048P.
PR   20-JUL-1999;   99US-0144758P.
PR   26-JUL-1999;   99US-0145698P.
PR   28-JUL-1999;   99US-0146222P.
PR   17-AUG-1999;   99US-0149396P.
PR   15-SEP-1999;   99WO-US021090.
PR   15-SEP-1999;   99WO-US021547.
PR   08-OCT-1999;   99US-0158663P.
PR   30-NOV-1999;   99WO-US028313.
PR   01-DEC-1999;   99WO-US028301.
PR   16-DEC-1999;   99WO-US030095.
PR   20-DEC-1999;   99WO-US030911.
PR   05-JAN-2000; 2000WO-US000219.
PR   06-JAN-2000; 2000WO-US000376.
PR   11-FEB-2000; 2000WO-US003565.
PR   18-FEB-2000; 2000WO-US004341.
PR   22-FEB-2000; 2000WO-US004414.
PR   24-FEB-2000; 2000WO-US004914.
PR   24-FEB-2000; 2000WO-US005004.
PR   02-MAR-2000; 2000WO-US005841.
PR   15-MAR-2000; 2000WO-US006884.
PR   20-MAR-2000; 2000WO-US007377.
XX
PA   (GETH ) GENENTECH INC.
XX
PI   Ashkenazi AJ,  Baker KP,  Botstein D,  Desnoyers L,  Eaton DL;
PI   Ferrara N,  Fong S,  Gerber H,  Gerritsen ME,  Goddard A,  Godowski PJ;
PI   Grimaldi CJ,  Gurney AL,  Kljavin IJ,  Napier MA,  Pan J,  Paoni NF;
PI   Roy MA,  Stewart TA,  Tumas D,  Watanabe CK,  Williams PM,  Wood WI;
PI   Zhang Z;
XX
DR   WPI; 2001-032160/04.
DR   N-PSDB; AAF44186.
XX
PT   PRO polynucleotides used to produce polypeptides used to target bioactive
PT   molecules such as toxins, radiolabels or antibodies, to specific cells,
PT   to cause targeted cell death.
XX
PS   Claim 12; Fig 171; 935pp; English.
XX
CC   The present invention describes human secreted and transmembrane PRO
CC   proteins. The PRO proteins have cytostatic activity. The PRO proteins can
CC   be used for targeted delivery of bioactive molecules, such as toxins,
CC   radiolabels or antibodies, that cause cell death. PRO nucleotide
CC   sequences, and their fragments, can be used as hybridisation probes, in
CC   chromosomal and gene mapping, and in the generation of anti-sense RNA and
CC   DNA. They may also be used to produce transgenic animals which are used
CC   to develop and screen therapeutically useful reagents. The PRO nucleotide
CC   and protein sequence can be used for tissue typing and in treating
CC   cancer. Anti-PRO antibodies can be used in diagnostic assays. AAF44270 to
CC   AAF44470 represent PCR primers and hybridisation probes used in the
CC   isolation of human PRO sequences. AAF44087 to AAF44269 and AAB65154 to
CC   AAB65300 represent human PRO polynucleotide and protein sequences given
CC   in the exemplification of the present invention
XX
SQ   Sequence 335 AA;

  Query Match             100.0%;  Score 1772;  DB 4;  Length 335;
  Best Local Similarity   100.0%;  Pred. No. 6.9e-163;
```

```
  Matches  335;  Conservative    0;  Mismatches    0;  Indels    0;  Gaps    0;

Qy          1 MAGSPTCLTLIYILWQLTGSAASGPVKELVGSVGGAVTFPLKSKVKQVDSIVWTFNTTPL 60
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db          1 MAGSPTCLTLIYILWQLTGSAASGPVKELVGSVGGAVTFPLKSKVKQVDSIVWTFNTTPL 60

Qy         61 VTIQPEGGTIIVTQNRNRERVDFPDGGYSLKLSKLKKNDSGIYYVGIYSSSLQQPSTQEY 120
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db         61 VTIQPEGGTIIVTQNRNRERVDFPDGGYSLKLSKLKKNDSGIYYVGIYSSSLQQPSTQEY 120

Qy        121 VLHVYEHLSKPKVTMGLQSNKNGTCVTNLTCCMEHGEEDVIYTWKALGQAANESHNGSIL 180
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        121 VLHVYEHLSKPKVTMGLQSNKNGTCVTNLTCCMEHGEEDVIYTWKALGQAANESHNGSIL 180

Qy        181 PISWRWGESDMTFICVARNPVSRNFSSPILARKLCEGAADDPDSSMVLLCLLLVPLLLSL 240
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        181 PISWRWGESDMTFICVARNPVSRNFSSPILARKLCEGAADDPDSSMVLLCLLLVPLLLSL 240

Qy        241 FVLGLFLWFLKRERQEEYIEEKKRVDICRETPNICPHSGENTEYDTIPHTNRTILKEDPA 300
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        241 FVLGLFLWFLKRERQEEYIEEKKRVDICRETPNICPHSGENTEYDTIPHTNRTILKEDPA 300

Qy        301 NTVYSTVEIPKKMENPHSLLTMPDTPRLFAYENVI 335
              ||||||||||||||||||||||||||||||||||||
Db        301 NTVYSTVEIPKKMENPHSLLTMPDTPRLFAYENVI 335


RESULT 8
ABG95873
ID   ABG95873 standard; protein; 335 AA.
XX
AC   ABG95873;
XX
DT   10-DEC-2002  (first entry)
XX
DE   Human secreted/transmembrane protein PRO1138.
XX
KW   Human; secreted protein; transmembrane protein; antirheumatic;
KW   antiarthritic; osteopathic; sports-related joint problem;
KW   articular cartilage defect; osteoarthritis; rheumatoid arthritis.
XX
OS   Homo sapiens.
XX
PN   US2002119130-A1.
XX
PD   29-AUG-2002.
XX
PF   06-DEC-2001; 2001US-00006867.
XX
PR   29-OCT-1997;   97US-0063435P.
PR   29-OCT-1997;   97US-0064215P.
PR   22-APR-1998;   98US-0082797P.
PR   29-APR-1998;   98US-0083495P.
PR   15-MAY-1998;   98US-0085579P.
PR   02-JUN-1998;   98US-0087759P.
PR   04-JUN-1998;   98US-0088021P.
PR   04-JUN-1998;   98US-0088029P.
PR   04-JUN-1998;   98US-0088030P.
PR   10-JUN-1998;   98US-0088734P.
PR   10-JUN-1998;   98US-0088740P.
PR   10-JUN-1998;   98US-0088811P.
PR   10-JUN-1998;   98US-0088824P.
PR   10-JUN-1998;   98US-0088825P.
PR   11-JUN-1998;   98US-0088863P.
PR   12-JUN-1998;   98US-0089105P.
PR   16-JUN-1998;   98US-0089514P.
PR   17-JUN-1998;   98US-0089653P.
PR   19-JUN-1998;   98US-0089952P.
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PR   06-OCT-1998;   98US-0103449P.
PR   08-MAR-1999;   99WO-US005028.
PR   14-MAY-1999;   99WO-US010733.
PR   02-JUN-1999;   99WO-US012252.
PR   01-SEP-1999;   99WO-US020111.
PR   15-SEP-1999;   99WO-US021090.
PR   15-SEP-1999;   99WO-US021194.
PR   22-DEC-1999;   99WO-US030720.
PR   18-FEB-2000; 2000WO-US004341.
PR   18-FEB-2000; 2000WO-US004342.
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PR   02-JUN-2000; 2000WO-US015264.
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PR   01-DEC-2000; 2000WO-US032378.
PR   20-DEC-2000; 2000WO-US034956.
PR   28-FEB-2001; 2001WO-US006520.
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PR   01-JUN-2001; 2001WO-US017800.
PR   20-JUN-2001; 2001WO-US019692.
PR   29-JUN-2001; 2001WO-US021066.
PR   09-JUL-2001; 2001WO-US021735.
XX
PA   (GETH ) GENENTECH INC.
XX
PI   Eaton DL,  Filvaroff E,  Gerritsen ME,  Goddard A,  Godowski PJ;
PI   Grimaldi JC,  Gurney AL,  Watanabe CK,  Wood WI;
XX
DR   WPI; 2002-731348/79.
DR   N-PSDB; ABS74400.
XX
PT   New isolated secreted and transmembrane PRO polypeptide useful for
PT   modulating biological activity of a cell, or for treating sports-related
PT   joint problems, osteoarthritis or rheumatoid arthritis.
XX
PS   Claim 20; Fig 46; 399pp; English.
XX
CC   The invention relates to an isolated secreted and transmembrane PRO
CC   polypeptide having 80 % sequence identity to a sequence appearing as
CC   ABG95851-ABG95934 or their associated signal peptide, or a sequence of an
CC   extracellular domain of the proteins with their associated signal peptide
CC   or lacking its associated signal peptide. Also included are the nucleic
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CC   acids encoding the proteins, vectors, host cells, fusion proteins and
CC   antibodies which specifically bind to the proteins. The proteins are
CC   useful for detecting a polypeptide designated as A, B, C or D in a sample
CC   suspected of containing an A, B, C or D polypeptide, by contacting the
CC   sample with a polypeptide designated as E, F, G, H or I (or vice versa)
CC   and determining the formation of a A/E, B/F, B/G, C/H or D/I polypeptide
CC   conjugate in the sample, where the formation of the conjugate is
CC   indicative of the presence of an A, B, C or D polypeptide in the sample,
CC   where A is a PRO10272 polypeptide, B is a PRO20110 polypeptide, C is a
CC   PRO10096 polypeptide, D is a PRO19760 polypeptide, E is a PRO5801
CC   polypeptide, F is a PRO1 polypeptide, G is a PRO20040 polypeptide, H is a
CC   PRO20233 polypeptide and I is a PRO1890 polypeptide. The sample comprises
CC   a cell suspected of expressing the A, B, C or D polypeptide. The E, F, G,
CC   H or I polypeptide is labeled with a detectable label or is attached to a
CC   solid support. The proteins are useful for linking a bioactive molecule
CC   to a cell expressing a polypeptide designated as A, B, C or D or E, F, G,
CC   H or I. The bioactive molecule is a toxin, a radiolabel or an antibody.
CC   The bioactive molecule causes death of the cell. A, B, C, D, E, F, G, H,
CC   or I, or antibodies against them are useful for modulating a biological
CC   activity of a cell expressing a polypeptide designated as A, B, C or D or
CC   E, F, G, H, or I. The cell is killed. The proteins are useful for
CC   identifying agonists or antagonists, for the preparation of a medicament
CC   useful in the treatment of a condition which is responsive to the
CC   proteins, as molecular weight markers for protein electrophoresis
CC   purposes, and as therapeutic agents for treating sports-related joint
CC   problems, articular cartilage defects, osteoarthritis or rheumatoid
CC   arthritis. Nucleic acids encoding the proteins are useful as
CC   hybridisation probes, in chromosome and gene mapping, in the generation
CC   of anti-sense RNA and DNA, for the preparation of the proteins, to
CC   generate transgenic or knockout animals which are useful in the
CC   development and screening of therapeutic useful reagents, for chromosome
CC   identification, and in gene therapy. The antibody is useful as a
CC   therapeutic agent, in a diagnostic assay and for affinity purification of
CC   the protein from recombinant cell culture natural sources. The present
CC   sequence represents a novel secreted or transmembrane protein of the
CC   invention
XX
SQ   Sequence 335 AA;

  Query Match             100.0%;  Score 1772;  DB 5;  Length 335;
  Best Local Similarity   100.0%;  Pred. No. 6.9e-163;
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Db          1 MAGSPTCLTLIYILWQLTGSAASGPVKELVGSVGGAVTFPLKSKVKQVDSIVWTFNTTPL 60

Qy         61 VTIQPEGGTIIVTQNRNRERVDFPDGGYSLKLSKLKKNDSGIYYVGIYSSSLQQPSTQEY 120
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Db         61 VTIQPEGGTIIVTQNRNRERVDFPDGGYSLKLSKLKKNDSGIYYVGIYSSSLQQPSTQEY 120

Qy        121 VLHVYEHLSKPKVTMGLQSNKNGTCVTNLTCCMEHGEEDVIYTWKALGQAANESHNGSIL 180
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Qy        181 PISWRWGESDMTFICVARNPVSRNFSSPILARKLCEGAADDPDSSMVLLCLLLVPLLLSL 240
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Db        181 PISWRWGESDMTFICVARNPVSRNFSSPILARKLCEGAADDPDSSMVLLCLLLVPLLLSL 240

Qy        241 FVLGLFLWFLKRERQEEYIEEKKRVDICRETPNICPHSGENTEYDTIPHTNRTILKEDPA 300
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Db        241 FVLGLFLWFLKRERQEEYIEEKKRVDICRETPNICPHSGENTEYDTIPHTNRTILKEDPA 300

Qy        301 NTVYSTVEIPKKMENPHSLLTMPDTPRLFAYENVI 335
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Db        301 NTVYSTVEIPKKMENPHSLLTMPDTPRLFAYENVI 335


RESULT 9
ABU58495
ID   ABU58495 standard; protein; 335 AA.
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AC   ABU58495;
XX
DT   15-APR-2003  (first entry)
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DE   Human PRO polypeptide #96.
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KW   Human; PRO; cytostatic; tumour; cancer; breast; lung; stomach; liver;
KW   dog; cat; cow; horse; sheep; pig; goat; rabbit; ADEPT;
KW   antibody-dependent enzyme mediated prodrug therapy.
XX
OS   Homo sapiens.
XX
PN   US2003027272-A1.
XX
PD   06-FEB-2003.
XX
PF   21-JUN-2002; 2002US-00176492.
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PR   18-SEP-1997;   97US-0059263P.
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PR 01-OCT-1998; 98US-0102687P.
PR 02-OCT-1998; 98US-0102965P.
PR 06-OCT-1998; 98US-0103258P.
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PR 07-OCT-1998; 98US-00168978.

Query Match 100.0%; Score 1772; DB 6; Length 335;
Best Local Similarity 100.0%; Pred. No. 6.9e-163;
Matches 335; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

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Db          1 MAGSPTCLTLIYILWQLTGSAASGPVKELVGSVGGAVTPPLKSKVKQVDSIVWTFNTTPL 60

Qy         61 VTIQPEGGTIIVTQNRNRERVDFPDGGYSLKLSKLKKNDSGIYYVGIYSSSLQQPSTQEY 120
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Qy        181 PISWRWGESDMTFICVARNPVSRNFSSPILARKLCEGAADDPDSSMVLLCLLLVPLLLSL 240
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RESULT 10
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ID   ABU88043 standard; protein; 335 AA.
XX
AC   ABU88043;
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DT   07-JUL-2003  (first entry)
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DE   Novel human secreted and transmembrane protein PRO1138.
XX
KW   Human; secreted and transmembrane protein: PRO; gene therapy;
KW   tumour necrosis factor-alpha release; TNF-alpha release;
KW   chondrocyte proliferation; chondrocyte differentiation; tumour;
KW   adrenal tumour; lung tumour; colon tumour; breast tumour;
KW   prostate tumour; rectal tumour; cervical tumour; liver tumour.
XX
OS   Homo sapiens.
XX
PN   US2003032127-A1.
XX
PD   13-FEB-2003.
XX
PF   26-JUN-2002; 2002US-00183012.
XX
PR   18-SEP-1997;   97US-0059263P.
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PR   17-OCT-1997;   97US-0062250P.
PR   21-OCT-1997;   97US-0063486P.
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DT 02-AUG-2003 (first entry)
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KW tumour necrosis factor alpha; chondrocyte cell; tumour; gene therapy;
KW tissue typing.
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PN US2003032112-A1.
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PD 13-FEB-2003.
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PF 21-JUN-2002; 2002US-00176756.
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DT   05-AUG-2003 (first entry)
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KW   extracellular domain; tumour necrosis factor-alpha; TNF-alpha;
KW   chondrocyte; proliferation; differentiation; cartilage disorder;
KW   bone disorder; arthritis; sports injury; cancer; tumour; diagnosis;
KW   adrenal tumour; lung; colon; breast; prostate; kidney; rectum; cervix;
KW   liver; drug screening; transgenic animal; genetic analysis;
KW   antiarthritic; vulnerary; gene therapy.
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XX
PN   US2003027278-A1.
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PD   06-FEB-2003.
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PF   21-JUN-2002; 2002US-00176987.
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PR   18-SEP-1997;   97US-0059263P.
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DT 05-AUG-2003 (first entry)
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KW extracellular domain; tumour necrosis factor-alpha; TNF-alpha;
KW chondrocyte; proliferation; differentiation; cartilage disorder;
KW bone disorder; arthritis; sports injury; cancer; tumour; diagnosis;
KW adrenal tumour; lung; colon; breast; prostate; kidney; rectum; cervix;
KW liver; drug screening; transgenic animal; genetic analysis;
KW antiarthritic; vulnerary; gene therapy.
XX
OS Homo sapiens.
XX
PN US2003036159-A1.
XX
PD 20-FEB-2003.
XX
PF 02-JUL-2002; 2002US-00188773.
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RESULT 14
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ID   ABU99562 standard; protein; 335 AA.
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AC   ABU99562;
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DT   09-AUG-2003  (first entry)
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DE   Human secreted/transmembrane protein (PRO) #96.
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KW   Human; secreted and transmembrane protein; PRO; TNF-alpha;
KW   tumour necrosis factor alpha; chondrocyte cell; tumour; gene therapy;
KW   tissue typing.
XX
OS   Homo sapiens.
XX
PN   US2003040070-A1.
XX
PD   27-FEB-2003.
XX
PF   27-JUN-2002; 2002US-00184627.
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PR   18-SEP-1997;   97US-0059266P.
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              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        121 VLHVYEHLSKPKVTMGLQSNKNGTCVTNLTCCMEHGEEDVIYTWKALGQAANESHNGSIL 180

Qy        181 PISWRWGESDMTFICVARNPVSRNFSSPILARKLCEGAADDPDSSMVLLCLLLVPLLLSL 240
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        181 PISWRWGESDMTFICVARNPVSRNFSSPILARKLCEGAADDPDSSMVLLCLLLVPLLLSL 240

Qy        241 FVLGLFLWFLKRERQEEYIEEKKRVDICRETPNICPHSGENTEYDTIPHTNRTILKEDPA 300
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        241 FVLGLFLWFLKRERQEEYIEEKKRVDICRETPNICPHSGENTEYDTIPHTNRTILKEDPA 300

Qy        301 NTVYSTVEIPKKMENPHSLLTMPDTPRLFAYENVI 335
              |||||||||||||||||||||||||||||||||||
Db        301 NTVYSTVEIPKKMENPHSLLTMPDTPRLFAYENVI 335

Search completed: August 18, 2004, 15:51:13
Job time : 59 secs
```

OM protein - protein search, using sw model

Run on: August 18, 2004, 15:56:34 ; Search time 39 Seconds
(without alignments)
2710.220 Million cell updates/sec

Title: US-10-063-549-46
Perfect score: 335
Sequence: 1 MAGSPTCLTLIYILWQLTGS.....PHSLLTMPDTPRLFAYENVI 335

Scoring table: OLIGO
Gapop 60.0 , Gapext 60.0

Searched: 1017041 seqs, 315518202 residues

Word size : 0

Total number of hits satisfying chosen parameters: 1017041

Minimum DB seq length: 0
Maximum DB seq length: 2000000000

Post-processing: Listing first 700 summaries

Database : SPTREMBL_25:*
1: sp_archea:*
2: sp_bacteria:*
3: sp_fungi:*
4: sp_human:*
5: sp_invertebrate:*
6: sp_mammal:*
7: sp_mhc:*
8: sp_organelle:*
9: sp_phage:*
10: sp_plant:*
11: sp_rodent:*
12: sp_virus:*
13: sp_vertebrate:*
14: sp_unclassified:*
15: sp_rvirus:*
16: sp_bacteriap:*
17: sp_archeap:*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	% Query Match	Length	DB	ID	Description
1	335	100.0	335	4	Q9NQ25	Q9nq25 homo sapien
2	257	76.7	296	4	Q8N6Y8	Q8n6y8 homo sapien
3	257	76.7	328	4	Q9NY23	Q9ny23 homo sapien
4	234	69.9	335	4	Q9NY08	Q9ny08 homo sapien
5	210	62.7	228	4	Q8ND32	Q8nd32 homo sapien
6	9	2.7	156	17	Q9YC18	Q9yc18 aeropyrum p
7	9	2.7	294	11	Q91XA0	Q91xa0 mus musculu
8	9	2.7	300	11	Q8CJ63	Q8cj63 mus musculu
9	9	2.7	333	11	Q8BHK6	Q8bhk6 mus musculu
10	9	2.7	335	11	Q8CJ65	Q8cj65 mus musculu
11	9	2.7	335	11	Q8CJ64	Q8cj64 mus musculu
12	9	2.7	335	11	Q8BTL2	Q8btl2 mus musculu
13	8	2.4	83	16	Q884T6	Q884t6 pseudomonas
14	8	2.4	91	10	Q94E37	Q94e37 oryza sativ
15	8	2.4	129	4	Q8IVU0	Q8ivu0 homo sapien
16	8	2.4	173	16	Q55866	Q55866 synechocyst
17	8	2.4	202	16	Q7V2B6	Q7v2b6 prochloroco
18	8	2.4	211	2	Q9S488	Q9s488 prochloroco
19	8	2.4	286	16	Q9KR71	Q9kr71 vibrio chol
20	8	2.4	317	7	Q9TPE7	Q9tpe7 monodelphis
21	8	2.4	328	6	Q9BDP0	Q9bdp0 aotus trivi
22	8	2.4	347	7	Q9TPK7	Q9tpk7 monodelphis
23	8	2.4	348	16	Q7USC6	Q7usc6 rhodopirell
24	8	2.4	360	4	Q96S86	Q96s86 homo sapien
25	8	2.4	362	7	Q9TPL0	Q9tpl0 monodelphis
26	8	2.4	412	16	Q89RV6	Q89rv6 bradyrhizob
27	8	2.4	467	16	Q8D7P9	Q8d7p9 vibrio vuln
28	8	2.4	533	16	Q8KCC4	Q8kcc4 chlorobium
29	8	2.4	671	16	Q829E0	Q829e0 streptomyce
30	8	2.4	705	10	Q03871	Q03871 triticum ae
31	8	2.4	720	10	Q94IJ6	Q94ij6 triticum ae
32	8	2.4	720	10	Q84TG6	Q84tg6 triticum tu
33	8	2.4	868	5	Q9VH63	Q9vh63 drosophila
34	8	2.4	1053	5	Q8IAQ8	Q8iaq8 plasmodium
35	8	2.4	1235	4	O95428	O95428 homo sapien
36	7	2.1	66	11	Q9QWE3	Q9qwe3 mus sp. alp
37	7	2.1	75	17	Q8TVA7	Q8tva7 methanopyru
38	7	2.1	90	6	Q9GK67	Q9gk67 oryctolagus
39	7	2.1	96	16	Q83E08	Q83e08 coxiella bu
40	7	2.1	97	6	Q9TTS6	Q9tts6 bos taurus
41	7	2.1	97	11	Q9Z318	Q9z318 cavia porce
42	7	2.1	101	16	Q82M02	Q82m02 streptomyce
43	7	2.1	105	5	Q23329	Q23329 caenorhabdi
44	7	2.1	115	2	Q8KX15	Q8kx15 synechococc
45	7	2.1	117	6	Q8HXK4	Q8hxk4 macaca fasc
46	7	2.1	120	5	Q9VNS7	Q9vns7 drosophila
47	7	2.1	124	5	Q9BNJ9	Q9bnj9 platydesmus
48	7	2.1	126	6	Q9BE60	Q9be60 macaca fasc
49	7	2.1	135	10	Q8GWH4	Q8gwh4 arabidopsis
50	7	2.1	143	4	Q86SP9	Q86sp9 homo sapien
51	7	2.1	145	17	Q8TY49	Q8ty49 methanopyru
52	7	2.1	150	2	Q9RFN9	Q9rfn9 mycoplasma
53	7	2.1	153	2	Q9X6K5	Q9x6k5 klebsiella
54	7	2.1	156	12	Q9EMQ1	Q9emq1 amsacta moo
55	7	2.1	159	11	Q9D0N8	Q9d0n8 mus musculu
56	7	2.1	159	11	Q8BRC2	Q8brc2 mus musculu
57	7	2.1	160	16	Q7TUK7	Q7tuk7 prochloroco
58	7	2.1	161	16	Q9ZKH9	Q9zkh9 helicobacte
59	7	2.1	162	16	Q98P38	Q98p38 rhizobium l
60	7	2.1	165	5	Q7YXD5	Q7yxd5 globodera r
61	7	2.1	165	16	Q98J36	Q98j36 rhizobium l
62	7	2.1	167	2	Q46295	Q46295 clostridium
63	7	2.1	167	16	Q8XPC3	Q8xpc3 clostridium
64	7	2.1	169	8	Q94SJ6	Q94sj6 zenopsis ne
65	7	2.1	170	16	Q8Z0K6	Q8z0k6 anabaena sp
66	7	2.1	171	8	Q85DH2	Q85dh2 corydoras r
67	7	2.1	173	8	Q94YR3	Q94yr3 engraulis j
68	7	2.1	173	8	Q8HQL0	Q8hql0 amia calva
69	7	2.1	174	3	Q870Y3	Q870y3 neurospora
70	7	2.1	174	8	Q8HL82	Q8hl82 synbranchus
71	7	2.1	175	8	Q9MJA5	Q9mja5 talpa europ
72	7	2.1	175	8	Q7Y8E4	Q7y8e4 mogera wogu
73	7	2.1	175	8	Q7Y8D2	Q7y8d2 urotrichus
74	7	2.1	179	16	Q9I0B8	Q9i0b8 pseudomonas
75	7	2.1	179	16	Q97EJ3	Q97ej3 clostridium
76	7	2.1	182	16	Q8Y365	Q8y365 ralstonia s
77	7	2.1	182	16	Q8UG92	Q8ug92 agrobacteri
78	7	2.1	183	13	Q8JH31	Q8jh31 gallus gall
79	7	2.1	185	15	Q7ZH80	Q7zh80 human immun
80	7	2.1	185	15	Q7ZH77	Q7zh77 human immun
81	7	2.1	186	11	Q80UC0	Q80uc0 mus musculu
82	7	2.1	187	16	Q9EUJ8	Q9euj8 salmonella
83	7	2.1	189	15	Q7ZH75	Q7zh75 human immun
84	7	2.1	189	15	Q7ZH70	Q7zh70 human immun
85	7	2.1	189	15	Q7ZH66	Q7zh66 human immun
86	7	2.1	190	15	Q7ZH74	Q7zh74 human immun
87	7	2.1	190	15	Q7ZH73	Q7zh73 human immun
88	7	2.1	190	15	Q7ZH72	Q7zh72 human immun
89	7	2.1	190	15	Q7ZH71	Q7zh71 human immun

90	7	2.1	190	15	Q7ZH68	Q7zh68 human immun
91	7	2.1	190	15	Q7ZH67	Q7zh67 human immun
92	7	2.1	191	12	Q9J4B8	Q9j4b8 baboon cyto
93	7	2.1	193	17	Q8U0S5	Q8u0s5 pyrococcus
94	7	2.1	195	15	Q7ZH61	Q7zh61 human immun
95	7	2.1	195	15	Q7ZH58	Q7zh58 human immun
96	7	2.1	195	15	Q7ZH57	Q7zh57 human immun
97	7	2.1	195	15	Q7ZH53	Q7zh53 human immun
98	7	2.1	195	15	Q7ZH52	Q7zh52 human immun
99	7	2.1	195	15	Q7ZH51	Q7zh51 human immun
100	7	2.1	195	15	Q7ZH48	Q7zh48 human immun
101	7	2.1	196	2	Q9AG89	Q9ag89 bdellovibri
102	7	2.1	199	2	O87756	O87756 klebsiella
103	7	2.1	204	12	Q66087	Q66087 canine herp
104	7	2.1	210	3	Q9UW23	Q9uw23 candida alb
105	7	2.1	212	8	Q8LUT5	Q8lut5 gymnogobius
106	7	2.1	212	8	Q8LVD0	Q8lvd0 gymnogobius
107	7	2.1	212	8	Q8LWK7	Q8lwk7 gymnogobius
108	7	2.1	212	8	Q8LWL1	Q8lwl1 gymnogobius
109	7	2.1	212	8	Q8LVD2	Q8lvd2 gymnogobius
110	7	2.1	212	8	Q8LWK8	Q8lwk8 gymnogobius
111	7	2.1	212	8	Q8LWL0	Q8lwl0 gymnogobius
112	7	2.1	212	8	Q8LWL2	Q8lwl2 gymnogobius
113	7	2.1	212	8	Q8LWK9	Q8lwk9 gymnogobius
114	7	2.1	212	8	Q8LWK6	Q8lwk6 gymnogobius
115	7	2.1	212	8	Q8LVD1	Q8lvd1 gymnogobius
116	7	2.1	215	9	Q8W6N4	Q8w6n4 bacteriopha
117	7	2.1	215	10	Q9FGS6	Q9fgs6 arabidopsis
118	7	2.1	216	16	Q8EZ54	Q8ez54 leptospira
119	7	2.1	220	10	Q94EG4	Q94eg4 arabidopsis
120	7	2.1	220	16	Q9RRZ0	Q9rrz0 deinococcus
121	7	2.1	221	12	Q7TFI2	Q7tfi2 rhesus cyto
122	7	2.1	224	2	Q93NK7	Q93nk7 yersinia en
123	7	2.1	224	2	Q9KKH2	Q9kkh2 yersinia en
124	7	2.1	224	9	Q8W6X2	Q8w6x2 cyanophage
125	7	2.1	226	16	Q99YA8	Q99ya8 streptococc
126	7	2.1	226	16	Q8NZL3	Q8nzl3 streptococc
127	7	2.1	226	16	Q8K607	Q8k607 streptococc
128	7	2.1	233	16	Q82DQ3	Q82dq3 streptomyce
129	7	2.1	238	16	P97032	P97032 bacillus su
130	7	2.1	238	16	Q9PPZ8	Q9ppz8 ureaplasma
131	7	2.1	239	10	Q9LES6	Q9les6 arabidopsis
132	7	2.1	244	8	Q35892	Q35892 squatina ne
133	7	2.1	246	10	Q8L655	Q8l655 oryza sativ
134	7	2.1	246	10	Q9AWH6	Q9awh6 oryza sativ
135	7	2.1	246	16	Q8G7M3	Q8g7m3 bifidobacte
136	7	2.1	246	16	Q8E7M3	Q8e7m3 streptococc
137	7	2.1	246	16	Q8E263	Q8e263 streptococc
138	7	2.1	248	16	Q886J4	Q886j4 pseudomonas
139	7	2.1	266	16	Q8A871	Q8a871 bacteroides
140	7	2.1	274	16	Q9L2E8	Q912e8 streptomyce
141	7	2.1	274	17	Q9HRP3	Q9hrp3 halobacteri
142	7	2.1	290	5	Q9TVH2	Q9tvh2 caenorhabdi
143	7	2.1	290	16	Q986W0	Q986w0 rhizobium l
144	7	2.1	300	16	Q830P3	Q830p3 enterococcu
145	7	2.1	301	2	O50573	O50573 bacillus ps
146	7	2.1	301	2	Q93FJ1	Q93fj1 citrobacter
147	7	2.1	301	4	Q8TE98	Q8te98 homo sapien
148	7	2.1	301	16	Q81WD1	Q81wd1 bacillus an
149	7	2.1	301	16	Q819Q4	Q819q4 bacillus ce
150	7	2.1	302	16	Q9RUT6	Q9rut6 deinococcus
151	7	2.1	304	16	Q89EI1	Q89ei1 bradyrhizob
152	7	2.1	306	16	Q82BN1	Q82bn1 streptomyce
153	7	2.1	309	12	Q91T37	Q91t37 lumpy skin
154	7	2.1	309	16	Q8DJ14	Q8dj14 synechococc
155	7	2.1	315	16	Q88H04	Q88h04 pseudomonas
156	7	2.1	317	12	Q86915	Q86915 capripoxvir
157	7	2.1	323	8	Q8LW43	Q8lw43 bubo virgin
158	7	2.1	323	10	Q8LK49	Q8lk49 leucaena gl
159	7	2.1	325	16	Q98B70	Q98b70 rhizobium l
160	7	2.1	328	12	Q8JU20	Q8ju20 lumpy skin
161	7	2.1	329	16	Q986Z1	Q986z1 rhizobium l
162	7	2.1	331	5	Q19173	Q19173 caenorhabdi
163	7	2.1	332	4	Q86UT8	Q86ut8 homo sapien
164	7	2.1	335	8	Q8LWB8	Q8lwb8 glaucidium
165	7	2.1	336	10	Q7XVK0	Q7xvk0 oryza sativ
166	7	2.1	341	12	Q91MZ1	Q91mz1 lumpy skin
167	7	2.1	341	12	Q8JTX8	Q8jtx8 lumpy skin
168	7	2.1	341	16	Q8A7Q3	Q8a7q3 bacteroides
169	7	2.1	342	8	Q8HIE5	Q8hie5 otus atrica
170	7	2.1	343	11	Q8R0W2	Q8r0w2 mus musculu
171	7	2.1	344	8	Q8HIV9	Q8hiv9 bubo ascala
172	7	2.1	344	12	Q8V3G4	Q8v3g4 swinepox vi
173	7	2.1	345	16	Q7VH06	Q7vh06 helicobacte
174	7	2.1	347	8	Q8HIV8	Q8hiv8 bubo bubo (
175	7	2.1	347	8	Q8HIV7	Q8hiv7 bubo bubo (
176	7	2.1	347	8	Q8HIV6	Q8hiv6 bubo bubo (
177	7	2.1	347	8	Q8HCI1	Q8hci1 bubo bubo (
178	7	2.1	347	8	Q8HCG3	Q8hcg3 bubo bubo (
179	7	2.1	347	8	Q8HBR5	Q8hbr5 bubo bubo (
180	7	2.1	347	8	Q8HAS5	Q8has5 bubo bubo (
181	7	2.1	348	17	Q9HPV6	Q9hpv6 halobacteri
182	7	2.1	349	16	Q98NI7	Q98ni7 rhizobium l
183	7	2.1	351	16	Q9PF30	Q9pf30 xylella fas
184	7	2.1	351	16	Q87AJ8	Q87aj8 xylella fas
185	7	2.1	353	16	Q8P6S6	Q8p6s6 xanthomonas
186	7	2.1	356	8	Q9TBF0	Q9tbf0 bubo virgin
187	7	2.1	360	11	Q8VIF0	Q8vif0 rattus norv
188	7	2.1	364	5	Q9VBF5	Q9vbf5 drosophila
189	7	2.1	367	16	Q88QG3	Q88qg3 pseudomonas
190	7	2.1	369	5	Q9XVU2	Q9xvu2 caenorhabdi
191	7	2.1	378	8	Q85DZ8	Q85dz8 eigenmannia
192	7	2.1	378	9	Q859L5	Q8591S staphylococ
193	7	2.1	378	9	Q859J4	Q859j4 staphylococ
194	7	2.1	380	8	Q9XKJ7	Q9xkj7 himantura s
195	7	2.1	381	8	O79571	O79571 mustelus ma
196	7	2.1	381	16	Q8PL48	Q8pl48 xanthomonas
197	7	2.1	388	2	Q8VQV8	Q8vqv8 kitasatospo
198	7	2.1	392	11	Q8K1Q8	Q8k1q8 petromus ty
199	7	2.1	392	11	Q8K1N8	Q8k1n8 thryonomys
200	7	2.1	394	2	Q8KNC8	Q8knc8 micromonosp
201	7	2.1	394	11	Q8VIE8	Q8vie8 rattus norv
202	7	2.1	395	11	Q8VIE9	Q8vie9 rattus norv
203	7	2.1	399	4	Q8N772	Q8n772 homo sapien
204	7	2.1	404	16	Q82IH5	Q82ih5 streptomyce
205	7	2.1	406	10	Q9AUU8	Q9auu8 oryza sativ
206	7	2.1	410	16	Q9PLM2	Q9plm2 chlamydia m
207	7	2.1	411	5	Q9NF81	Q9nf81 leishmania
208	7	2.1	413	10	Q9LYC2	Q9lyc2 arabidopsis
209	7	2.1	419	16	Q89M64	Q89m64 bradyrhizob
210	7	2.1	427	16	Q834I0	Q834i0 enterococcu
211	7	2.1	428	16	Q8ZPG6	Q8zpg6 salmonella
212	7	2.1	428	16	Q8Z716	Q8z716 salmonella
213	7	2.1	430	16	Q88NK6	Q88nk6 pseudomonas
214	7	2.1	433	2	Q84HJ4	Q84hj4 streptomyce
215	7	2.1	439	16	Q8AA31	Q8aa31 bacteroides
216	7	2.1	442	8	Q8HQ09	Q8hq09 thrips imag
217	7	2.1	443	5	Q9V6N4	Q9v6n4 drosophila
218	7	2.1	445	2	P97001	P97001 streptococc
219	7	2.1	448	2	Q45513	Q45513 bacillus su
220	7	2.1	448	16	Q81VN2	Q81vn2 bacillus an
221	7	2.1	452	8	Q8WP40	Q8wf40 venerupis p
222	7	2.1	452	8	Q7YF52	Q7yf52 venerupis (
223	7	2.1	452	8	Q7YF51	Q7yf51 venerupis (
224	7	2.1	452	8	Q7YF50	Q7yf50 venerupis (
225	7	2.1	452	8	Q7YF47	Q7yf47 venerupis (
226	7	2.1	452	8	Q7YF45	Q7yf45 venerupis (
227	7	2.1	454	5	Q9U3P6	Q9u3p6 caenorhabdi
228	7	2.1	458	17	O26297	O26297 methanobact
229	7	2.1	460	13	Q803K4	Q803k4 brachydanio
230	7	2.1	463	16	O34474	O34474 bacillus su
231	7	2.1	464	16	Q92E77	Q92e77 listeria in
232	7	2.1	464	16	Q8Y9F4	Q8y9f4 listeria mo
233	7	2.1	464	16	Q836T7	Q836t7 enterococcu
234	7	2.1	467	17	Q97U81	Q97u81 sulfolobus
235	7	2.1	469	8	Q9B6C8	Q9b6c8 yarrowia li

236	7	2.1	469	16	Q81NB5	Q81nb5 bacillus an
237	7	2.1	469	16	Q81F82	Q81f82 bacillus ce
238	7	2.1	470	5	Q9N4J9	Q9n4j9 caenorhabdi
239	7	2.1	475	10	Q9M3D9	Q9m3d9 arabidopsis
240	7	2.1	480	16	Q8UG85	Q8ug85 agrobacteri
241	7	2.1	487	5	Q9VZ97	Q9vz97 drosophila
242	7	2.1	492	16	Q9A4F0	Q9a4f0 caulobacter
243	7	2.1	493	10	Q9AXF0	Q9axf0 oryza sativ
244	7	2.1	496	5	Q961I9	Q961i9 drosophila
245	7	2.1	496	5	Q9VX74	Q9vx74 drosophila
246	7	2.1	500	10	Q9LKG1	Q9lkg1 mesembryant
247	7	2.1	501	4	Q9BU25	Q9bu25 homo sapien
248	7	2.1	501	16	Q92X18	Q92x18 rhizobium m
249	7	2.1	504	6	Q95LK5	Q95lk5 macaca fasc
250	7	2.1	505	5	Q8IMI4	Q8imi4 drosophila
251	7	2.1	505	13	Q8JG64	Q8jg64 gallus gall
252	7	2.1	507	11	Q8VIF1	Q8vif1 rattus norv
253	7	2.1	509	5	Q8IQ93	Q8iq93 drosophila
254	7	2.1	513	11	Q8K052	Q8k052 mus musculu
255	7	2.1	513	17	Q9HMS7	Q9hms7 halobacteri
256	7	2.1	514	3	Q872D0	Q872d0 neurospora
257	7	2.1	517	2	Q8KY45	Q8ky45 streptomyce
258	7	2.1	518	10	Q7Y0Y8	Q7y0y8 oryza sativ
259	7	2.1	522	16	Q8NP67	Q8np67 corynebacte
260	7	2.1	524	12	Q86404	Q86404 rabies viru
261	7	2.1	524	12	Q9DKD1	Q9dkd1 rabies viru
262	7	2.1	524	12	Q86393	Q86393 rabies viru
263	7	2.1	524	12	Q86385	Q86385 rabies viru
264	7	2.1	532	5	Q9VCQ0	Q9vcq0 drosophila
265	7	2.1	532	10	Q94CQ5	Q94cq5 oryza sativ
266	7	2.1	532	11	Q99J23	Q99j23 mus musculu
267	7	2.1	532	11	Q99J92	Q99j92 mus musculu
268	7	2.1	539	11	Q99LI2	Q99li2 mus musculu
269	7	2.1	540	16	Q888X4	Q888x4 pseudomonas
270	7	2.1	541	11	Q9WU61	Q9wu61 rattus norv
271	7	2.1	551	4	Q96S66	Q96s66 homo sapien
272	7	2.1	572	16	Q8UHB4	Q8uhb4 agrobacteri
273	7	2.1	577	16	Q8KE38	Q8ke38 chlorobium
274	7	2.1	577	16	Q8KAB6	Q8kab6 chlorobium
275	7	2.1	579	5	Q8T7M1	Q8t7m1 physarum po
276	7	2.1	582	16	Q8PRA6	Q8pra6 xanthomonas
277	7	2.1	588	5	O01465	O01465 caenorhabdi
278	7	2.1	591	11	Q8K3H8	Q8k3h8 cricetulus
279	7	2.1	600	16	Q8FPD5	Q8fpd5 corynebacte
280	7	2.1	602	4	Q86YJ9	Q86yj9 homo sapien
281	7	2.1	613	16	Q98C87	Q98c87 rhizobium l
282	7	2.1	617	11	Q8VDQ7	Q8vdq7 mus musculu
283	7	2.1	619	5	Q9VJK5	Q9vjk5 drosophila
284	7	2.1	624	5	Q9BNQ2	Q9bnq2 abacion mag
285	7	2.1	643	16	Q7UVL7	Q7uvl7 rhodopirell
286	7	2.1	643	17	Q9YCH6	Q9ych6 aeropyrum p
287	7	2.1	646	16	Q9KMZ5	Q9kmz5 vibrio chol
288	7	2.1	650	4	Q8NA84	Q8na84 homo sapien
289	7	2.1	656	5	Q9Y114	Q9y114 drosophila
290	7	2.1	660	16	Q8ZMN7	Q8zmn7 salmonella
291	7	2.1	693	4	Q96MV6	Q96mv6 homo sapien
292	7	2.1	694	16	Q7UNZ3	Q7unz3 rhodopirell
293	7	2.1	695	8	Q32508	Q32508 lycium cest
294	7	2.1	695	8	Q32700	Q32700 nolana spat
295	7	2.1	695	8	Q33168	Q33168 salpiglossi
296	7	2.1	696	5	O17479	O17479 hyalophora
297	7	2.1	705	5	Q9VLC6	Q9vlc6 drosophila
298	7	2.1	708	17	Q8ZXU4	Q8zxu4 pyrobaculum
299	7	2.1	715	5	Q8WS55	Q8ws55 oikopleura
300	7	2.1	716	16	Q87CY5	Q87cy5 xylella fas
301	7	2.1	726	2	Q8GFR4	Q8gfr4 citrobacter
302	7	2.1	728	5	Q8IEM1	Q8iem1 plasmodium
303	7	2.1	730	8	O98698	O98698 exacum affi
304	7	2.1	732	4	Q9P0Y2	Q9p0y2 homo sapien
305	7	2.1	732	4	Q9BQ33	Q9bq33 homo sapien
306	7	2.1	737	13	Q802D0	Q802d0 brachydanio
307	7	2.1	744	4	Q8N261	Q8n261 homo sapien
308	7	2.1	765	5	Q20479	Q20479 caenorhabdi
309	7	2.1	797	3	Q9UTK6	Q9utk6 schizosacch
310	7	2.1	801	5	Q8IFG4	Q8ifg4 trypanosoma
311	7	2.1	803	10	Q9LWV8	Q9lwv8 oryza sativ
312	7	2.1	814	10	Q8S808	Q8s808 oryza sativ
313	7	2.1	847	6	Q95KP7	Q95kp7 canis famil
314	7	2.1	870	4	Q8N639	Q8n639 homo sapien
315	7	2.1	870	4	Q7Z3F1	Q7z3f1 homo sapien
316	7	2.1	878	3	Q9USU3	Q9usu3 schizosacch
317	7	2.1	892	4	Q9Y438	Q9y438 homo sapien
318	7	2.1	946	5	O44825	O44825 caenorhabdi
319	7	2.1	946	16	Q827G6	Q827g6 streptomyce
320	7	2.1	947	5	Q9BIA3	Q9bia3 caenorhabdi
321	7	2.1	951	5	Q8MUT5	Q8mut5 helicoverpa
322	7	2.1	951	5	Q8MU79	Q8mu79 helicoverpa
323	7	2.1	951	5	Q86QI6	Q86qi6 helicoverpa
324	7	2.1	951	5	Q7Z268	Q7z268 helicoverpa
325	7	2.1	957	16	Q83QA2	Q83qa2 shigella fl
326	7	2.1	959	16	Q7U3Q5	Q7u3q5 synechococc
327	7	2.1	963	11	Q8BX19	Q8bx19 mus musculu
328	7	2.1	964	16	Q7V9K4	Q7v9k4 prochloroco
329	7	2.1	965	2	Q9RA59	Q9ra59 thermus cal
330	7	2.1	965	2	Q7WUI5	Q7wui5 thermus the
331	7	2.1	969	16	Q7WR47	Q7wr47 bordetella
332	7	2.1	969	16	Q7UZJ5	Q7uzj5 prochloroco
333	7	2.1	977	5	Q8WRU7	Q8wru7 trypanosoma
334	7	2.1	1019	11	Q8BJQ7	Q8bjq7 mus musculu
335	7	2.1	1031	6	Q8HZ52	Q8hz52 felis silve
336	7	2.1	1057	5	Q8MRS3	Q8mrs3 drosophila
337	7	2.1	1057	5	Q869U6	Q869u6 dictyosteli
338	7	2.1	1070	10	Q9SV36	Q9sv36 arabidopsis
339	7	2.1	1133	5	Q8MKU4	Q8mku4 drosophila
340	7	2.1	1142	13	Q7SZV2	Q7szv2 xenopus lae
341	7	2.1	1244	11	Q8CHI5	Q8chi5 rattus norv
342	7	2.1	1271	11	Q8CHR1	Q8chr1 mus musculu
343	7	2.1	1277	5	O17517	O17517 caenorhabdi
344	7	2.1	1285	11	Q8K3T3	Q8k3t3 spalax juda
345	7	2.1	1345	1	Q54437	Q54437 staphylothe
346	7	2.1	1383	12	O89232	O89232 canine herp
347	7	2.1	1415	16	Q8A9R6	Q8a9r6 bacteroides
348	7	2.1	1422	6	Q95KU4	Q95ku4 canis famil
349	7	2.1	1487	11	Q03626	Q03626 rattus norv
350	7	2.1	1543	4	Q8WWZ4	Q8wwz4 homo sapien
351	7	2.1	1543	4	Q7Z2I9	Q7z2i9 homo sapien
352	7	2.1	1552	10	O49370	O49370 arabidopsis
353	7	2.1	1560	11	O88323	O88323 mus musculu
354	7	2.1	1560	11	Q925J9	Q925j9 mus musculu
355	7	2.1	1560	11	Q925K0	Q925k0 mus musculu
356	7	2.1	1585	16	Q8UBT4	Q8ubt4 agrobacteri
357	7	2.1	1620	5	Q24984	Q24984 giardia lam
358	7	2.1	1781	5	Q86KF8	Q86kf8 dictyosteli
359	7	2.1	1785	5	Q7YY85	Q7yy85 cryptospori
360	7	2.1	2055	10	Q7X9V2	Q7x9v2 arabidopsis
361	7	2.1	2061	10	Q9LTV5	Q9ltv5 arabidopsis
362	7	2.1	2087	5	Q8MXL2	Q8mxl2 leishmania
363	7	2.1	2747	2	Q9L800	Q9l800 aeromonas s
364	7	2.1	3410	5	O18290	O18290 caenorhabdi
365	7	2.1	3436	5	Q86NG1	Q86ng1 caenorhabdi
366	7	2.1	3436	5	Q86NF9	Q86nf9 caenorhabdi
367	7	2.1	3436	5	Q86NF8	Q86nf8 caenorhabdi
368	7	2.1	3522	5	Q86NF7	Q86nf7 caenorhabdi
369	7	2.1	4091	5	O96204	O96204 plasmodium
370	7	2.1	4340	2	O30764	O30764 streptomyce
371	7	2.1	4545	11	Q61291	Q61291 mus musculu
372	7	2.1	4918	5	Q867N2	Q867n2 caenorhabdi
373	7	2.1	4929	5	Q867D9	Q867d9 caenorhabdi
374	7	2.1	4944	5	Q86NG0	Q86ng0 caenorhabdi
375	7	2.1	6145	16	Q93H84	Q93h84 streptomyce
376	7	2.1	6239	16	Q9S0R7	Q9s0r7 streptomyce
377	6	1.8	21	4	Q9UMU6	Q9umu6 homo sapien
378	6	1.8	22	8	Q9T2R5	Q9t2r5 solanum tub
379	6	1.8	26	11	Q9QVZ8	Q9qvz8 mus sp. b c
380	6	1.8	29	11	O88224	O88224 mus musculu
381	6	1.8	30	8	Q34897	Q34897 lasiorhinus

382	6	1.8	35	8	Q8M1N3	Q8m1n3 limbodessus
383	6	1.8	36	16	O25409	O25409 helicobacte
384	6	1.8	37	16	Q8F9D8	Q8f9d8 leptospira
385	6	1.8	38	4	Q7Z6X7	Q7z6x7 homo sapien
386	6	1.8	39	16	Q98RB8	Q98rb8 mycoplasma
387	6	1.8	41	2	Q93LW0	Q93lw0 helicobacte
388	6	1.8	41	2	Q93LW5	Q93lw5 helicobacte
389	6	1.8	41	2	Q93LW3	Q93lw3 helicobacte
390	6	1.8	43	2	O82949	O82949 chromatium
391	6	1.8	44	2	Q93UZ3	Q93uz3 chromatium
392	6	1.8	46	2	Q93LT1	Q93lt1 helicobacte
393	6	1.8	46	2	Q93LS1	Q93ls1 helicobacte
394	6	1.8	46	2	Q93LS3	Q93ls3 helicobacte
395	6	1.8	46	2	Q93LU0	Q93lu0 helicobacte
396	6	1.8	46	2	Q93LU3	Q93lu3 helicobacte
397	6	1.8	46	2	Q93LT2	Q93lt2 helicobacte
398	6	1.8	46	2	Q93LT0	Q93lt0 helicobacte
399	6	1.8	46	2	Q93LS6	Q93ls6 helicobacte
400	6	1.8	48	16	Q8G233	Q8g233 brucella su
401	6	1.8	49	16	Q8G004	Q8g004 brucella su
402	6	1.8	51	4	Q9UDD2	Q9udd2 homo sapien
403	6	1.8	52	12	Q91G27	Q91g27 chilo iride
404	6	1.8	53	12	Q8VA91	Q8va91 polyomaviru
405	6	1.8	53	16	Q82EM7	Q82em7 streptomyce
406	6	1.8	54	16	Q82AA3	Q82aa3 streptomyce
407	6	1.8	56	17	O27388	O27388 methanobact
408	6	1.8	57	16	Q92X78	Q92x78 rhizobium m
409	6	1.8	58	2	Q51751	Q51751 pseudomonas
410	6	1.8	60	12	Q69131	Q69131 human herpe
411	6	1.8	60	12	Q04361	Q04361 epstein-bar
412	6	1.8	60	12	Q8AZJ2	Q8azj2 human herpe
413	6	1.8	61	12	O37321	O37321 heliothis a
414	6	1.8	61	16	Q836K7	Q836k7 enterococcu
415	6	1.8	63	5	O96374	O96374 manduca sex
416	6	1.8	63	10	Q940T4	Q940t4 arabidopsis
417	6	1.8	64	16	Q8G2Q6	Q8g2q6 brucella su
418	6	1.8	66	16	Q99U22	Q99u22 staphylococ
419	6	1.8	66	16	Q8NWN2	Q8nwn2 staphylococ
420	6	1.8	66	16	Q8K6N7	Q8k6n7 streptococc
421	6	1.8	67	8	Q7Y8G4	Q7y8g4 hemiechinus
422	6	1.8	67	12	Q86132	Q86132 vesicular s
423	6	1.8	68	2	Q93LL6	Q93ll6 nostoc punc
424	6	1.8	68	13	Q98SP3	Q98sp3 brachydanio
425	6	1.8	68	16	Q8DX22	Q8dx22 streptococc
426	6	1.8	72	5	Q8T1A1	Q8t1a1 dictyosteli
427	6	1.8	72	10	Q7XUP3	Q7xup3 oryza sativ
428	6	1.8	72	10	Q7XSB4	Q7xsb4 oryza sativ
429	6	1.8	72	16	Q9HYJ4	Q9hyj4 pseudomonas
430	6	1.8	72	16	Q817F6	Q817f6 bacillus ce
431	6	1.8	73	2	O32310	O32310 bacillus th
432	6	1.8	73	5	Q9XVG6	Q9xvg6 caenorhabdi
433	6	1.8	73	8	Q85WY1	Q85wy1 pinus korai
434	6	1.8	73	9	O03922	O03922 bacteriopha
435	6	1.8	74	16	Q97P87	Q97p87 streptococc
436	6	1.8	75	6	Q9TTQ1	Q9ttq1 equus cabal
437	6	1.8	75	10	Q941C7	Q941c7 arabidopsis
438	6	1.8	75	16	Q92UZ5	Q92uz5 rhizobium m
439	6	1.8	76	5	Q24505	Q24505 drosophila
440	6	1.8	77	16	Q8YP97	Q8yp97 anabaena sp
441	6	1.8	78	9	Q7Y2F7	Q7y2f7 bacteriopha
442	6	1.8	78	17	Q8Q0K6	Q8q0k6 methanosarc
443	6	1.8	81	6	Q9TTQ2	Q9ttq2 equus cabal
444	6	1.8	82	13	Q7ZTT8	Q7ztt8 brachydanio
445	6	1.8	82	16	Q9PPD2	Q9ppd2 campylobact
446	6	1.8	83	11	O70182	O70182 mus musculu
447	6	1.8	83	17	Q978H2	Q978h2 thermoplasm
448	6	1.8	84	10	Q94CU0	Q94cu0 oryza sativ
449	6	1.8	84	12	Q8QS40	Q8qs40 chimpanzee
450	6	1.8	85	6	Q9TUZ8	Q9tuz8 ovis aries
451	6	1.8	85	10	Q7XQI9	Q7xqi9 oryza sativ
452	6	1.8	86	2	Q9EXM6	Q9exm6 enterobacte
453	6	1.8	86	2	Q53845	Q53845 spiroplasma
454	6	1.8	86	2	Q9EUC4	Q9euc4 serratia ma
455	6	1.8	86	2	Q9EXM8	Q9exm8 enterobacte
456	6	1.8	86	10	Q84JY6	Q84jy6 arabidopsis
457	6	1.8	86	16	Q8YU64	Q8yu64 anabaena sp
458	6	1.8	88	2	O31217	O31217 desulfovibr
459	6	1.8	88	2	O66207	O66207 klebsiella
460	6	1.8	88	2	O66193	O66193 enterobacte
461	6	1.8	88	2	O66217	O66217 pantoea ana
462	6	1.8	88	2	O66195	O66195 enterobacte
463	6	1.8	88	2	O66203	O66203 serratia fi
464	6	1.8	88	2	O66199	O66199 pantoea agg
465	6	1.8	88	2	O66215	O66215 pantoea agg
466	6	1.8	88	2	O66219	O66219 erwinia car
467	6	1.8	88	2	O66191	O66191 enterobacte
468	6	1.8	88	2	O66221	O66221 erwinia aph
469	6	1.8	88	2	O66197	O66197 enterobacte
470	6	1.8	88	2	O66213	O66213 klebsiella
471	6	1.8	88	2	O66201	O66201 serratia ru
472	6	1.8	88	2	O66211	O66211 klebsiella
473	6	1.8	88	2	O66205	O66205 serratia ma
474	6	1.8	88	2	O66209	O66209 klebsiella
475	6	1.8	88	2	O66189	O66189 enterobacte
476	6	1.8	89	2	O33687	O33687 primary end
477	6	1.8	89	5	Q8IEE1	Q8iee1 plasmodium
478	6	1.8	89	10	Q8LJ37	Q8lj37 oryza sativ
479	6	1.8	89	16	Q8DJC2	Q8djc2 synechococc
480	6	1.8	91	5	Q86BD7	Q86bd7 drosophila
481	6	1.8	91	6	Q9N038	Q9n038 macaca fasc
482	6	1.8	93	2	Q9X7B6	Q9x7b6 mycobacteri
483	6	1.8	94	8	Q9ZZM7	Q9zzm7 rattus sp.
484	6	1.8	95	2	Q9AJB6	Q9ajb6 pseudoalter
485	6	1.8	95	16	Q8FYN4	Q8fyn4 brucella su
486	6	1.8	96	2	Q8KIW6	Q8kiw6 buchnera sp
487	6	1.8	96	2	Q8KIW8	Q8kiw8 buchnera sp
488	6	1.8	96	9	Q8W6C5	Q8w6c5 bacteriopha
489	6	1.8	96	16	Q83DL6	Q83dl6 coxiella bu
490	6	1.8	97	2	Q9F4B9	Q9f4b9 bacillus ma
491	6	1.8	97	5	Q8MXM8	Q8mxm8 dictyosteli
492	6	1.8	97	16	Q7U349	Q7u349 candidatus
493	6	1.8	98	6	Q8WN12	Q8wn12 ovis aries
494	6	1.8	98	8	Q8LWP4	Q8lwp4 tupaia bela
495	6	1.8	98	8	Q9G3R5	Q9g3r5 chalinolobu
496	6	1.8	98	8	Q9B996	Q9b996 muntiacus v
497	6	1.8	98	8	Q94YC5	Q94yc5 pipistrellu
498	6	1.8	98	8	Q9B991	Q9b991 muntiacus m
499	6	1.8	98	8	Q9GA22	Q9ga22 tupaia bela
500	6	1.8	98	8	Q9B1C5	Q9b1c5 muntiacus c
501	6	1.8	98	8	Q85RW9	Q85rw9 muntiacus m
502	6	1.8	98	8	Q7Y8H3	Q7y8h3 elephantulu
503	6	1.8	98	10	Q7X8I1	Q7x8i1 oryza sativ
504	6	1.8	98	12	Q9QEW0	Q9qew0 porcine res
505	6	1.8	98	12	Q9QEW1	Q9qew1 porcine res
506	6	1.8	98	12	Q9QEW2	Q9qew2 porcine res
507	6	1.8	99	2	Q8GFN4	Q8gfn4 anabaena cf
508	6	1.8	99	2	Q8GFI8	Q8gfi8 anabaena sp
509	6	1.8	99	2	Q8GFI7	Q8gfi7 anabaena sp
510	6	1.8	99	2	Q8GFI6	Q8gfi6 anabaena sp
511	6	1.8	99	2	Q8GFI5	Q8gfi5 anabaena sp
512	6	1.8	99	2	Q8GFI4	Q8gfi4 anabaena sp
513	6	1.8	99	2	Q8GBZ0	Q8gbz0 nostoc sp.
514	6	1.8	99	2	Q8GBW5	Q8gbw5 planktothri
515	6	1.8	99	2	Q8GBW4	Q8gbw4 planktothri
516	6	1.8	99	2	Q8GBW3	Q8gbw3 planktothri
517	6	1.8	99	2	Q8GBW2	Q8gbw2 planktothri
518	6	1.8	99	2	Q8GBW1	Q8gbw1 plantothrix
519	6	1.8	99	2	Q8GBW0	Q8gbw0 planktothri
520	6	1.8	99	2	Q8GBV9	Q8gbv9 planktothri
521	6	1.8	99	2	Q8GBV8	Q8gbv8 planktothri
522	6	1.8	99	3	Q9C225	Q9c225 neurospora
523	6	1.8	99	6	Q8MKC8	Q8mkc8 equus cabal
524	6	1.8	99	6	Q9TTQ3	Q9ttq3 equus cabal
525	6	1.8	99	6	Q8HYQ0	Q8hyq0 macaca mula
526	6	1.8	99	6	Q865F4	Q865f4 macaca neme
527	6	1.8	99	8	P92624	P92624 diodora asp

528	6	1.8	99	13	Q8UV71	Q8uv71 brachydanio
529	6	1.8	99	15	Q8ULI6	Q8uli6 human immun
530	6	1.8	99	15	Q9IXS2	Q9ixs2 human immun
531	6	1.8	99	15	Q98X59	Q98x59 human immun
532	6	1.8	100	2	Q93IA4	Q93ia4 staphylococ
533	6	1.8	100	4	Q9P0F3	Q9p0f3 homo sapien
534	6	1.8	100	5	Q8IRP7	Q8irp7 drosophila
535	6	1.8	100	6	Q95MD5	Q95md5 bos taurus
536	6	1.8	100	6	Q9TTQ4	Q9ttq4 equus cabal
537	6	1.8	100	10	Q8LN51	Q8ln51 oryza sativ
538	6	1.8	100	16	Q8ZDL6	Q8zdl6 yersinia pe
539	6	1.8	100	16	Q8XFA3	Q8xfa3 salmonella
540	6	1.8	101	5	Q8MKN8	Q8mkn8 drosophila
541	6	1.8	101	6	Q95K94	Q95k94 macaca fasc
542	6	1.8	102	13	Q9DFZ5	Q9dfz5 xenopus lae
543	6	1.8	102	15	Q9YVG5	Q9yvg5 human immun
544	6	1.8	102	15	O91931	O91931 human immun
545	6	1.8	103	5	Q8IPR1	Q8ipr1 drosophila
546	6	1.8	103	15	O91930	O91930 human immun
547	6	1.8	103	16	Q8XK86	Q8xk86 clostridium
548	6	1.8	103	16	Q89MS9	Q89ms9 bradyrhizob
549	6	1.8	104	5	Q8T4J5	Q8t4j5 scylla serr
550	6	1.8	104	10	Q42028	Q42028 arabidopsis
551	6	1.8	104	15	O91929	O91929 human immun
552	6	1.8	104	15	O91934	O91934 human immun
553	6	1.8	104	16	Q9FBM5	Q9fbm5 streptomyce
554	6	1.8	105	4	O60384	O60384 homo sapien
555	6	1.8	106	2	Q847N9	Q847n9 aster yello
556	6	1.8	106	15	O91932	O91932 human immun
557	6	1.8	106	15	O91928	O91928 human immun
558	6	1.8	106	16	Q92IZ5	Q92iz5 rickettsia
559	6	1.8	107	11	Q8C4E6	Q8c4e6 mus musculu
560	6	1.8	107	12	Q91TU9	Q91tu9 tupaia herp
561	6	1.8	107	15	Q9YVG7	Q9yvg7 human immun
562	6	1.8	107	15	O91910	O91910 human immun
563	6	1.8	107	15	Q9YIL5	Q9yil5 human immun
564	6	1.8	107	15	Q9YVF6	Q9yvf6 human immun
565	6	1.8	107	15	O91927	O91927 human immun
566	6	1.8	107	15	Q9YVH2	Q9yvh2 human immun
567	6	1.8	107	15	O91920	O91920 human immun
568	6	1.8	107	16	O51651	O51651 borrelia bu
569	6	1.8	107	16	Q88J53	Q88j53 pseudomonas
570	6	1.8	108	2	Q8KVR7	Q8kvr7 bacteroides
571	6	1.8	108	2	Q45800	Q45800 bacteroides
572	6	1.8	108	2	Q44706	Q44706 borrelia bu
573	6	1.8	108	11	Q9CV78	Q9cv78 mus musculu
574	6	1.8	109	4	Q7Z7Q8	Q7z7q8 homo sapien
575	6	1.8	109	16	Q88CE9	Q88ce9 pseudomonas
576	6	1.8	109	17	O58093	O58093 pyrococcus
577	6	1.8	110	5	Q8T4I6	Q8t4i6 drosophila
578	6	1.8	110	13	O42454	O42454 trachemys s
579	6	1.8	111	10	Q8LHY8	Q8lhy8 oryza sativ
580	6	1.8	111	11	Q811A7	Q811a7 rattus norv
581	6	1.8	111	16	Q9HW55	Q9hw55 pseudomonas
582	6	1.8	111	17	Q9UY95	Q9uy95 pyrococcus
583	6	1.8	112	2	Q93IB3	Q93ib3 staphylococ
584	6	1.8	112	3	Q03884	Q03884 saccharomyc
585	6	1.8	112	16	Q8Y0L8	Q8y0l8 ralstonia s
586	6	1.8	112	17	Q8ZTR9	Q8ztr9 pyrobaculum
587	6	1.8	113	2	Q8RQR1	Q8rqr1 lactobacill
588	6	1.8	113	8	Q35015	Q35015 meloidogyne
589	6	1.8	113	16	Q8ZPH6	Q8zph6 salmonella
590	6	1.8	113	16	Q886Z6	Q886z6 pseudomonas
591	6	1.8	113	16	Q7WK58	Q7wk58 bordetella
592	6	1.8	113	16	Q7W8U8	Q7w8u8 bordetella
593	6	1.8	113	16	Q7VXG6	Q7vxg6 bordetella
594	6	1.8	114	4	Q8IWS4	Q8iws4 homo sapien
595	6	1.8	114	10	Q94AF8	Q94af8 arabidopsis
596	6	1.8	114	16	Q7USA6	Q7usa6 rhodopirell
597	6	1.8	115	15	Q7ZEJ9	Q7zej9 human immun
598	6	1.8	115	16	Q8YJ66	Q8yj66 brucella me
599	6	1.8	115	16	Q8CMN1	Q8cmn1 staphylococ
600	6	1.8	116	5	Q7YX03	Q7yx03 caenorhabdi
601	6	1.8	116	16	Q8XJV0	Q8xjv0 clostridium
602	6	1.8	116	16	Q823C0	Q823c0 chlamydophi
603	6	1.8	117	4	Q96A31	Q96a31 homo sapien
604	6	1.8	117	11	Q63063	Q63063 rattus norv
605	6	1.8	117	16	Q8Y1U1	Q8y1u1 ralstonia s
606	6	1.8	118	6	Q862Z6	Q862z6 pan troglod
607	6	1.8	118	11	Q8R2H0	Q8r2h0 rattus norv
608	6	1.8	118	11	Q9CRB3	Q9crb3 mus musculu
609	6	1.8	118	16	Q8UD05	Q8ud05 agrobacteri
610	6	1.8	118	16	Q8UCV9	Q8ucv9 agrobacteri
611	6	1.8	119	16	Q8PQM8	Q8pqm8 xanthomonas
612	6	1.8	119	16	Q8PDQ7	Q8pdq7 xanthomonas
613	6	1.8	119	16	Q7W7B7	Q7w7b7 bordetella
614	6	1.8	120	5	Q86JJ5	Q86jj5 dictyosteli
615	6	1.8	120	11	Q8C699	Q8c699 mus musculu
616	6	1.8	121	5	Q95TD0	Q95td0 drosophila
617	6	1.8	122	2	Q9AF23	Q9af23 uncultured
618	6	1.8	122	4	Q8WU89	Q8wu89 homo sapien
619	6	1.8	122	4	Q9NV16	Q9nv16 homo sapien
620	6	1.8	122	4	Q8N8P7	Q8n8p7 homo sapien
621	6	1.8	122	11	Q8CID7	Q8cid7 mus musculu
622	6	1.8	122	16	Q9HZU9	Q9hzu9 pseudomonas
623	6	1.8	122	16	Q89YH2	Q89yh2 bacteroides
624	6	1.8	122	17	Q8U1X6	Q8u1x6 pyrococcus
625	6	1.8	122	17	Q8PS76	Q8ps76 methanosarc
626	6	1.8	123	11	Q90137	Q90137 marmota mon
627	6	1.8	123	13	Q9DDX9	Q9ddx9 xenopus lae
628	6	1.8	123	16	Q9RT46	Q9rt46 deinococcus
629	6	1.8	124	12	Q65085	Q65085 foot-and-mo
630	6	1.8	124	16	Q92B29	Q92b29 listeria in
631	6	1.8	124	16	Q7WPD6	Q7wpd6 bordetella
632	6	1.8	125	5	Q9U1P6	Q9u1p6 caenorhabdi
633	6	1.8	125	13	Q9DFZ6	Q9dfz6 xenopus lae
634	6	1.8	126	1	P95861	P95861 sulfolobus
635	6	1.8	126	10	Q7Y1C7	Q7y1c7 oryza sativ
636	6	1.8	126	16	Q7UB47	Q7ub47 shigella fl
637	6	1.8	126	17	Q9YEE3	Q9yee3 aeropyrum p
638	6	1.8	127	12	O10461	O10461 venezuelan
639	6	1.8	127	12	O10457	O10457 venezuelan
640	6	1.8	127	12	O10460	O10460 venezuelan
641	6	1.8	127	12	O39813	O39813 encephalomy
642	6	1.8	127	13	Q9DDY1	Q9ddy1 xenopus lae
643	6	1.8	127	16	Q8EIW3	Q8eiw3 shewanella
644	6	1.8	128	2	Q7X3J9	Q7x3j9 pseudomonas
645	6	1.8	128	9	Q9B030	Q9b030 bacteriopha
646	6	1.8	128	10	Q94I63	Q94i63 oryza sativ
647	6	1.8	128	11	Q8C2V3	Q8c2v3 mus musculu
648	6	1.8	128	16	Q9RVX6	Q9rvx6 deinococcus
649	6	1.8	128	16	Q928A1	Q928a1 listeria in
650	6	1.8	128	16	Q8Y4F2	Q8y4f2 listeria mo
651	6	1.8	129	2	Q84GY0	Q84gy0 photorhabdu
652	6	1.8	129	5	Q86KR5	Q86kr5 dictyosteli
653	6	1.8	129	6	Q862M3	Q862m3 bos taurus
654	6	1.8	129	16	Q8NNM5	Q8nnm5 corynebacte
655	6	1.8	129	17	Q8TR81	Q8tr81 methanosarc
656	6	1.8	132	5	Q8T9B2	Q8t9b2 drosophila
657	6	1.8	132	5	Q9W2M8	Q9w2m8 drosophila
658	6	1.8	132	8	Q7Y7V2	Q7y7v2 cunninghame
659	6	1.8	132	12	O39815	O39815 encephalomy
660	6	1.8	132	16	Q9RT34	Q9rt34 deinococcus
661	6	1.8	132	16	Q9KA40	Q9ka40 bacillus ha
662	6	1.8	132	16	Q9A895	Q9a895 caulobacter
663	6	1.8	133	2	Q55212	Q55212 streptococc
664	6	1.8	133	16	Q7UVZ6	Q7uvz6 rhodopirell
665	6	1.8	134	10	Q9ARU5	Q9aru5 oryza sativ
666	6	1.8	134	13	Q9DDX4	Q9ddx4 xenopus lae
667	6	1.8	134	16	O69567	O69567 mycobacteri
668	6	1.8	134	16	Q7V2U6	Q7v2u6 prochloroco
669	6	1.8	135	6	Q29049	Q29049 sus scrofa
670	6	1.8	135	16	P95012	P95012 mycobacteri
671	6	1.8	135	16	Q9I380	Q9i380 pseudomonas
672	6	1.8	135	16	Q9CBH3	Q9cbh3 mycobacteri
673	6	1.8	135	16	Q8DVR5	Q8dvr5 streptococc

674	6	1.8	135	16	Q7TYC5	Q7tyc5 mycobacteri
675	6	1.8	136	5	O45582	O45582 caenorhabdi
676	6	1.8	136	5	Q9XYH8	Q9xyh8 leishmania
677	6	1.8	136	6	Q8WNA0	Q8wna0 cynocephalu
678	6	1.8	136	11	Q9CQK5	Q9cqk5 mus musculu
679	6	1.8	136	13	Q9DDX3	Q9ddx3 xenopus lae
680	6	1.8	137	5	Q9BI29	Q9bi29 chlamys isl
681	6	1.8	137	12	Q9E2N0	Q9e2n0 hepatitis c
682	6	1.8	137	16	Q8CVY5	Q8cvy5 escherichia
683	6	1.8	137	16	Q88MD0	Q88md0 pseudomonas
684	6	1.8	137	16	Q83KM3	Q83km3 shigella fl
685	6	1.8	138	2	Q93KI8	Q93ki8 uncultured
686	6	1.8	138	12	Q91CE6	Q91ce6 west nile v
687	6	1.8	138	12	Q7T7N4	Q7t7n4 bubaline he
688	6	1.8	138	13	Q9DDY2	Q9ddy2 xenopus lae
689	6	1.8	138	17	Q8ZZA5	Q8zza5 pyrobaculum
690	6	1.8	139	2	Q99Q68	Q99q68 uncultured
691	6	1.8	139	2	Q9AF44	Q9af44 uncultured
692	6	1.8	139	2	Q9AF45	Q9af45 uncultured
693	6	1.8	139	2	Q9AF46	Q9af46 uncultured
694	6	1.8	139	5	Q9BNG1	Q9bng1 carcinoscor
695	6	1.8	139	5	Q9BNF2	Q9bnf2 chthonius t
696	6	1.8	139	16	Q89S26	Q89s26 bradyrhizob
697	6	1.8	139	16	Q88F26	Q88f26 pseudomonas
698	6	1.8	140	3	Q92276	Q92276 saccharomyc
699	6	1.8	140	16	Q9K0F8	Q9k0f8 neisseria m
700	6	1.8	140	16	Q8U957	Q8u957 agrobacteri

ALIGNMENTS

RESULT 1
Q9NQ25
ID Q9NQ25 PRELIMINARY; PRT; 335 AA.
AC Q9NQ25;
DT 01-OCT-2000 (TrEMBLrel. 15, Created)
DT 01-OCT-2000 (TrEMBLrel. 15, Last sequence update)
DT 01-OCT-2003 (TrEMBLrel. 25, Last annotation update)
DE BA404F10.4 (Novel LY9 (Lymphocyte antigen 9) like protein) (NK cell
DE receptor) (Membrane protein FOAP-12) (CD2-like receptor activating
DE cytotoxic cells).
GN BA404F10.4 OR CS1.
OS Homo sapiens (Human).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
OX NCBI_TaxID=9606;
RN [1]
RP SEQUENCE FROM N.A.
RA Bates K.;
RL Submitted (APR-2000) to the EMBL/GenBank/DDBJ databases.
RN [2]
RP SEQUENCE FROM N.A.
RA Boles K.S., Mathew P.A. Sr.;
RT "Cloning of a new member of the CD2 subset of receptors expressed on
RT NK cells.";
RL Submitted (AUG-2000) to the EMBL/GenBank/DDBJ databases.
RN [3]
RP SEQUENCE FROM N.A.
RC TISSUE=Macrophage;
RA Fujii Y., Takayama K., Tsuritani K., Yajima Y., Amemiya T., Ukai Y.,
RA Naito K., Kawaguchi A.;
RT "Homo sapiens mRNA for FOAP-12 protein, complete cds.";
RL Submitted (MAY-1999) to the EMBL/GenBank/DDBJ databases.
RN [4]
RP SEQUENCE FROM N.A.
RA Bouchon A., Cella M., Grierson H.L., Cohen J.I., Colonna M.;
RT "Cutting Edge: Activation of NK Cell-Mediated Cytotoxicity by a SAP-
RT Independent Receptor of the CD2 Family.";
RL J. Immunol. 167:0-0(2001).
DR EMBL; AL121985; CAC00579.1; -.
DR EMBL; AF291815; AAK11549.1; -.
DR EMBL; AB027233; BAB61022.1; -.
DR EMBL; AF390894; AAL26989.1; -.
DR GO; GO:0004872; F:receptor activity; IEA.
DR InterPro; IPR003599; Ig.
DR InterPro; IPR007110; Ig-like.
DR SMART; SM00409; IG; 1.
DR PROSITE; PS50835; IG_LIKE; 1.
KW Receptor.
SQ SEQUENCE 335 AA; 37421 MW; D09ABBCFF74BE8D4 CRC64;

Query Match 100.0%; Score 335; DB 4; Length 335;
Best Local Similarity 100.0%; Pred. No. 0;
Matches 335; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

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Qy          1 MAGSPTCLTLIYILWQLTGSAASGPVKELVGSVGGAVTFPLKSKVKQVDSIVWTFNTTPL 60
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Db          1 MAGSPTCLTLIYILWQLTGSAASGPVKELVGSVGGAVTFPLKSKVKQVDSIVWTFNTTPL 60

Qy         61 VTIQPEGGTIIVTQNRNRERVDFPDGGYSLKLSKLKKNDSGIYYVGIYSSSLQQPSTQEY 120
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db         61 VTIQPEGGTIIVTQNRNRERVDFPDGGYSLKLSKLKKNDSGIYYVGIYSSSLQQPSTQEY 120

Qy        121 VLHVYEHLSKPKVTMGLQSNKNGTCVTNLTCCMEHGEEDVIYTWKALGQAANESHNGSIL 180
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        121 VLHVYEHLSKPKVTMGLQSNKNGTCVTNLTCCMEHGEEDVIYTWKALGQAANESHNGSIL 180

Qy        181 PISWRWGESDMTFICVARNPVSRNFSSPILARKLCEGAADDPDSSMVLLCLLLVPLLLSL 240
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        181 PISWRWGESDMTFICVARNPVSRNFSSPILARKLCEGAADDPDSSMVLLCLLLVPLLLSL 240

Qy        241 FVLGLFLWFLKRERQEEYIEEKKRVDICRETPNICPHSGENTEYDTIPHTNRTILKEDPA 300
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        241 FVLGLFLWFLKRERQEEYIEEKKRVDICRETPNICPHSGENTEYDTIPHTNRTILKEDPA 300

Qy        301 NTVYSTVEIPKKMENPHSLLTMPDTPRLFAYENVI 335
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Db        301 NTVYSTVEIPKKMENPHSLLTMPDTPRLFAYENVI 335
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RESULT 2
Q8N6Y8
ID Q8N6Y8 PRELIMINARY; PRT; 296 AA.
AC Q8N6Y8;
DT 01-OCT-2002 (TrEMBLrel. 22, Created)
DT 01-OCT-2002 (TrEMBLrel. 22, Last sequence update)
DT 01-OCT-2003 (TrEMBLrel. 25, Last annotation update)
DE 19A24 protein.
OS Homo sapiens (Human).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
OX NCBI_TaxID=9606;
RN [1]
RP SEQUENCE FROM N.A.
RC TISSUE=Lung;
RA Strausberg R.;
RL Submitted (APR-2002) to the EMBL/GenBank/DDBJ databases.
DR EMBL; BC027867; AAH27867.1; -.
DR InterPro; IPR007110; Ig-like.
DR PROSITE; PS50835; IG_LIKE; 1.
SQ SEQUENCE 296 AA; 32581 MW; E85D277192494EEC CRC64;

Query Match 76.7%; Score 257; DB 4; Length 296;
Best Local Similarity 100.0%; Pred. No. 5e-259;
Matches 257; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

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Db          1 MAGSPTCLTLIYILWQLTGSAASGPVKELVGSVGGAVTFPLKSKVKQVDSIVWTFNTTPL 60

Qy         61 VTIQPEGGTIIVTQNRNRERVDFPDGGYSLKLSKLKKNDSGIYYVGIYSSSLQQPSTQEY 120
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Db         61 VTIQPEGGTIIVTQNRNRERVDFPDGGYSLKLSKLKKNDSGIYYVGIYSSSLQQPSTQEY 120

Qy        121 VLHVYEHLSKPKVTMGLQSNKNGTCVTNLTCCMEHGEEDVIYTWKALGQAANESHNGSIL 180
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Db        121 VLHVYEHLSKPKVTMGLQSNKNGTCVTNLTCCMEHGEEDVIYTWKALGQAANESHNGSIL 180

Qy        181 PISWRWGESDMTFICVARNPVSRNFSSPILARKLCEGAADDPDSSMVLLCLLLVPLLLSL 240
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Db        181 PISWRWGESDMTFICVARNPVSRNFSSPILARKLCEGAADDPDSSMVLLCLLLVPLLLSL 240

Qy        241 FVLGLFLWFLKRERQEE 257
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Db        241 FVLGLFLWFLKRERQEE 257


RESULT 3
Q9NY23
ID   Q9NY23      PRELIMINARY;      PRT;   328 AA.
AC   Q9NY23;
DT   01-OCT-2000 (TrEMBLrel. 15, Created)
DT   01-OCT-2000 (TrEMBLrel. 15, Last sequence update)
DT   01-OCT-2003 (TrEMBLrel. 25, Last annotation update)
DE   19A24 protein.
GN   19A24.
OS   Homo sapiens (Human).
OC   Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC   Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
OX   NCBI_TaxID=9606;
RN   [1]
RP   SEQUENCE FROM N.A.
RC   TISSUE=Peripheral blood;
RA   Murphy J.J., Norton J.D., Hobby P., Sutton B.J.;
RT   "An early response gene that encodes an immunoglobulin superfamily
RT   member with structural similarity to CD2.";
RL   Submitted (FEB-2000) to the EMBL/GenBank/DDBJ databases.
DR   EMBL; AJ271869; CAB76561.1; -.
DR   InterPro; IPR003599; Ig.
DR   InterPro; IPR007110; Ig-like.
DR   SMART; SM00409; IG; 1.
DR   PROSITE; PS50835; IG_LIKE; 1.
SQ   SEQUENCE   328 AA;  36490 MW;  E68A7243964380DB CRC64;

  Query Match            76.7%;  Score 257;  DB 4;  Length 328;
  Best Local Similarity  100.0%;  Pred. No. 5.5e-259;
  Matches  257;  Conservative    0;  Mismatches    0;  Indels    0;  Gaps    0;

Qy          1 MAGSPTCLTLIYILWQLTGSAASGPVKELVGSVGGAVTFPLKSKVKQVDSIVWTFNTTPL 60
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Db          1 MAGSPTCLTLIYILWQLTGSAASGPVKELVGSVGGAVTFPLKSKVKQVDSIVWTFNTTPL 60

Qy         61 VTIQPEGGTIIVTQNRNRERVDFPDGGYSLKLSKLKKNDSGIYYVGIYSSSLQQPSTQEY 120
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Db         61 VTIQPEGGTIIVTQNRNRERVDFPDGGYSLKLSKLKKNDSGIYYVGIYSSSLQQPSTQEY 120

Qy        121 VLHVYEHLSKPKVTMGLQSNKNGTCVTNLTCCMEHGEEDVIYTWKALGQAANESHNGSIL 180
                ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        121 VLHVYEHLSKPKVTMGLQSNKNGTCVTNLTCCMEHGEEDVIYTWKALGQAANESHNGSIL 180

Qy        181 PISWRWGESDMTFICVARNPVSRNFSSPILARKLCEGAADDPDSSMVLLCLLLVPLLLSL 240
                ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        181 PISWRWGESDMTFICVARNPVSRNFSSPILARKLCEGAADDPDSSMVLLCLLLVPLLLSL 240

Qy        241 FVLGLFLWFLKRERQEE 257
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Db        241 FVLGLFLWFLKRERQEE 257


RESULT 4
Q9NY08
ID   Q9NY08      PRELIMINARY;      PRT;   335 AA.
AC   Q9NY08;
DT   01-OCT-2000 (TrEMBLrel. 15, Created)
DT   01-MAR-2001 (TrEMBLrel. 16, Last sequence update)
DT   01-OCT-2003 (TrEMBLrel. 25, Last annotation update)
DE   19A protein.
GN   19A.
OS   Homo sapiens (Human).
OC   Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC   Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
OX   NCBI_TaxID=9606;
RN   [1]
RP   SEQUENCE FROM N.A.
RA   Murphy J.J., Norton J.D., Hobby P., Sutton B.J.;
RT   "An early response gene that encodes an immunoglobulin superfamily
RT   member with structural similarity to CD2.";
RL   Submitted (JAN-2001) to the EMBL/GenBank/DDBJ databases.
DR   EMBL; AJ276429; CAB81950.2; -.
DR   InterPro; IPR003599; Ig.
DR   InterPro; IPR007110; Ig-like.
DR   SMART; SM00409; IG; 1.
DR   PROSITE; PS50835; IG_LIKE; 1.
SQ   SEQUENCE   335 AA;  37403 MW;  BB758E505CA4DDD5 CRC64;

  Query Match            69.9%;  Score 234;  DB 4;  Length 335;
  Best Local Similarity  99.7%;  Pred. No. 5.4e-235;
  Matches  334;  Conservative    0;  Mismatches    1;  Indels    0;  Gaps    0;

Qy          1 MAGSPTCLTLIYILWQLTGSAASGPVKELVGSVGGAVTFPLKSKVKQVDSIVWTFNTTPL 60
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Db          1 MAGSPTCLTLIYILWQLTGSAASGPVKELVGSVGGAVTFPLKSKVKQVDSIVWTFNTTPL 60

Qy         61 VTIQPEGGTIIVTQNRNRERVDFPDGGYSLKLSKLKKNDSGIYYVGIYSSSLQQPSTQEY 120
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Db         61 VTIQPEGGTIIVTQNRNRERVDFPDGGYSLKLSKLKKNDSGIYYVGIYSSSLQQPSTQEY 120

Qy        121 VLHVYEHLSKPKVTMGLQSNKNGTCVTNLTCCMEHGEEDVIYTWKALGQAANESHNGSIL 180
                ||||||||||||||| ||||||||||||||||||||||||||||||||||||||||||||||||
Db        121 VLHVYEHLSKPKVTLGLQSNKNGTCVTNLTCCMEHGEEDVIYTWKALGQAANESHNGSIL 180

Qy        181 PISWRWGESDMTFICVARNPVSRNFSSPILARKLCEGAADDPDSSMVLLCLLLVPLLLSL 240
                ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        181 PISWRWGESDMTFICVARNPVSRNFSSPILARKLCEGAADDPDSSMVLLCLLLVPLLLSL 240

Qy        241 FVLGLFLWFLKRERQEEYIEEKKRVDICRETPNICPHSGENTEYDTIPHTNRTILKEDPA 300
                ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        241 FVLGLFLWFLKRERQEEYIEEKKRVDICRETPNICPHSGENTEYDTIPHTNRTILKEDPA 300

Qy        301 NTVYSTVEIPKKMENPHSLLTMPDTPRLFAYENVI 335
                |||||||||||||||||||||||||||||||||
Db        301 NTVYSTVEIPKKMENPHSLLTMPDTPRLFAYENVI 335


RESULT 5
Q8ND32
ID   Q8ND32      PRELIMINARY;      PRT;   228 AA.
AC   Q8ND32;
DT   01-OCT-2002 (TrEMBLrel. 22, Created)
DT   01-OCT-2002 (TrEMBLrel. 22, Last sequence update)
DT   01-OCT-2003 (TrEMBLrel. 25, Last annotation update)
DE   Hypothetical protein.
GN   DKFZP667F126.
OS   Homo sapiens (Human).
OC   Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC   Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
OX   NCBI_TaxID=9606;
RN   [1]
RP   SEQUENCE FROM N.A.
RC   TISSUE=Lymph node;
RA   Bloecker H., Boecher M., Brandt P., Mewes H.W., Weil B., Wiemann S.;
RL   Submitted (JUL-2002) to the EMBL/GenBank/DDBJ databases.
DR   EMBL; AL834424; CAD39085.1; -.
DR   InterPro; IPR007110; Ig-like.
DR   PROSITE; PS50835; IG_LIKE; 1.
KW   Hypothetical protein.
SQ   SEQUENCE   228 AA;  25831 MW;  2B01DB70E7BBFC14 CRC64;

  Query Match            62.7%;  Score 210;  DB 4;  Length 228;
  Best Local Similarity  100.0%;  Pred. No. 4e-210;
  Matches  210;  Conservative    0;  Mismatches    0;  Indels    0;  Gaps    0;
```

```
Qy        126 EHLSKPKVTMGLQSNKNGTCVTNLTCCMEHGEEDVIYTWKALGQAANESHNGSILPISWR 185
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db         19 EHLSKPKVTMGLQSNKNGTCVTNLTCCMEHGEEDVIYTWKALGQAANESHNGSILPISWR 78

Qy        186 WGESDMTFICVARNPVSRNFSSPILARKLCEGAADDPDSSMVLLCLLLVPLLLSLFVLGL 245
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db         79 WGESDMTFICVARNPVSRNFSSPILARKLCEGAADDPDSSMVLLCLLLVPLLLSLFVLGL 138

Qy        246 FLWFLKRERQEEYIEEKKRVDICRETPNICPHSGENTEYDTIPHTNRTILKEDPANTVYS 305
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        139 FLWFLKRERQEEYIEEKKRVDICRETPNICPHSGENTEYDTIPHTNRTILKEDPANTVYS 198

Qy        306 TVEIPKKMENPHSLLTMPDTPRLFAYENVI 335
              |||||||||||||||||||||||||||||
Db        199 TVEIPKKMENPHSLLTMPDTPRLFAYENVI 228
```

```
RESULT 6
Q9YC18
ID   Q9YC18      PRELIMINARY;      PRT;   156 AA.
AC   Q9YC18;
DT   01-NOV-1999 (TrEMBLrel. 12, Created)
DT   01-NOV-1999 (TrEMBLrel. 12, Last sequence update)
DT   01-JUN-2003 (TrEMBLrel. 24, Last annotation update)
DE   Hypothetical protein APE1433.
GN   APE1433.
OS   Aeropyrum pernix.
OC   Archaea; Crenarchaeota; Thermoprotei; Desulfurococcales;
OC   Desulfurococcaceae; Aeropyrum.
OX   NCBI_TaxID=56636;
RN   [1]
RP   SEQUENCE FROM N.A.
RC   STRAIN=K1;
RX   MEDLINE=99310339; PubMed=10382966;
RA   Kawarabayasi Y., Hino Y., Horikawa H., Yamazaki S., Haikawa Y.,
RA   Jin-no K., Takahashi M., Sekine M., Baba S.-I., Ankai A., Kosugi H.,
RA   Hosoyama A., Fukui S., Nagai Y., Nishijima K., Nakazawa H.,
RA   Takamiya M., Masuda S., Funahashi T., Tanaka T., Kudoh Y.,
RA   Yamazaki J., Kushida N., Oguchi A., Aoki K.-I., Kubota K.,
RA   Nakamura Y., Nomura N., Sako Y., Kikuchi H.;
RT   "Complete genome sequence of an aerobic hyper-thermophilic
RT   crenarchaeon, Aeropyrum pernix K1.";
RL   DNA Res. 6:83-101(1999).
DR   EMBL; AP000061; BAA80430.1; -.
DR   PIR; H72621; H72621.
KW   Hypothetical protein; Complete proteome.
SQ   SEQUENCE   156 AA;  15954 MW;  73BBB5C99FBE453D CRC64;

  Query Match             2.7%;  Score 9;  DB 17;  Length 156;
  Best Local Similarity   100.0%;  Pred. No. 1;
  Matches    9;  Conservative    0;  Mismatches    0;  Indels    0;  Gaps    0;

Qy         17 LTGSAASGP 25
              |||||||||
Db        105 LTGSAASGP 113
```

```
RESULT 7
Q91XA0
ID   Q91XA0      PRELIMINARY;      PRT;   294 AA.
AC   Q91XA0;
DT   01-DEC-2001 (TrEMBLrel. 19, Created)
DT   01-DEC-2001 (TrEMBLrel. 19, Last sequence update)
DT   01-OCT-2003 (TrEMBLrel. 25, Last annotation update)
DE   Similar to 19A24 protein.
GN   4930560D03RIK.
OS   Mus musculus (Mouse).
OC   Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC   Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus.
OX   NCBI_TaxID=10090;
RN   [1]
RP   SEQUENCE FROM N.A.
RC   TISSUE=Salivary gland;
RA   Strausberg R.;
RL   Submitted (JUL-2001) to the EMBL/GenBank/DDBJ databases.
DR   EMBL; BC011154; AAH11154.1; -.
DR   MGD; MGI:1922595; 4930560D03Rik.
DR   InterPro; IPR007110; Ig-like.
DR   PROSITE; PS50835; IG_LIKE; 1.
SQ   SEQUENCE   294 AA;  32782 MW;  F4C88BC4CFAA1AFB CRC64;

  Query Match             2.7%;  Score 9;  DB 11;  Length 294;
  Best Local Similarity   100.0%;  Pred. No. 1.8;
  Matches    9;  Conservative    0;  Mismatches    0;  Indels    0;  Gaps    0;

Qy        138 QSNKNGTCV 146
              |||||||||
Db        135 QSNKNGTCV 143
```

```
RESULT 8
Q8CJ63
ID   Q8CJ63      PRELIMINARY;      PRT;   300 AA.
AC   Q8CJ63;
DT   01-MAR-2003 (TrEMBLrel. 23, Created)
DT   01-MAR-2003 (TrEMBLrel. 23, Last sequence update)
DT   01-OCT-2003 (TrEMBLrel. 25, Last annotation update)
DE   Leukocyte cell-surface antigen isoform s.
GN   4930560D03RIK.
OS   Mus musculus (Mouse).
OC   Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC   Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus.
OX   NCBI_TaxID=10090;
RN   [1]
RP   SEQUENCE FROM N.A.
RC   STRAIN=BALB/c; TISSUE=Thymus;
RX   MEDLINE=22226696; PubMed=12242590;
RA   Tovar V., Del Valle J., Zapater N., Martin M., Romero X., Pizcueta P.,
RA   Bosch J., Terhorst C., Engel P.;
RT   "Mouse novel Ly9: a new member of the expanding CD150 (SLAM) family of
RT   leukocyte cell-surface receptors.";
RL   Immunogenetics 54:394-402(2002).
DR   EMBL; AF467911; AAN63160.1; -.
DR   PIR; PT0566; PT0566.
DR   MGD; MGI:1922595; 4930560D03Rik.
DR   InterPro; IPR007110; Ig-like.
DR   PROSITE; PS50835; IG_LIKE; 1.
SQ   SEQUENCE   300 AA;  33332 MW;  9948108710BEBC3D CRC64;

  Query Match             2.7%;  Score 9;  DB 11;  Length 300;
  Best Local Similarity   100.0%;  Pred. No. 1.8;
  Matches    9;  Conservative    0;  Mismatches    0;  Indels    0;  Gaps    0;

Qy        138 QSNKNGTCV 146
              |||||||||
Db        135 QSNKNGTCV 143
```

```
RESULT 9
Q8BHK6
ID   Q8BHK6      PRELIMINARY;      PRT;   333 AA.
AC   Q8BHK6;
DT   01-MAR-2003 (TrEMBLrel. 23, Created)
DT   01-MAR-2003 (TrEMBLrel. 23, Last sequence update)
DT   01-OCT-2003 (TrEMBLrel. 25, Last annotation update)
DE   Similar to 19A24 protein homolog.
GN   4930560D03RIK.
OS   Mus musculus (Mouse).
OC   Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC   Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus.
OX   NCBI_TaxID=10090;
RN   [1]
RP   SEQUENCE FROM N.A.
RC   STRAIN=Aorta;
RX   MEDLINE=22354683; PubMed=12466851;
```

```
RA   The FANTOM Consortium,
RA   the RIKEN Genome Exploration Research Group Phase I & II Team;
RT   "Analysis of the mouse transcriptome based on functional annotation of
RT   60,770 full-length cDNAs.";
RL   Nature 420:563-573(2002).
DR   EMBL; AK030135; BAC26801.1; -.
DR   EMBL; AK030148; BAC26810.1; -.
DR   EMBL; AK040678; BAC30665.1; -.
DR   PIR; PT0566; PT0566.
DR   MGD; MGI:1922595; 4930560D03Rik.
DR   InterPro; IPR007110; Ig-like.
DR   PROSITE; PS50835; IG_LIKE; 1.
SQ   SEQUENCE   333 AA;  37217 MW;  0CC9A0AAFEACD46E CRC64;

  Query Match             2.7%;  Score 9;  DB 11;  Length 333;
  Best Local Similarity   100.0%;  Pred. No. 2;
  Matches    9;  Conservative    0;  Mismatches    0;  Indels    0;  Gaps    0;

Qy        138 QSNKNGTCV 146
              |||||||||
Db        135 QSNKNGTCV 143


RESULT 10
Q8CJ65
ID   Q8CJ65      PRELIMINARY;      PRT;   335 AA.
AC   Q8CJ65;
DT   01-MAR-2003 (TrEMBLrel. 23, Created)
DT   01-MAR-2003 (TrEMBLrel. 23, Last sequence update)
DT   01-OCT-2003 (TrEMBLrel. 25, Last annotation update)
DE   Leukocyte cell-surface antigen.
GN   4930560D03RIK.
OS   Mus musculus (Mouse).
OC   Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC   Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus.
OX   NCBI_TaxID=10090;
RN   [1]
RP   SEQUENCE FROM N.A.
RC   STRAIN=C57BL/6J; TISSUE=Thymus;
RX   MEDLINE=22226696; PubMed=12242590;
RA   Tovar V., Del Valle J., Zapater N., Martin M., Romero X., Pizcueta P.,
RA   Bosch J., Terhorst C., Engel P.;
RT   "Mouse novel Ly9: a new member of the expanding CD150 (SLAM) family of
RT   leukocyte cell-surface receptors.";
RL   Immunogenetics 54:394-402(2002).
DR   EMBL; AF467909; AAN63158.1; -.
DR   PIR; PT0566; PT0566.
DR   MGD; MGI:1922595; 4930560D03Rik.
DR   InterPro; IPR007110; Ig-like.
DR   PROSITE; PS50835; IG_LIKE; 1.
SQ   SEQUENCE   335 AA;  37493 MW;  C210E9CEADC8F3EB CRC64;

  Query Match             2.7%;  Score 9;  DB 11;  Length 335;
  Best Local Similarity   100.0%;  Pred. No. 2;
  Matches    9;  Conservative    0;  Mismatches    0;  Indels    0;  Gaps    0;

Qy        138 QSNKNGTCV 146
              |||||||||
Db        135 QSNKNGTCV 143


RESULT 11
Q8CJ64
ID   Q8CJ64      PRELIMINARY;      PRT;   335 AA.
AC   Q8CJ64;
DT   01-MAR-2003 (TrEMBLrel. 23, Created)
DT   01-MAR-2003 (TrEMBLrel. 23, Last sequence update)
DT   01-OCT-2003 (TrEMBLrel. 25, Last annotation update)
DE   Leukocyte cell-surface antigen.
GN   4930560D03RIK.
OS   Mus musculus (Mouse).
OC   Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC   Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus.
OX   NCBI_TaxID=10090;
RN   [1]
RP   SEQUENCE FROM N.A.
RC   STRAIN=BALB/c; TISSUE=Thymus;
RX   MEDLINE=22226696; PubMed=12242590;
RA   Tovar V., Del Valle J., Zapater N., Martin M., Romero X., Pizcueta P.,
RA   Bosch J., Terhorst C., Engel P.;
RT   "Mouse novel Ly9: a new member of the expanding CD150 (SLAM) family of
RT   leukocyte cell-surface receptors.";
RL   Immunogenetics 54:394-402(2002).
DR   EMBL; AF467910; AAN63159.1; -.
DR   PIR; PT0566; PT0566.
DR   MGD; MGI:1922595; 4930560D03Rik.
DR   InterPro; IPR007110; Ig-like.
DR   PROSITE; PS50835; IG_LIKE; 1.
SQ   SEQUENCE   335 AA;  37590 MW;  85F00ABDFC8B90A0 CRC64;

  Query Match             2.7%;  Score 9;  DB 11;  Length 335;
  Best Local Similarity   100.0%;  Pred. No. 2;
  Matches    9;  Conservative    0;  Mismatches    0;  Indels    0;  Gaps    0;

Qy        138 QSNKNGTCV 146
              |||||||||
Db        135 QSNKNGTCV 143


RESULT 12
Q8BTL2
ID   Q8BTL2      PRELIMINARY;      PRT;   335 AA.
AC   Q8BTL2;
DT   01-MAR-2003 (TrEMBLrel. 23, Created)
DT   01-MAR-2003 (TrEMBLrel. 23, Last sequence update)
DT   01-OCT-2003 (TrEMBLrel. 25, Last annotation update)
DE   Similar to 19A24 protein homolog.
GN   4930560D03RIK.
OS   Mus musculus (Mouse).
OC   Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC   Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus.
OX   NCBI_TaxID=10090;
RN   [1]
RP   SEQUENCE FROM N.A.
RC   STRAIN=C57BL/6J;
RX   MEDLINE=22354683; PubMed=12466851;
RA   The FANTOM Consortium,
RA   the RIKEN Genome Exploration Research Group Phase I & II Team;
RT   "Analysis of the mouse transcriptome based on functional annotation of
RT   60,770 full-length cDNAs.";
RL   Nature 420:563-573(2002).
DR   EMBL; AK089525; BAC40914.1; -.
DR   PIR; PT0566; PT0566.
DR   MGD; MGI:1922595; 4930560D03Rik.
DR   InterPro; IPR007110; Ig-like.
DR   PROSITE; PS50835; IG_LIKE; 1.
SQ   SEQUENCE   335 AA;  37521 MW;  99E8802E55A98A03 CRC64;

  Query Match             2.7%;  Score 9;  DB 11;  Length 335;
  Best Local Similarity   100.0%;  Pred. No. 2;
  Matches    9;  Conservative    0;  Mismatches    0;  Indels    0;  Gaps    0;

Qy        138 QSNKNGTCV 146
              |||||||||
Db        135 QSNKNGTCV 143


RESULT 13
Q884T6
ID   Q884T6      PRELIMINARY;      PRT;    83 AA.
AC   Q884T6;
DT   01-JUN-2003 (TrEMBLrel. 24, Created)
DT   01-JUN-2003 (TrEMBLrel. 24, Last sequence update)
DT   01-JUN-2003 (TrEMBLrel. 24, Last annotation update)
DE   Prevent-host-death family protein.
GN   PSPTO2000.
```

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OS   Pseudomonas syringae (pv. tomato).
OC   Bacteria; Proteobacteria; Gammaproteobacteria; Pseudomonadales;
OC   Pseudomonadaceae; Pseudomonas.
OX   NCBI_TaxID=323;
RN   [1]
RP   SEQUENCE FROM N.A.
RC   STRAIN=DC3000;
RA   Buell R., Joardar V., Khouri H., Fedorova N., Tran B., Russell D.,
RA   Berry K., Utterback T., Van Aken S., Feldblyum T., Gwinn M.,
RA   Dodson R., DeBoy R., Durkin A., Kolonay J., Madupu R., Daugherty S.,
RA   Brinkac L., Beanan M., Haft D., Selengut J., Nelson W., Davidsen T.,
RA   White O., Fraser C., Collmer A.;
RT   "Complete sequence of Pseudomonas syringae.";
RL   Submitted (MAR-2003) to the EMBL/GenBank/DDBJ databases.
DR   EMBL; AE016862; AAO55518.1; -.
DR   TIGR; PSPTO2000; -.
KW   Complete proteome.
SQ   SEQUENCE   83 AA;  8993 MW;  ED9080CB44BCD3EE CRC64;

  Query Match           2.4%;  Score 8;  DB 16;  Length 83;
  Best Local Similarity   100.0%;  Pred. No. 6.2;
  Matches    8;  Conservative    0;  Mismatches    0;  Indels    0;  Gaps    0;

Qy         16 QLTGSAAS 23
              ||||||||
Db         46 QLTGSAAS 53


RESULT 14
Q94E37
ID   Q94E37      PRELIMINARY;      PRT;    91 AA.
AC   Q94E37;
DT   01-DEC-2001 (TrEMBLrel. 19, Created)
DT   01-DEC-2001 (TrEMBLrel. 19, Last sequence update)
DT   01-OCT-2002 (TrEMBLrel. 22, Last annotation update)
DE   OSJNBb0032H19.17 protein.
OS   Oryza sativa (Rice).
OC   Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta;
OC   Spermatophyta; Magnoliophyta; Liliopsida; Poales; Poaceae;
OC   Ehrhartoideae; Oryzeae; Oryza.
OX   NCBI_TaxID=4530;
RN   [1]
RP   SEQUENCE FROM N.A.
RC   STRAIN=cv. Nipponbare;
RA   Sasaki T., Matsumoto T., Yamamoto K.;
RT   "Oryza sativa nipponbare(GA3) genomic DNA, chromosome 1, BAC
RT   clone:OSJNBb0032H19.";
RL   Submitted (FEB-2001) to the EMBL/GenBank/DDBJ databases.
DR   EMBL; AP003219; BAB61185.1; -.
DR   Gramene; Q94E37; -.
SQ   SEQUENCE   91 AA;  9789 MW;  D9D559FB49BF71B2 CRC64;

  Query Match           2.4%;  Score 8;  DB 10;  Length 91;
  Best Local Similarity   100.0%;  Pred. No. 6.8;
  Matches    8;  Conservative    0;  Mismatches    0;  Indels    0;  Gaps    0;

Qy        236 LLLSLFVL 243
              ||||||||
Db         16 LLLSLFVL 23


RESULT 15
Q8IVU0
ID   Q8IVU0      PRELIMINARY;      PRT;   129 AA.
AC   Q8IVU0;
DT   01-MAR-2003 (TrEMBLrel. 23, Created)
DT   01-MAR-2003 (TrEMBLrel. 23, Last sequence update)
DT   01-JUN-2003 (TrEMBLrel. 24, Last annotation update)
DE   Similar to papilin, proteoglycan-like sulfated glycoprotein.
OS   Homo sapiens (Human).
OC   Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC   Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
OX   NCBI_TaxID=9606;
RN   [1]
RP   SEQUENCE FROM N.A.
RC   TISSUE=Ovary;
RA   Strausberg R.;
RL   Submitted (DEC-2002) to the EMBL/GenBank/DDBJ databases.
DR   EMBL; BC042057; AAH42057.1; -.
DR   InterPro; IPR000884; TSP1.
DR   InterPro; IPR008085; TSP_1.
DR   Pfam; PF00090; tsp_1; 1.
DR   PRINTS; PR01705; TSP1REPEAT.
DR   SMART; SM00209; TSP1; 1.
DR   PROSITE; PS50092; TSP1; 1.
SQ   SEQUENCE   129 AA;  14368 MW;  D51144A494C12B3B CRC64;

  Query Match           2.4%;  Score 8;  DB 4;  Length 129;
  Best Local Similarity   100.0%;  Pred. No. 9.3;
  Matches    8;  Conservative    0;  Mismatches    0;  Indels    0;  Gaps    0;

Qy        231 LLLVPLLL 238
              ||||||||
Db          4 LLLVPLLL 11


Search completed: August 18, 2004, 16:00:33
Job time : 46 secs
```

GenCore version 5.1.6

OM protein - protein search, using sw model

Run on: August 18, 2004, 15:48:32 ; Search time 39 Seconds
(without alignments)
2710.220 Million cell updates/sec

Title: US-10-063-549-46
Perfect score: 1772
Sequence: 1 MAGSPTCLTLIYILWQLTGS.....PHSLLTMPDTPRLFAYENVI 335

Scoring table: BLOSUM62
Gapop 10.0 , Gapext 0.5

Searched: 1017041 seqs, 315518202 residues

Total number of hits satisfying chosen parameters: 1017041

Minimum DB seq length: 0
Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%
Maximum Match 100%
Listing first 700 summaries

Database : SPTREMBL_25:*
1: sp_archea:*
2: sp_bacteria:*
3: sp_fungi:*
4: sp_human:*
5: sp_invertebrate:*
6: sp_mammal:*
7: sp_mhc:*
8: sp_organelle:*
9: sp_phage:*
10: sp_plant:*
11: sp_rodent:*
12: sp_virus:*
13: sp_vertebrate:*
14: sp_unclassified:*
15: sp_rvirus:*
16: sp_bacteriap:*
17: sp_archeap:*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	% Query Match	Length	DB	ID	Description
1	1772	100.0	335	4	Q9NQ25	Q9nq25 homo sapien
2	1769	99.8	335	4	Q9NY08	Q9ny08 homo sapien
3	1392.5	78.6	328	4	Q9NY23	Q9ny23 homo sapien
4	1349	76.1	296	4	Q8N6Y8	Q8n6y8 homo sapien
5	1160.5	65.5	228	4	Q8ND32	Q8nd32 homo sapien
6	817	46.1	333	11	Q8BHK6	Q8bhk6 mus musculu
7	778.5	43.9	335	11	Q8CJ64	Q8cj64 mus musculu
8	773.5	43.7	335	11	Q8BTL2	Q8btl2 mus musculu
9	769.5	43.4	335	11	Q8CJ65	Q8cj65 mus musculu
10	651	36.7	300	11	Q8CJ63	Q8cj63 mus musculu
11	637.5	36.0	294	11	Q91XA0	Q91xa0 mus musculu
12	362.5	20.5	328	4	O15430	O15430 homo sapien
13	362.5	20.5	328	7	Q8WLP1	Q8wlp1 homo sapien
14	362.5	20.5	329	11	Q9Z178	Q9z178 mus musculu
15	359	20.3	339	4	Q8WWI8	Q8wwi8 homo sapien
16	358	20.2	345	4	Q9UIB8	Q9uib8 homo sapien
17	354.5	20.0	649	11	Q7TMP7	Q7tmp7 mus musculu
18	353.5	19.9	544	11	Q8C2D4	Q8c2d4 mus musculu
19	330.5	18.7	289	4	Q96A28	Q96a28 homo sapien
20	329	18.6	538	11	Q8C9E4	Q8c9e4 mus musculu
21	315.5	17.8	331	4	Q96DV0	Q96dv0 homo sapien
22	311.5	17.6	285	11	Q8BTK0	Q8btk0 mus musculu
23	311	17.6	332	4	Q96DU3	Q96du3 homo sapien
24	308.5	17.4	285	11	Q8VE93	Q8ve93 mus musculu
25	308	17.4	280	4	O95660	O95660 homo sapien
26	307.5	17.4	285	11	Q9D780	Q9d780 mus musculu
27	304	17.2	272	4	Q9UIB7	Q9uib7 homo sapien
28	290.5	16.4	241	4	Q9UIB6	Q9uib6 homo sapien
29	281	15.9	197	4	Q9UIT7	Q9uit7 homo sapien
30	225.5	12.7	331	11	Q9ET40	Q9et40 mus musculu
31	225.5	12.7	351	11	Q9ET39	Q9et39 mus musculu
32	204.5	11.5	338	6	Q95MM6	Q95mm6 bos taurus
33	187.5	10.6	336	6	Q9GJT3	Q9gjt3 saguinus oe
34	183.5	10.4	335	4	Q96QR3	Q96qr3 homo sapien
35	183	10.3	266	11	Q9CUC8	Q9cuc8 mus musculu
36	179	10.1	278	11	Q9D3G2	Q9d3g2 mus musculu
37	178	10.0	278	11	Q8R3T7	Q8r3t7 mus musculu
38	171	9.7	329	4	Q9NQD2	Q9nqd2 homo sapien
39	170	9.6	365	4	Q9Y288	Q9y288 homo sapien
40	168.5	9.5	342	6	Q95L99	Q95199 canis famil
41	167.5	9.5	342	6	Q95MM9	Q95mm9 canis famil
42	159.5	9.0	370	4	Q9BZW8	Q9bzw8 homo sapien
43	158.5	8.9	326	11	Q8CAU4	Q8cau4 mus musculu
44	152	8.6	288	4	Q9NQ26	Q9nq26 homo sapien
45	150.5	8.5	285	4	Q9P0V8	Q9p0v8 homo sapien
46	145.5	8.2	416	4	Q8N7I3	Q8n7i3 homo sapien
47	144	8.1	344	11	Q9R201	Q9r201 mus musculu
48	142	8.0	207	4	Q9HBE9	Q9hbe9 homo sapien
49	133.5	7.5	394	11	Q9EQK9	Q9eqk9 rattus norv
50	132.5	7.5	372	13	Q90Y50	Q90y50 brachydanio
51	128.5	7.3	253	6	Q28753	Q28753 ovis sp. lf
52	126.5	7.1	461	4	O60430	O60430 homo sapien
53	125.5	7.1	430	4	Q15600	Q15600 homo sapien
54	125.5	7.1	464	4	Q16170	Q16170 homo sapien
55	125.5	7.1	468	4	Q96CA7	Q96ca7 homo sapien
56	124.5	7.0	344	4	Q13774	Q13774 homo sapien
57	124.5	7.0	461	4	Q13854	Q13854 homo sapien
58	123.5	7.0	227	6	Q28754	Q28754 ovis sp. lf
59	123	6.9	140	11	Q8BFV0	Q8bfv0 mus musculu
60	123	6.9	311	11	Q9JLM2	Q9jlm2 rattus norv
61	122.5	6.9	298	13	Q804R4	Q804r4 brachydanio
62	122.5	6.9	458	11	Q61351	Q61351 mus musculu
63	122.5	6.9	521	11	Q61352	Q61352 mus musculu
64	122	6.9	326	6	Q9N166	Q9n166 papio hamad
65	122	6.9	344	4	Q9UKV4	Q9ukv4 homo sapien
66	121.5	6.9	377	11	Q80V04	Q80v04 mus musculu
67	121.5	6.9	536	11	Q8BJE2	Q8bje2 mus musculu
68	119.5	6.7	332	13	Q9IB08	Q9ib08 sphoeroides
69	118.5	6.7	520	11	Q925P2	Q925p2 mus musculu
70	115	6.5	357	13	Q90ZL5	Q90zl5 anas platyr
71	114.5	6.5	430	4	Q8N4F1	Q8n4f1 homo sapien
72	114.5	6.5	702	4	Q8N4D0	Q8n4d0 homo sapien
73	113.5	6.4	454	11	Q91W54	Q91w54 mus musculu
74	113.5	6.4	521	11	Q925P3	Q925p3 mus musculu
75	113	6.4	373	4	Q9H6B4	Q9h6b4 homo sapien
76	113	6.4	621	11	Q811T7	Q811t7 mus musculu
77	111	6.3	372	11	Q8K1G0	Q8k1g0 rattus norv
78	110	6.2	539	6	Q8HXQ6	Q8hxq6 sus scrofa
79	109	6.2	316	11	Q8VE98	Q8ve98 mus musculu
80	109	6.2	924	10	Q7XTP5	Q7xtp5 oryza sativ
81	108.5	6.1	365	6	Q8WMV3	Q8wmv3 bos taurus
82	108	6.1	304	11	Q9CVA4	Q9cva4 mus musculu
83	108	6.1	316	11	Q7TPB4	Q7tpb4 rattus norv
84	107.5	6.1	398	11	Q07763	Q07763 mus musculu
85	107	6.0	399	11	Q9ESE5	Q9ese5 mus musculu
86	106.5	6.0	752	5	Q9XYS4	Q9xys4 hydra atten
87	106.5	6.0	4138	5	Q8I1Y3	Q8i1y3 plasmodium
88	106	6.0	397	11	Q9JIE0	Q9jie0 mus musculu
89	106	6.0	897	10	Q9SJY2	Q9sjy2 arabidopsis

90	105.5	6.0	335	13	Q9PWR4	Q9pwr4 gallus gall
91	105.5	6.0	398	11	Q9JIE1	Q9jie1 mus musculu
92	105	5.9	340	11	O88654	O88654 mus musculu
93	104.5	5.9	319	6	Q9TU79	Q9tu79 sus scrofa
94	104.5	5.9	1271	16	Q8A321	Q8a321 bacteroides
95	104	5.9	455	11	Q920L8	Q92018 mus musculu
96	104	5.9	535	11	Q9EQT7	Q9eqt7 mus musculu
97	103.5	5.8	319	6	Q9TU80	Q9tu80 canis famil
98	103.5	5.8	323	6	Q9BDB8	Q9bdb8 cercocebus
99	103.5	5.8	373	11	Q8R373	Q8r373 mus musculu
100	103.5	5.8	406	4	Q8N7T8	Q8n7t8 homo sapien
101	103	5.8	1062	13	Q8AXC7	Q8axc7 fugu rubrip
102	103	5.8	1078	13	Q8AXC8	Q8axc8 fugu rubrip
103	102.5	5.8	304	12	Q8JSP1	Q8jsp1 african swi
104	102.5	5.8	323	6	Q9BDM4	Q9bdm4 macaca mula
105	102.5	5.8	335	13	Q9YGH1	Q9ygh1 gallus gall
106	102.5	5.8	373	11	Q920S5	Q920s5 mus musculu
107	102	5.8	1482	5	Q9V4Y0	Q9v4y0 drosophila
108	101.5	5.7	761	10	O22271	O22271 arabidopsis
109	100.5	5.7	259	16	Q9CFA4	Q9cfa4 lactococcus
110	100.5	5.7	280	13	Q8UWL2	Q8uwl2 ictalurus p
111	100.5	5.7	323	6	Q9BDM2	Q9bdm2 cercopithec
112	99.5	5.6	323	6	Q9BDM9	Q9bdm9 macaca neme
113	99.5	5.6	335	13	Q9YGV5	Q9ygv5 gallus gall
114	99.5	5.6	658	5	Q86J55	Q86j55 dictyosteli
115	98.5	5.6	229	11	Q8BNV8	Q8bnv8 mus musculu
116	98.5	5.6	348	4	Q96ST1	Q96st1 homo sapien
117	98.5	5.6	404	4	Q9GZZ9	Q9gzz9 homo sapien
118	98.5	5.6	733	6	Q8SQ83	Q8sq83 trichosurus
119	98.5	5.6	1227	5	Q21038	Q21038 caenorhabdi
120	98.5	5.6	16215	5	Q9NFS3	Q9nfs3 drosophila
121	97.5	5.5	2772	5	Q9VAV4	Q9vav4 drosophila
122	97.5	5.5	2776	5	Q869A0	Q869a0 drosophila
123	97.5	5.5	2898	5	Q868Z9	Q868z9 drosophila
124	97	5.5	352	11	Q91W66	Q91w66 mus musculu
125	97	5.5	484	5	Q26475	Q26475 schistocerc
126	96.5	5.4	204	11	Q9JLM3	Q9jlm3 rattus norv
127	96.5	5.4	402	12	Q89501	Q89501 african swi
128	96.5	5.4	533	4	Q8NCB6	Q8ncb6 homo sapien
129	96.5	5.4	534	4	Q8NBI8	Q8nbi8 homo sapien
130	96.5	5.4	1896	13	Q9IAJ1	Q9iaj1 xenopus lae
131	96	5.4	339	13	Q9IAZ7	Q9iaz7 sphoeroides
132	96	5.4	341	11	Q61354	Q61354 mus musculu
133	96	5.4	359	5	Q9V6C2	Q9v6c2 drosophila
134	96	5.4	526	4	Q9H458	Q9h458 homo sapien
135	95.5	5.4	248	11	Q9D0T4	Q9d0t4 mus musculu
136	95.5	5.4	340	11	Q61349	Q61349 mus musculu
137	95.5	5.4	365	11	Q9DBJ8	Q9dbj8 mus musculu
138	95.5	5.4	448	11	Q9JHL7	Q9jhl7 rattus norv
139	95.5	5.4	458	11	Q63093	Q63093 rattus norv
140	95.5	5.4	459	11	Q9JHL6	Q9jhl6 rattus norv
141	95	5.4	814	4	Q8IVU1	Q8ivu1 homo sapien
142	94.5	5.3	280	13	Q8UWK3	Q8uwk3 ictalurus p
143	94.5	5.3	286	6	O46535	O46535 bos taurus
144	94.5	5.3	379	11	Q8BLX5	Q8blx5 mus musculu
145	94.5	5.3	397	11	Q8BFX8	Q8bfx8 mus musculu
146	94	5.3	336	6	Q8WNV8	Q8wnv8 felis silve
147	94	5.3	344	11	Q9R067	Q9r067 rattus norv
148	94	5.3	419	4	Q96QL5	Q96ql5 homo sapien
149	94	5.3	828	11	Q8C8T7	Q8c8t7 mus musculu
150	93.5	5.3	358	11	Q9R066	Q9r066 rattus norv
151	93	5.2	316	4	Q9BXR1	Q9bxr1 homo sapien
152	93	5.2	339	5	Q9V5T7	Q9v5t7 drosophila
153	93	5.2	342	13	Q9IB00	Q9ib00 sphoeroides
154	93	5.2	752	13	Q9DGN6	Q9dgn6 gallus gall
155	93	5.2	793	11	O70246	O70246 mus musculu
156	93	5.2	813	11	Q8BQC3	Q8bqc3 mus musculu
157	93	5.2	1788	13	Q9IAJ0	Q9iaj0 xenopus lae
158	92.5	5.2	160	11	Q8C239	Q8c239 mus musculu
159	92.5	5.2	485	13	Q801W5	Q801w5 brachydanio
160	92.5	5.2	544	13	Q7ZZ85	Q7zz85 brachydanio
161	92.5	5.2	760	16	Q8EBB5	Q8ebb5 shewanella
162	92.5	5.2	761	10	Q9C9S3	Q9c9s3 arabidopsis
163	92.5	5.2	782	12	Q8JYB8	Q8jyb8 porcine lym
164	92.5	5.2	782	12	Q8B3U9	Q8b3u9 porcine lym
165	92	5.2	297	11	Q63476	Q63476 rattus norv
166	92	5.2	426	4	O60410	O60410 homo sapien
167	92	5.2	609	12	Q9YKD7	Q9ykd7 rinderpest
168	92	5.2	667	11	Q8CHA6	Q8cha6 mus musculu
169	92	5.2	700	11	Q7TSU7	Q7tsu7 mus musculu
170	92	5.2	822	10	Q9ZQX3	Q9zqx3 arabidopsis
171	92	5.2	1020	11	Q8BIE6	Q8bie6 mus musculu
172	92	5.2	1087	13	Q7ZY71	Q7zy71 xenopus lae
173	92	5.2	2828	4	Q9NR99	Q9nr99 homo sapien
174	91.5	5.2	160	11	Q8C254	Q8c254 mus musculu
175	91.5	5.2	226	4	Q8NHI1	Q8nhi1 homo sapien
176	91.5	5.2	230	13	Q90Z86	Q90z86 brachydanio
177	91.5	5.2	230	13	Q8UV30	Q8uv30 brachydanio
178	91.5	5.2	1079	12	Q9YW56	Q9yw56 melanoplus
179	91	5.1	388	4	Q8NC34	Q8nc34 homo sapien
180	91	5.1	467	11	Q91VT9	Q91vt9 mus musculu
181	91	5.1	467	11	Q8C6F2	Q8c6f2 mus musculu
182	91	5.1	510	6	Q9BGY6	Q9bgy6 macaca fasc
183	91	5.1	1496	4	Q92626	Q92626 homo sapien
184	91	5.1	1840	11	Q9JI03	Q9ji03 rattus norv
185	91	5.1	1842	4	Q8IZY3	Q8izy3 homo sapien
186	91	5.1	2053	4	Q8WXU7	Q8wxu7 homo sapien
187	91	5.1	2053	4	Q8IZY4	Q8izy4 homo sapien
188	91	5.1	2113	4	Q8TD84	Q8td84 homo sapien
189	90.5	5.1	230	13	Q801W9	Q801w9 brachydanio
190	90.5	5.1	306	11	Q7TSA3	Q7tsa3 mus musculu
191	90.5	5.1	412	11	Q63611	Q63611 rattus norv
192	90.5	5.1	412	11	Q9R1E1	Q9r1e1 rattus norv
193	90.5	5.1	417	4	Q96BJ1	Q96bj1 homo sapien
194	90.5	5.1	483	13	Q7SX76	Q7sx76 brachydanio
195	90.5	5.1	922	10	Q9LTL7	Q91tl7 arabidopsis
196	90.5	5.1	1016	11	Q8C310	Q8c310 mus musculu
197	90	5.1	309	11	Q91YV7	Q91yv7 mus musculu
198	90	5.1	348	11	Q80Z24	Q80z24 mus musculu
199	90	5.1	428	4	Q9P1W5	Q9p1w5 homo sapien
200	90	5.1	609	12	Q9WHH7	Q9whh7 rinderpest
201	90	5.1	1431	11	Q80U60	Q80u60 mus musculu
202	89.5	5.1	756	16	Q8CJW2	Q8cjw2 streptomyce
203	89.5	5.1	770	16	Q89LN9	Q89ln9 bradyrhizob
204	89.5	5.1	833	5	Q9BPQ7	Q9bpq7 halocynthia
205	89.5	5.1	845	4	Q9H156	Q9h156 homo sapien
206	89.5	5.1	2214	4	O95425	O95425 homo sapien
207	89	5.0	240	4	Q9BRW0	Q9brw0 homo sapien
208	89	5.0	292	11	Q80T70	Q80t70 mus musculu
209	89	5.0	314	11	Q61238	Q61238 mus musculu
210	89	5.0	315	4	Q96DM5	Q96dm5 homo sapien
211	89	5.0	322	13	Q9PTR8	Q9ptr8 sphoeroides
212	89	5.0	323	5	Q8MKZ7	Q8mkz7 drosophila
213	89	5.0	325	4	O95791	O95791 homo sapien
214	89	5.0	328	11	Q9Z109	Q9z109 mus musculu
215	89	5.0	356	11	Q64381	Q64381 mus musculu
216	89	5.0	5175	5	Q8I0L3	Q8i0l3 caenorhabdi
217	89	5.0	5198	5	O76518	O76518 caenorhabdi
218	88.5	5.0	271	12	O40948	O40948 kaposi's sa
219	88.5	5.0	315	13	Q9DGI5	Q9dgi5 gallus gall
220	88.5	5.0	325	13	Q8UWL3	Q8uwl3 ictalurus p
221	88.5	5.0	344	13	O93242	O93242 gallus gall
222	88.5	5.0	532	4	Q8WWV6	Q8wwv6 homo sapien
223	88.5	5.0	534	4	Q96SA2	Q96sa2 homo sapien
224	88.5	5.0	554	5	Q9W4R3	Q9w4r3 drosophila
225	88.5	5.0	583	11	Q8CDA5	Q8cda5 mus musculu
226	88.5	5.0	1081	5	Q8T4N8	Q8t4n8 penaeus sem
227	88	5.0	324	11	Q7TMH2	Q7tmh2 mus musculu
228	88	5.0	329	6	Q9TTF2	Q9ttf2 canis famil
229	88	5.0	337	13	Q9IAZ4	Q9iaz4 sphoeroides
230	88	5.0	339	13	Q9IB09	Q9ib09 sphoeroides
231	88	5.0	343	11	Q8R4Y0	Q8r4y0 mus musculu
232	88	5.0	422	17	O58124	O58124 pyrococcus
233	88	5.0	457	11	Q61396	Q61396 mus musculu
234	88	5.0	530	11	Q80XJ5	Q80xj5 mus musculu
235	88	5.0	699	11	Q61042	Q61042 mus musculu

236	88	5.0	837	16	Q8G518	Q8g518 bifidobacte
237	88	5.0	986	13	Q8UVR9	Q8uvr9 fugu rubrip
238	88	5.0	1379	5	Q8I3S7	Q8i3s7 plasmodium
239	88	5.0	1925	4	Q8IZJ2	Q8izj2 homo sapien
240	88	5.0	1985	4	Q9Y4D7	Q9y4d7 homo sapien
241	88	5.0	3007	4	Q14215	Q14215 homo sapien
242	87.5	4.9	276	12	Q64861	Q64861 human adeno
243	87.5	4.9	276	12	Q98822	Q98822 human adeno
244	87.5	4.9	325	6	O02838	O02838 sus scrofa
245	87.5	4.9	403	11	Q8VE47	Q8ve47 mus musculu
246	87.5	4.9	487	13	Q7T2H2	Q7t2h2 gallus gall
247	87.5	4.9	583	11	O35112	O35112 rattus norv
248	87.5	4.9	583	11	Q8R2T0	Q8r2t0 mus musculu
249	87.5	4.9	652	12	Q89703	Q89703 cassava vei
250	87.5	4.9	1087	13	Q9PUF6	Q9puf6 gallus gall
251	87.5	4.9	2307	12	Q80IV2	Q80iv2 theiler-lik
252	87.5	4.9	2340	11	Q64736	Q64736 mus musculu
253	87.5	4.9	4162	13	Q98918	Q98918 gallus gall
254	87.5	4.9	4283	11	Q9ERV0	Q9erv0 rattus norv
255	87.5	4.9	18074	5	Q9I7U4	Q9i7u4 drosophila
256	87	4.9	229	11	Q9R121	Q9r121 rattus norv
257	87	4.9	291	11	Q8C6C3	Q8c6c3 mus musculu
258	87	4.9	326	11	Q8CI91	Q8ci91 mus musculu
259	87	4.9	341	11	Q61353	Q61353 mus musculu
260	87	4.9	403	11	Q9CYD6	Q9cyd6 mus musculu
261	87	4.9	415	11	Q8C6X8	Q8c6x8 mus musculu
262	87	4.9	491	11	Q8BQZ8	Q8bqz8 mus musculu
263	87	4.9	514	11	Q8BH18	Q8bh18 mus musculu
264	87	4.9	521	6	O46651	O46651 oryctolagus
265	87	4.9	522	16	Q8F7F1	Q8f7f1 leptospira
266	87	4.9	873	11	Q8CD46	Q8cd46 mus musculu
267	87	4.9	1501	11	Q7TT17	Q7tt17 mus musculu
268	87	4.9	1904	11	Q64699	Q64699 mus musculu
269	87	4.9	2673	4	Q96SC3	Q96sc3 homo sapien
270	86.5	4.9	293	13	Q8AXN8	Q8axn8 cyprinus ca
271	86.5	4.9	313	11	O35531	O35531 rattus norv
272	86.5	4.9	324	13	Q9IAY9	Q9iay9 sphoeroides
273	86.5	4.9	354	4	Q8NAQ3	Q8naq3 homo sapien
274	86.5	4.9	474	6	P79355	P79355 felis silve
275	86.5	4.9	528	16	Q9RTP5	Q9rtp5 deinococcus
276	86.5	4.9	650	16	Q88BN9	Q88bn9 pseudomonas
277	86.5	4.9	846	11	Q810C0	Q810c0 mus musculu
278	86	4.9	259	4	Q9Y5B2	Q9y5b2 homo sapien
279	86	4.9	280	13	Q8UWK1	Q8uwk1 ictalurus p
280	86	4.9	339	13	Q9IAZ1	Q9iaz1 sphoeroides
281	86	4.9	354	12	Q98VN1	Q98vn1 human herpe
282	86	4.9	428	4	Q9BRW2	Q9brw2 homo sapien
283	86	4.9	486	16	Q82NI6	Q82ni6 streptomyce
284	86	4.9	487	16	Q82MI3	Q82mi3 streptomyce
285	86	4.9	545	5	Q9VCT4	Q9vct4 drosophila
286	86	4.9	687	10	Q9MAJ5	Q9maj5 arabidopsis
287	86	4.9	731	6	Q8SPI6	Q8spi6 macropus eu
288	86	4.9	885	10	Q8L3R3	Q8l3r3 arabidopsis
289	86	4.9	885	10	Q8L3Y7	Q8l3y7 arabidopsis
290	86	4.9	885	10	O81401	O81401 arabidopsis
291	86	4.9	885	10	Q8LGP8	Q8lgp8 arabidopsis
292	86	4.9	1187	13	Q98TF0	Q98tf0 cyprinus ca
293	86	4.9	1327	4	O15070	O15070 homo sapien
294	86	4.9	18412	13	Q7ZZ61	Q7zz61 brachydanio
295	85.5	4.8	324	4	Q9UPK9	Q9upk9 homo sapien
296	85.5	4.8	326	4	Q9UPK8	Q9upk8 homo sapien
297	85.5	4.8	333	4	O75238	O75238 homo sapien
298	85.5	4.8	335	4	O75237	O75237 homo sapien
299	85.5	4.8	393	11	Q7TNZ6	Q7tnz6 rattus norv
300	85.5	4.8	650	4	Q8NA84	Q8na84 homo sapien
301	85.5	4.8	657	2	Q93D79	Q93d79 bacillus th
302	85.5	4.8	789	2	Q45793	Q45793 bacillus th
303	85.5	4.8	789	2	O69270	O69270 bacillus th
304	85.5	4.8	789	2	Q45792	Q45792 bacillus th
305	85.5	4.8	789	2	Q938Z1	Q938z1 bacillus th
306	85.5	4.8	1101	10	Q9FWL8	Q9fwl8 oryza sativ
307	85.5	4.8	1101	10	Q7XDJ5	Q7xdj5 oryza sativ
308	85.5	4.8	1354	5	Q9VIC7	Q9vic7 drosophila
309	85.5	4.8	2115	5	Q8IE55	Q8ie55 plasmodium
310	85.5	4.8	2491	4	Q96PT5	Q96pt5 homo sapien
311	85.5	4.8	2491	4	Q7Z7G9	Q7z7g9 homo sapien
312	85.5	4.8	2588	11	O88491	O88491 mus musculu
313	85	4.8	224	3	Q870G0	Q870g0 podospora a
314	85	4.8	280	13	Q8UWL1	Q8uwl1 ictalurus p
315	85	4.8	332	16	Q8EXS1	Q8exs1 leptospira
316	85	4.8	375	2	Q93GD6	Q93gd6 desulfovibr
317	85	4.8	379	11	Q80UL9	Q80ul9 mus musculu
318	85	4.8	583	6	Q9BH13	Q9bh13 bos taurus
319	85	4.8	684	5	Q21138	Q21138 caenorhabdi
320	85	4.8	709	6	Q9XSJ2	Q9xsj2 sus scrofa
321	85	4.8	875	11	Q91ZY7	Q91zy7 mus musculu
322	85	4.8	1376	12	Q8AZ23	Q8az23 porcine lym
323	85	4.8	1598	4	Q9P214	Q9p214 homo sapien
324	85	4.8	1723	11	Q8CHB2	Q8chb2 mus musculu
325	85	4.8	2487	6	Q9N1T0	Q9n1t0 ornithorhyn
326	84.5	4.8	280	16	Q899D0	Q899d0 clostridium
327	84.5	4.8	303	4	Q9UKJ1	Q9ukj1 homo sapien
328	84.5	4.8	355	4	Q7Z3B1	Q7z3b1 homo sapien
329	84.5	4.8	394	11	Q9D0G8	Q9d0g8 mus musculu
330	84.5	4.8	656	10	O04533	O04533 arabidopsis
331	84.5	4.8	798	5	Q86K66	Q86k66 dictyosteli
332	84.5	4.8	840	16	Q7VQI2	Q7vqi2 candidatus
333	84.5	4.8	1164	17	Q8PX58	Q8px58 methanosarc
334	84.5	4.8	1608	17	Q8PVI0	Q8pvi0 methanosarc
335	84.5	4.8	4311	6	Q7YQK5	Q7yqk5 canis famil
336	84	4.7	262	13	Q9PTR7	Q9ptr7 sphoeroides
337	84	4.7	333	13	Q9IB04	Q9ib04 sphoeroides
338	84	4.7	343	11	Q8BYS4	Q8bys4 mus musculu
339	84	4.7	403	16	Q8ENX5	Q8enx5 oceanobacil
340	84	4.7	556	13	Q7ZZU8	Q7zzu8 brachydanio
341	84	4.7	593	3	Q8NKB1	Q8nkb1 emericella
342	84	4.7	775	6	O97754	O97754 oryctolagus
343	84	4.7	800	10	Q8H329	Q8h329 oryza sativ
344	84	4.7	810	5	Q8T3J2	Q8t3j2 drosophila
345	84	4.7	811	5	Q9VK54	Q9vk54 drosophila
346	84	4.7	812	5	Q8MZ57	Q8mz57 drosophila
347	84	4.7	851	17	Q9UX76	Q9ux76 sulfolobus
348	84	4.7	880	5	P91643	P91643 drosophila
349	84	4.7	992	10	Q7XTP4	Q7xtp4 oryza sativ
350	84	4.7	1062	12	Q997A4	Q997a4 american pl
351	84	4.7	1193	5	Q9VQW1	Q9vqw1 drosophila
352	84	4.7	1499	13	Q90815	Q90815 gallus gall
353	83.5	4.7	284	6	Q9GL33	Q9gl33 bos taurus
354	83.5	4.7	289	11	Q8K3J3	Q8k3j3 meriones un
355	83.5	4.7	315	17	O50082	O50082 pyrococcus
356	83.5	4.7	392	5	O76708	O76708 caenorhabdi
357	83.5	4.7	408	11	Q91WP1	Q91wp1 mus musculu
358	83.5	4.7	408	11	Q8BVF6	Q8bvf6 mus musculu
359	83.5	4.7	408	11	Q8K094	Q8k094 mus musculu
360	83.5	4.7	515	4	Q96RE0	Q96re0 homo sapien
361	83.5	4.7	515	4	Q96PJ5	Q96pj5 homo sapien
362	83.5	4.7	528	5	P91670	P91670 drosophila
363	83.5	4.7	577	16	Q81H34	Q81h34 bacillus ce
364	83.5	4.7	646	16	Q899Y4	Q899y4 clostridium
365	83.5	4.7	1059	13	Q9DE49	Q9de49 brachydanio
366	83.5	4.7	1463	11	O55124	O55124 mus musculu
367	83.5	4.7	1501	11	Q9QW00	Q9qw00 rattus sp.
368	83.5	4.7	1556	16	Q83NF7	Q83nf7 tropheryma
369	83.5	4.7	1802	12	Q9J5C2	Q9j5c2 fowlpox vir
370	83.5	4.7	1863	11	Q64605	Q64605 rattus norv
371	83	4.7	151	6	Q7YS89	Q7ys89 sus scrofa
372	83	4.7	231	4	Q8WYY6	Q8wyy6 homo sapien
373	83	4.7	234	11	Q61401	Q61401 mus musculu
374	83	4.7	273	4	Q9NQD3	Q9nqd3 homo sapien
375	83	4.7	281	11	Q8CJE8	Q8cje8 mesocricetu
376	83	4.7	319	11	Q9JKA5	Q9jka5 mus musculu
377	83	4.7	339	13	Q9IAZ2	Q9iaz2 sphoeroides
378	83	4.7	369	2	Q93EW5	Q93ew5 desulfovibr
379	83	4.7	373	17	Q8TU74	Q8tu74 methanosarc
380	83	4.7	401	6	Q08835	Q08835 cercopithec
381	83	4.7	437	13	Q90WI4	Q90wi4 gallus gall

382	83	4.7	514	4	Q9H0C3	Q9h0c3 homo sapien
383	83	4.7	538	13	Q9DFU0	Q9dfu0 sparus aura
384	83	4.7	577	11	Q9D2Z1	Q9d2z1 mus musculu
385	83	4.7	885	10	Q8LGQ0	Q8lgq0 arabidopsis
386	83	4.7	885	10	Q8LGP9	Q8lgp9 arabidopsis
387	83	4.7	885	10	Q8LGP7	Q8lgp7 arabidopsis
388	83	4.7	925	5	Q9U4E4	Q9u4e4 caenorhabdi
389	83	4.7	925	5	Q9UB95	Q9ub95 caenorhabdi
390	83	4.7	925	5	Q9UB94	Q9ub94 caenorhabdi
391	83	4.7	925	5	O44191	O44191 caenorhabdi
392	83	4.7	1106	5	Q8IBR5	Q8ibr5 plasmodium
393	83	4.7	2421	6	Q95MJ1	Q95mj1 lemur catta
394	83	4.7	2489	3	Q06116	Q06116 saccharomyc
395	82.5	4.7	155	4	Q96P81	Q96p81 homo sapien
396	82.5	4.7	230	13	Q8UV76	Q8uv76 brachydanio
397	82.5	4.7	244	6	Q7YS40	Q7ys40 sus scrofa
398	82.5	4.7	270	4	Q9H564	Q9h564 homo sapien
399	82.5	4.7	319	11	Q922D5	Q922d5 mus musculu
400	82.5	4.7	330	11	P97269	P97269 cavia porce
401	82.5	4.7	373	10	Q9SSH0	Q9ssh0 arabidopsis
402	82.5	4.7	378	10	Q8L4Y2	Q8l4y2 arabidopsis
403	82.5	4.7	393	10	Q9C9P8	Q9c9p8 arabidopsis
404	82.5	4.7	446	3	Q8NK03	Q8nk03 emericella
405	82.5	4.7	462	10	Q8LBP4	Q8lbp4 arabidopsis
406	82.5	4.7	576	17	Q8TQK0	Q8tqk0 methanosarc
407	82.5	4.7	833	5	Q9VHG1	Q9vhg1 drosophila
408	82.5	4.7	840	2	Q84BZ7	Q84bz7 spiroplasma
409	82.5	4.7	840	2	Q84BZ6	Q84bz6 spiroplasma
410	82.5	4.7	994	5	O96167	O96167 plasmodium
411	82.5	4.7	1028	4	Q9UQ52	Q9uq52 homo sapien
412	82.5	4.7	1241	16	Q83GQ1	Q83gq1 tropheryma
413	82.5	4.7	1319	5	Q9BJF3	Q9bjf3 oxytricha t
414	82.5	4.7	4256	6	Q8MJF3	Q8mjf3 canis famil
415	82.5	4.7	4650	4	Q15598	Q15598 homo sapien
416	82.5	4.7	26926	4	Q8WZB3	Q8wzb3 homo sapien
417	82.5	4.7	26926	4	Q10466	Q10466 homo sapien
418	82.5	4.7	34350	4	Q8WZ42	Q8wz42 homo sapien
419	82	4.6	151	6	Q7YS88	Q7ys88 sus scrofa
420	82	4.6	184	16	Q7VM71	Q7vm71 haemophilus
421	82	4.6	308	6	Q95K99	Q95k99 macaca fasc
422	82	4.6	324	4	Q8NBY8	Q8nby8 homo sapien
423	82	4.6	326	4	Q8NC17	Q8nc17 homo sapien
424	82	4.6	327	4	Q96IQ7	Q96iq7 homo sapien
425	82	4.6	331	13	Q9IB01	Q9ib01 sphoeroides
426	82	4.6	409	16	Q814M1	Q814m1 bacillus ce
427	82	4.6	412	6	Q8HY14	Q8hy14 oryctolagus
428	82	4.6	444	10	Q8S9I7	Q8s9i7 arabidopsis
429	82	4.6	449	3	P78721	P78721 orpinomyces
430	82	4.6	587	13	Q9IAA1	Q9iaa1 carassius a
431	82	4.6	634	3	Q9P8L1	Q9p8l1 cryptococcu
432	82	4.6	648	11	Q9EPF1	Q9epf1 mus musculu
433	82	4.6	709	6	Q9XSJ1	Q9xsj1 bos taurus
434	82	4.6	709	11	O08702	O08702 rattus norv
435	82	4.6	737	11	O70376	O70376 rattus norv
436	82	4.6	757	11	O70482	O70482 rattus norv
437	82	4.6	785	11	Q9QZF9	Q9qzf9 rattus norv
438	82	4.6	795	4	Q8ND69	Q8nd69 homo sapien
439	82	4.6	890	4	Q86YF3	Q86yf3 homo sapien
440	82	4.6	1038	11	Q8CHA3	Q8cha3 mus musculu
441	82	4.6	1166	11	Q80VP0	Q80vp0 mus musculu
442	82	4.6	2136	10	Q8RYW8	Q8ryw8 oryza sativ
443	82	4.6	2940	5	Q8IHP9	Q8ihp9 plasmodium
444	82	4.6	3173	16	Q882M6	Q882m6 pseudomonas
445	82	4.6	5636	4	Q96RW7	Q96rw7 homo sapien
446	81.5	4.6	275	13	Q8AVV1	Q8avv1 xenopus lae
447	81.5	4.6	329	13	Q9IAY6	Q9iay6 sphoeroides
448	81.5	4.6	336	13	Q90Z89	Q90z89 brachydanio
449	81.5	4.6	340	13	Q9IAZ6	Q9iaz6 sphoeroides
450	81.5	4.6	352	4	Q15403	Q15403 homo sapien
451	81.5	4.6	352	4	Q08266	Q08266 homo sapien
452	81.5	4.6	355	10	O65493	O65493 arabidopsis
453	81.5	4.6	411	4	Q15228	Q15228 homo sapien
454	81.5	4.6	438	13	Q7T0Z8	Q7t0z8 xenopus lae
455	81.5	4.6	473	16	Q8ZQD1	Q8zqd1 salmonella
456	81.5	4.6	502	2	Q842D1	Q842d1 escherichia
457	81.5	4.6	504	4	Q8N441	Q8n441 homo sapien
458	81.5	4.6	504	4	Q9H4D7	Q9h4d7 homo sapien
459	81.5	4.6	524	2	Q09012	Q09012 shigella so
460	81.5	4.6	606	5	Q9VMN6	Q9vmn6 drosophila
461	81.5	4.6	677	16	Q8A3Q5	Q8a3q5 bacteroides
462	81.5	4.6	708	10	Q9M1P4	Q9m1p4 arabidopsis
463	81.5	4.6	779	16	Q8AAG1	Q8aag1 bacteroides
464	81.5	4.6	824	16	Q8A3C4	Q8a3c4 bacteroides
465	81.5	4.6	873	13	O42595	O42595 xenopus lae
466	81.5	4.6	968	5	Q9VR40	Q9vr40 drosophila
467	81.5	4.6	1187	13	O93284	O93284 fugu rubrip
468	81.5	4.6	1194	3	O93962	O93962 glomus vers
469	81.5	4.6	1194	11	Q7TPV3	Q7tpv3 mus musculu
470	81.5	4.6	1214	4	O75054	O75054 homo sapien
471	81.5	4.6	1596	4	Q9HCL6	Q9hcl6 homo sapien
472	81.5	4.6	2212	4	Q8NHN3	Q8nhn3 homo sapien
473	81.5	4.6	2284	5	Q8I5Y7	Q8i5y7 plasmodium
474	81.5	4.6	6620	4	Q96AA2	Q96aa2 homo sapien
475	81	4.6	149	5	Q86L22	Q86l22 dictyosteli
476	81	4.6	151	6	Q867B8	Q867b8 sus scrofa
477	81	4.6	252	4	O95781	O95781 homo sapien
478	81	4.6	272	7	Q861J5	Q861j5 equus cabal
479	81	4.6	291	11	Q8CD40	Q8cd40 mus musculu
480	81	4.6	326	13	Q9IAY7	Q9iay7 sphoeroides
481	81	4.6	330	16	Q87W83	Q87w83 pseudomonas
482	81	4.6	338	4	Q8IV49	Q8iv49 homo sapien
483	81	4.6	374	10	Q43741	Q43741 bromheadia
484	81	4.6	423	5	Q9UAG6	Q9uag6 dictyosteli
485	81	4.6	438	11	Q920C3	Q920c3 mus musculu
486	81	4.6	451	16	Q8DDA0	Q8dda0 vibrio vuln
487	81	4.6	507	5	Q9U319	Q9u319 caenorhabdi
488	81	4.6	521	6	O46634	O46634 canis famil
489	81	4.6	624	10	Q94AX9	Q94ax9 arabidopsis
490	81	4.6	643	10	Q7Y231	Q7y231 arabidopsis
491	81	4.6	769	16	Q97IS9	Q97is9 clostridium
492	81	4.6	937	16	Q8G4P3	Q8g4p3 bifidobacte
493	81	4.6	1196	13	Q98TF1	Q98tf1 cyprinus ca
494	81	4.6	1220	3	Q9P3A8	Q9p3a8 schizosacch
495	81	4.6	1898	11	Q64604	Q64604 r protein-t
496	81	4.6	1901	16	Q7UI70	Q7ui70 rhodopirell
497	81	4.6	2219	16	Q88WI9	Q88wi9 lactobacill
498	81	4.6	2402	2	Q9AER7	Q9aer7 staphylococ
499	80.5	4.5	261	13	Q9W6V1	Q9w6v1 gallus gall
500	80.5	4.5	270	4	Q9UMT1	Q9umt1 homo sapien
501	80.5	4.5	290	16	Q8CRR9	Q8crr9 staphylococ
502	80.5	4.5	371	16	Q816Y2	Q816y2 bacillus ce
503	80.5	4.5	376	10	Q94B08	Q94b08 arabidopsis
504	80.5	4.5	376	10	O23195	O23195 arabidopsis
505	80.5	4.5	388	11	Q8R464	Q8r464 mus musculu
506	80.5	4.5	472	11	Q811T8	Q811t8 mus musculu
507	80.5	4.5	473	16	Q8Z809	Q8z809 salmonella
508	80.5	4.5	475	11	Q62056	Q62056 mus musculu
509	80.5	4.5	498	16	Q886D9	Q886d9 pseudomonas
510	80.5	4.5	540	16	Q8XEB5	Q8xeb5 escherichia
511	80.5	4.5	546	11	Q80X70	Q80x70 mus musculu
512	80.5	4.5	548	11	Q99NB3	Q99nb3 mus musculu
513	80.5	4.5	556	16	Q8DEW4	Q8dew4 vibrio vuln
514	80.5	4.5	564	13	Q7ZU00	Q7zu00 brachydanio
515	80.5	4.5	602	4	Q86YJ9	Q86yj9 homo sapien
516	80.5	4.5	662	4	O60926	O60926 homo sapien
517	80.5	4.5	707	10	Q7XNT7	Q7xnt7 oryza sativ
518	80.5	4.5	721	3	O13479	O13479 aspergillus
519	80.5	4.5	739	6	Q865P2	Q865f2 oryctolagus
520	80.5	4.5	789	2	Q8RSZ5	Q8rsz5 bacillus th
521	80.5	4.5	823	10	Q39594	Q39594 chlamydomon
522	80.5	4.5	932	11	Q7TQ14	Q7tq14 rattus norv
523	80.5	4.5	976	13	Q8JFR5	Q8jfr5 brachydanio
524	80.5	4.5	976	13	Q9W755	Q9w755 brachydanio
525	80.5	4.5	1146	13	Q9I8V6	Q9i8v6 gallus gall
526	80.5	4.5	1202	11	Q80U33	Q80u33 mus musculu
527	80.5	4.5	1465	4	Q7Z3Y2	Q7z3y2 homo sapien

528	80.5	4.5	2253	12	Q8JV20	Q8jv20 ljungan vir
529	80.5	4.5	2358	6	Q95MJ2	Q95mj2 macropus ru
530	80.5	4.5	2898	3	Q872P1	Q872p1 neurospora
531	80.5	4.5	3337	5	Q9TWY4	Q9twy4 caenorhabdi
532	80.5	4.5	8081	5	Q7Z120	Q7z120 caenorhabdi
533	80	4.5	184	4	Q8WVI8	Q8wvi8 homo sapien
534	80	4.5	227	4	Q9UKJ0	Q9ukj0 homo sapien
535	80	4.5	235	11	Q99M11	Q99m11 mus musculu
536	80	4.5	303	13	Q7T114	Q7t114 brachydanio
537	80	4.5	337	13	Q8UV29	Q8uv29 brachydanio
538	80	4.5	341	11	Q8BLK3	Q8blk3 mus musculu
539	80	4.5	343	16	Q8X5J1	Q8x5j1 escherichia
540	80	4.5	365	13	Q8AXL6	Q8axl6 oncorhynchu
541	80	4.5	436	4	Q99563	Q99563 homo sapien
542	80	4.5	440	6	Q8MK36	Q8mk36 macaca mula
543	80	4.5	509	11	Q920C2	Q920c2 mus musculu
544	80	4.5	516	4	Q8IWX2	Q8iwx2 homo sapien
545	80	4.5	529	11	Q91V87	Q91v87 mus musculu
546	80	4.5	624	10	Q8LG08	Q8lg08 arabidopsis
547	80	4.5	627	5	Q9VUL0	Q9vul0 drosophila
548	80	4.5	633	13	Q7SXC1	Q7sxc1 brachydanio
549	80	4.5	637	3	Q9P8P2	Q9p8p2 cryptococcu
550	80	4.5	681	5	Q86J56	Q86j56 dictyosteli
551	80	4.5	913	11	Q9QYM7	Q9qym7 cricetulus
552	80	4.5	1005	13	P79921	P79921 xenopus lae
553	80	4.5	1192	16	Q81YZ8	Q81yz8 bacillus an
554	80	4.5	1310	5	Q8I7I4	Q8i7i4 caenorhabdi
555	80	4.5	1431	16	Q8EW23	Q8ew23 mycoplasma
556	80	4.5	1925	12	Q9YRB3	Q9yrb3 nudaurelia
557	80	4.5	2456	5	Q8I7I5	Q8i7i5 caenorhabdi
558	79.5	4.5	151	11	Q8C2T1	Q8c2t1 mus musculu
559	79.5	4.5	244	6	Q8SQB6	Q8sqb6 sus scrofa
560	79.5	4.5	289	17	Q97XZ7	Q97xz7 sulfolobus
561	79.5	4.5	399	16	Q8EMV2	Q8emv2 oceanobacil
562	79.5	4.5	400	16	Q8ZHN7	Q8zhn7 yersinia pe
563	79.5	4.5	401	13	O93534	O93534 xenopus lae
564	79.5	4.5	446	16	O69885	O69885 streptomyce
565	79.5	4.5	474	13	Q7ZU39	Q7zu39 brachydanio
566	79.5	4.5	520	2	Q8GDL8	Q8gdl8 photorhabdu
567	79.5	4.5	641	5	Q86SD2	Q86sd2 ciona intes
568	79.5	4.5	821	11	Q8C756	Q8c756 mus musculu
569	79.5	4.5	845	11	Q91YY0	Q91yy0 mus musculu
570	79.5	4.5	961	11	Q80W87	Q80w87 rattus norv
571	79.5	4.5	1162	4	O75921	O75921 homo sapien
572	79.5	4.5	1162	4	Q9UNY4	Q9uny4 homo sapien
573	79.5	4.5	1171	11	Q8CGB2	Q8cgb2 mus musculu
574	79.5	4.5	1171	11	Q80YQ1	Q80yq1 mus musculu
575	79.5	4.5	1342	5	Q9GPP6	Q9gpp6 drosophila
576	79.5	4.5	1342	5	Q9VPZ7	Q9vpz7 drosophila
577	79.5	4.5	1838	11	O88207	O88207 mus musculu
578	79.5	4.5	2253	12	Q8JV21	Q8jv21 ljungan vir
579	79.5	4.5	2256	12	Q8JV19	Q8jv19 ljungan vir
580	79.5	4.5	2658	5	Q9GRL9	Q9gr19 leishmania
581	79.5	4.5	2706	5	O97292	O97292 plasmodium
582	79	4.5	158	4	Q15229	Q15229 homo sapien
583	79	4.5	210	16	Q9AC09	Q9ac09 caulobacter
584	79	4.5	222	6	Q8MK98	Q8mk98 macroscelid
585	79	4.5	226	5	Q86P32	Q86p32 drosophila
586	79	4.5	244	16	Q927X2	Q927x2 listeria in
587	79	4.5	271	7	Q95I61	Q95i61 gadus morhu
588	79	4.5	323	4	Q8NDD2	Q8ndd2 homo sapien
589	79	4.5	342	6	Q8MK29	Q8mk29 macaca mula
590	79	4.5	406	11	Q8BPP7	Q8bpp7 mus musculu
591	79	4.5	410	16	Q81JP5	Q81jp5 bacillus an
592	79	4.5	429	11	Q8BFS1	Q8bfs1 mus musculu
593	79	4.5	440	6	Q8MK37	Q8mk37 macaca mula
594	79	4.5	446	13	P79762	P79762 gallus gall
595	79	4.5	446	13	Q9PWF8	Q9pwf8 gallus gall
596	79	4.5	464	16	Q88KY8	Q88ky8 pseudomonas
597	79	4.5	479	16	Q9K6X5	Q9k6x5 bacillus ha
598	79	4.5	490	4	Q8WUZ1	Q8wuz1 homo sapien
599	79	4.5	491	10	Q8GZP5	Q8gzp5 lycopersico
600	79	4.5	517	4	O76021	O76021 homo sapien
601	79	4.5	524	9	Q8LTK1	Q8ltk1 lactococcus
602	79	4.5	526	11	Q80WA6	Q80wa6 mus musculu
603	79	4.5	584	4	Q9Y3Y8	Q9y3y8 homo sapien
604	79	4.5	590	3	Q9P4U4	Q9p4u4 candida tro
605	79	4.5	611	13	Q9IBF6	Q9ibf6 xenopus lae
606	79	4.5	611	13	Q9PTI0	Q9pti0 xenopus lae
607	79	4.5	619	10	Q9ASG9	Q9asg9 oryza sativ
608	79	4.5	657	16	P73359	P73359 synechocyst
609	79	4.5	711	11	Q80Y89	Q80y89 mus musculu
610	79	4.5	778	5	Q9N4B1	Q9n4b1 caenorhabdi
611	79	4.5	783	11	Q811H8	Q811h8 mus musculu
612	79	4.5	785	11	Q7TNP4	Q7tnp4 mus musculu
613	79	4.5	807	17	Q8PTE2	Q8pte2 methanosarc
614	79	4.5	903	5	Q19372	Q19372 caenorhabdi
615	79	4.5	920	10	Q8GZA0	Q8gza0 arabidopsis
616	79	4.5	1092	11	Q8BPZ4	Q8bpz4 mus musculu
617	79	4.5	1104	10	Q9FKR7	Q9fkr7 arabidopsis
618	79	4.5	1264	5	P91767	P91767 manduca sex
619	79	4.5	1728	11	Q80TC7	Q80tc7 mus musculu
620	79	4.5	1887	11	Q9QW67	Q9qw67 rattus sp.
621	79	4.5	4010	11	Q80T14	Q80t14 mus musculu
622	78.5	4.4	305	6	Q9BE65	Q9be65 macaca fasc
623	78.5	4.4	318	13	Q91664	Q91664 xenopus lae
624	78.5	4.4	388	4	Q8NFZ8	Q8nfz8 homo sapien
625	78.5	4.4	431	3	Q8X022	Q8x022 neurospora
626	78.5	4.4	452	5	O76773	O76773 lucilia cup
627	78.5	4.4	459	10	Q9SS39	Q9ss39 arabidopsis
628	78.5	4.4	471	11	Q9DAV5	Q9dav5 mus musculu
629	78.5	4.4	537	2	Q93E12	Q93e12 rhizobium l
630	78.5	4.4	539	10	O04252	O04252 arabidopsis
631	78.5	4.4	556	10	Q8L6Z9	Q8l6z9 arabidopsis
632	78.5	4.4	629	10	Q8LA44	Q8la44 arabidopsis
633	78.5	4.4	638	10	Q9LFS4	Q9lfs4 arabidopsis
634	78.5	4.4	651	16	Q88BU0	Q88bu0 pseudomonas
635	78.5	4.4	810	4	Q9Y5C8	Q9y5c8 homo sapien
636	78.5	4.4	844	3	Q875H9	Q875h9 candida alb
637	78.5	4.4	888	13	Q7ZWM9	Q7zwm9 xenopus lae
638	78.5	4.4	927	4	Q9Y5G3	Q9y5g3 homo sapien
639	78.5	4.4	1038	16	Q8YSN0	Q8ysn0 anabaena sp
640	78.5	4.4	1465	10	Q8GYU3	Q8gyu3 arabidopsis
641	78.5	4.4	1468	10	Q9SVE1	Q9sve1 arabidopsis
642	78.5	4.4	1788	4	O60612	O60612 homo sapien
643	78.5	4.4	1915	2	Q9RPL0	Q9rpl0 acetivibrio
644	78	4.4	236	4	Q8NEJ1	Q8nej1 homo sapien
645	78	4.4	257	16	Q97I62	Q97i62 clostridium
646	78	4.4	272	11	Q8R1N5	Q8r1n5 mus musculu
647	78	4.4	287	4	Q13984	Q13984 homo sapien
648	78	4.4	304	4	O43754	O43754 homo sapien
649	78	4.4	313	13	O57596	O57596 gallus gall
650	78	4.4	375	12	Q65280	Q65280 african swi
651	78	4.4	399	4	Q9Y279	Q9y279 homo sapien
652	78	4.4	402	11	O35444	O35444 mus musculu
653	78	4.4	412	16	Q8G6P7	Q8g6p7 bifidobacte
654	78	4.4	423	2	Q9RBI2	Q9rbi2 acinetobact
655	78	4.4	452	16	Q7VQM5	Q7vqm5 candidatus
656	78	4.4	491	5	Q9VKX6	Q9vkx6 drosophila
657	78	4.4	604	3	O74491	O74491 schizosacch
658	78	4.4	606	11	Q9ESS7	Q9ess7 mus musculu
659	78	4.4	608	16	Q8YCV9	Q8ycv9 brucella me
660	78	4.4	608	16	Q8FVG6	Q8fvg6 brucella su
661	78	4.4	634	3	Q8X0Z4	Q8x0z4 cryptococcu
662	78	4.4	634	3	Q96WX0	Q96wx0 cryptococcu
663	78	4.4	648	11	Q8R2Y2	Q8r2y2 mus musculu
664	78	4.4	706	11	Q8BM11	Q8bm11 mus musculu
665	78	4.4	836	9	O48483	O48483 bacteriopha
666	78	4.4	865	15	Q8Q7H7	Q8q7h7 human immun
667	78	4.4	905	3	O13955	O13955 schizosacch
668	78	4.4	1009	13	O93250	O93250 xenopus lae
669	78	4.4	1016	16	Q8A4W1	Q8a4w1 bacteroides
670	78	4.4	1147	13	Q9DDK1	Q9ddk1 meleagris g
671	78	4.4	1924	3	Q7Z8U6	Q7z8u6 aspergillus
672	78	4.4	3722	2	P94873	P94873 lysobacter
673	77.5	4.4	117	13	Q7ZZ67	Q7zz67 brachydanio

674	77.5	4.4	128	4	Q86UW2	Q86uw2 homo sapien
675	77.5	4.4	172	5	Q19627	Q19627 caenorhabdi
676	77.5	4.4	186	5	Q8MV99	Q8mv99 ixodes scap
677	77.5	4.4	214	16	Q99VY1	Q99vy1 staphylococ
678	77.5	4.4	258	4	Q9H563	Q9h563 homo sapien
679	77.5	4.4	284	4	Q9NX42	Q9nx42 homo sapien
680	77.5	4.4	294	11	Q8K1Z5	Q8k1z5 mus musculu
681	77.5	4.4	300	11	Q9JHY1	Q9jhy1 rattus norv
682	77.5	4.4	324	10	Q940M5	Q940m5 arabidopsis
683	77.5	4.4	326	13	Q9IAZ3	Q9iaz3 sphoeroides
684	77.5	4.4	345	8	Q9G9W4	Q9g9w4 teleogryllu
685	77.5	4.4	345	8	Q9G9W3	Q9g9w3 teleogryllu
686	77.5	4.4	351	2	Q9ADX7	Q9adx7 agrobacteri
687	77.5	4.4	356	13	Q8AXL7	Q8axl7 oncorhynchu
688	77.5	4.4	360	16	Q7VAZ7	Q7vaz7 prochloroco
689	77.5	4.4	371	16	Q81KQ7	Q81kq7 bacillus an
690	77.5	4.4	425	3	Q96VU0	Q96vu0 amanita mus
691	77.5	4.4	428	16	Q8F7J7	Q8f7j7 leptospira
692	77.5	4.4	433	11	O55054	O55054 mus musculu
693	77.5	4.4	460	5	Q7YTA8	Q7yta8 bombyx mori
694	77.5	4.4	476	11	Q9CU34	Q9cu34 mus musculu
695	77.5	4.4	536	16	Q7UZH7	Q7uzh7 prochloroco
696	77.5	4.4	539	10	Q9FX24	Q9fx24 arabidopsis
697	77.5	4.4	589	10	Q8RZH3	Q8rzh3 oryza sativ
698	77.5	4.4	591	16	Q9I1K8	Q9i1k8 pseudomonas
699	77.5	4.4	717	16	Q8U7P9	Q8u7p9 agrobacteri
700	77.5	4.4	735	10	Q9FG24	Q9fg24 arabidopsis

ALIGNMENTS

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RESULT 1
Q9NQ25
ID   Q9NQ25      PRELIMINARY;      PRT;   335 AA.
AC   Q9NQ25;
DT   01-OCT-2000 (TrEMBLrel. 15, Created)
DT   01-OCT-2000 (TrEMBLrel. 15, Last sequence update)
DT   01-OCT-2003 (TrEMBLrel. 25, Last annotation update)
DE   BA404F10.4 (Novel LY9 (Lymphocyte antigen 9) like protein) (NK cell
DE   receptor) (Membrane protein FOAP-12) (CD2-like receptor activating
DE   cytotoxic cells).
GN   BA404F10.4 OR CS1.
OS   Homo sapiens (Human).
OC   Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC   Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
OX   NCBI_TaxID=9606;
RN   [1]
RP   SEQUENCE FROM N.A.
RA   Bates K.;
RL   Submitted (APR-2000) to the EMBL/GenBank/DDBJ databases.
RN   [2]
RP   SEQUENCE FROM N.A.
RA   Boles K.S., Mathew P.A. Sr.;
RT   "Cloning of a new member of the CD2 subset of receptors expressed on
RT   NK cells.";
RL   Submitted (AUG-2000) to the EMBL/GenBank/DDBJ databases.
RN   [3]
RP   SEQUENCE FROM N.A.
RC   TISSUE=Macrophage;
RA   Fujii Y., Takayama K., Tsuritani K., Yajima Y., Amemiya T., Ukai Y.,
RA   Naito K., Kawaguchi A.;
RT   "Homo sapiens mRNA for FOAP-12 protein, complete cds.";
RL   Submitted (MAY-1999) to the EMBL/GenBank/DDBJ databases.
RN   [4]
RP   SEQUENCE FROM N.A.
RA   Bouchon A., Cella M., Grierson H.L., Cohen J.I., Colonna M.;
RT   "Cutting Edge: Activation of NK Cell-Mediated Cytotoxicity by a SAP-
RT   Independent Receptor of the CD2 Family.";
RL   J. Immunol. 167:0-0(2001).
DR   EMBL; AL121985; CAC00579.1; -.
DR   EMBL; AF291815; AAK11549.1; -.
DR   EMBL; AB027233; BAB61022.1; -.
DR   EMBL; AF390894; AAL26989.1; -.
DR   GO; GO:0004872; F:receptor activity; IEA.
DR   InterPro; IPR003599; Ig.
DR   InterPro; IPR007110; Ig-like.
DR   SMART; SM00409; IG; 1.
DR   PROSITE; PS50835; IG_LIKE; 1.
KW   Receptor.
SQ   SEQUENCE   335 AA;  37421 MW;  D09ABBCFF74BE8D4 CRC64;

  Query Match           100.0%;  Score 1772;  DB 4;  Length 335;
  Best Local Similarity  100.0%;  Pred. No. 6.5e-159;
  Matches  335;  Conservative    0;  Mismatches    0;  Indels    0;  Gaps    0;

Qy          1 MAGSPTCLTLIYILWQLTGSAASGPVKELVGSVGGAVTFPLKSKVKQVDSIVWTFNTTPL 60
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db          1 MAGSPTCLTLIYILWQLTGSAASGPVKELVGSVGGAVTFPLKSKVKQVDSIVWTFNTTPL 60

Qy         61 VTIQPEGGTIIVTQNRNRERVDFPDGGYSLKLSKLKKNDSGIYYVGIYSSSLQQPSTQEY 120
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db         61 VTIQPEGGTIIVTQNRNRERVDFPDGGYSLKLSKLKKNDSGIYYVGIYSSSLQQPSTQEY 120

Qy        121 VLHVYEHLSKPKVTMGLQSNKNGTCVTNLTCCMEHGEEDVIYTWKALGQAANESHNGSIL 180
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        121 VLHVYEHLSKPKVTMGLQSNKNGTCVTNLTCCMEHGEEDVIYTWKALGQAANESHNGSIL 180

Qy        181 PISWRWGESDMTFICVARNPVSRNFSSPILARKLCEGAADDPDSSMVLLCLLLVPLLLSL 240
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        181 PISWRWGESDMTFICVARNPVSRNFSSPILARKLCEGAADDPDSSMVLLCLLLVPLLLSL 240

Qy        241 FVLGLFLWFLKRERQEEYIEEKKRVDICRETPNICPHSGENTEYDTIPHTNRTILKEDPA 300
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        241 FVLGLFLWFLKRERQEEYIEEKKRVDICRETPNICPHSGENTEYDTIPHTNRTILKEDPA 300

Qy        301 NTVYSTVEIPKKMENPHSLLTMPDTPRLFAYENVI 335
              |||||||||||||||||||||||||||||||||||
Db        301 NTVYSTVEIPKKMENPHSLLTMPDTPRLFAYENVI 335


RESULT 2
Q9NY08
ID   Q9NY08      PRELIMINARY;      PRT;   335 AA.
AC   Q9NY08;
DT   01-OCT-2000 (TrEMBLrel. 15, Created)
DT   01-MAR-2001 (TrEMBLrel. 16, Last sequence update)
DT   01-OCT-2003 (TrEMBLrel. 25, Last annotation update)
DE   19A protein.
GN   19A.
OS   Homo sapiens (Human).
OC   Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC   Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
OX   NCBI_TaxID=9606;
RN   [1]
RP   SEQUENCE FROM N.A.
RA   Murphy J.J., Norton J.D., Hobby P., Sutton B.J.;
RT   "An early response gene that encodes an immunoglobulin superfamily
RT   member with structural similarity to CD2.";
RL   Submitted (JAN-2001) to the EMBL/GenBank/DDBJ databases.
DR   EMBL; AJ276429; CAB81950.2; -.
DR   InterPro; IPR003599; Ig.
DR   InterPro; IPR007110; Ig-like.
DR   SMART; SM00409; IG; 1.
DR   PROSITE; PS50835; IG_LIKE; 1.
SQ   SEQUENCE   335 AA;  37403 MW;  BB758E505CA4DDD5 CRC64;

  Query Match           99.8%;  Score 1769;  DB 4;  Length 335;
  Best Local Similarity  99.7%;  Pred. No. 1.2e-158;
  Matches  334;  Conservative    1;  Mismatches    0;  Indels    0;  Gaps    0;

Qy          1 MAGSPTCLTLIYILWQLTGSAASGPVKELVGSVGGAVTFPLKSKVKQVDSIVWTFNTTPL 60
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db          1 MAGSPTCLTLIYILWQLTGSAASGPVKELVGSVGGAVTFPLKSKVKQVDSIVWTFNTTPL 60

Qy         61 VTIQPEGGTIIVTQNRNRERVDFPDGGYSLKLSKLKKNDSGIYYVGIYSSSLQQPSTQEY 120
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                ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db          61 VTIQPEGGTIIVTQNRNRERVDFPDGGYSLKLSKLKKNDSGIYYVGIYSSSLQQPSTQEY 120

Qy         121 VLHVYEHLSKPKVTMGLQSNKNGTCVTNLTCCMEHGEEDVIYTWKALGQAANESHNGSIL 180
                |||||||||||||:||||||||||||||||||||||||||||||||||||||||||||||||
Db         121 VLHVYEHLSKPKVTLGLQSNKNGTCVTNLTCCMEHGEEDVIYTWKALGQAANESHNGSIL 180

Qy         181 PISWRWGESDMTFICVARNPVSRNFSSPILARKLCEGAADDPDSSMVLLCLLLVPLLLSL 240
                ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db         181 PISWRWGESDMTFICVARNPVSRNFSSPILARKLCEGAADDPDSSMVLLCLLLVPLLLSL 240

Qy         241 FVLGLFLWFLKRERQEEYIEEKKRVDICRETPNICPHSGENTEYDTIPHTNRTILKEDPA 300
                ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db         241 FVLGLFLWFLKRERQEEYIEEKKRVDICRETPNICPHSGENTEYDTIPHTNRTILKEDPA 300

Qy         301 NTVYSTVEIPKKMENPHSLLTMPDTPRLFAYENVI 335
                |||||||||||||||||||||||||||||||||||
Db         301 NTVYSTVEIPKKMENPHSLLTMPDTPRLFAYENVI 335


RESULT 3
Q9NY23
ID   Q9NY23      PRELIMINARY;      PRT;   328 AA.
AC   Q9NY23;
DT   01-OCT-2000 (TrEMBLrel. 15, Created)
DT   01-OCT-2000 (TrEMBLrel. 15, Last sequence update)
DT   01-OCT-2003 (TrEMBLrel. 25, Last annotation update)
DE   19A24 protein.
GN   19A24.
OS   Homo sapiens (Human).
OC   Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC   Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
OX   NCBI_TaxID=9606;
RN   [1]
RP   SEQUENCE FROM N.A.
RC   TISSUE=Peripheral blood;
RA   Murphy J.J., Norton J.D., Hobby P., Sutton B.J.;
RT   "An early response gene that encodes an immunoglobulin superfamily
RT   member with structural similarity to CD2.";
RL   Submitted (FEB-2000) to the EMBL/GenBank/DDBJ databases.
DR   EMBL; AJ271869; CAB76561.1; -.
DR   InterPro; IPR003599; Ig.
DR   InterPro; IPR007110; Ig-like.
DR   SMART; SM00409; IG; 1.
DR   PROSITE; PS50835; IG_LIKE; 1.
SQ   SEQUENCE   328 AA;  36490 MW;  E68A7243964380DB CRC64;

  Query Match             78.6%;  Score 1392.5;  DB 4;  Length 328;
  Best Local Similarity   86.4%;  Pred. No. 4.7e-123;
  Matches  273;  Conservative    3;  Mismatches    5;  Indels   35;  Gaps    3;

Qy           1 MAGSPTCLTLIYILWQLTGSAASGPVKELVGSVGGAVTFPLKSKVKQVDSIVWTFNTTPL 60
                ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db           1 MAGSPTCLTLIYILWQLTGSAASGPVKELVGSVGGAVTFPLKSKVKQVDSIVWTFNTTPL 60

Qy          61 VTIQPEGGTIIVTQNRNRERVDFPDGGYSLKLSKLKKNDSGIYYVGIYSSSLQQPSTQEY 120
                ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db          61 VTIQPEGGTIIVTQNRNRERVDFPDGGYSLKLSKLKKNDSGIYYVGIYSSSLQQPSTQEY 120

Qy         121 VLHVYEHLSKPKVTMGLQSNKNGTCVTNLTCCMEHGEEDVIYTWKALGQAANESHNGSIL 180
                ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db         121 VLHVYEHLSKPKVTMGLQSNKNGTCVTNLTCCMEHGEEDVIYTWKALGQAANESHNGSIL 180

Qy         181 PISWRWGESDMTFICVARNPVSRNFSSPILARKLCEGAADDPDSSMVLLCLLLVPLLLSL 240
                ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db         181 PISWRWGESDMTFICVARNPVSRNFSSPILARKLCEGAADDPDSSMVLLCLLLVPLLLSL 240

Qy         241 FVLGLFLWFLKRERQEEYIEEKKRVDICRETPNICPHSGENTEYDTIPHTNRTILKEDPA 300
                ||||||||||||||||  |       | :::|
Db         241 FVLGLFLWFLKRERQEE------------NNP-----KGRSSKYG-------------- 268

Qy         301 NTVYSTVEIPKKMENP 316
                ||||||||||||||
Db         269 ---YSTVEIPKKMENP 281


RESULT 4
Q8N6Y8
ID   Q8N6Y8      PRELIMINARY;      PRT;   296 AA.
AC   Q8N6Y8;
DT   01-OCT-2002 (TrEMBLrel. 22, Created)
DT   01-OCT-2002 (TrEMBLrel. 22, Last sequence update)
DT   01-OCT-2003 (TrEMBLrel. 25, Last annotation update)
DE   19A24 protein.
OS   Homo sapiens (Human).
OC   Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC   Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
OX   NCBI_TaxID=9606;
RN   [1]
RP   SEQUENCE FROM N.A.
RC   TISSUE=Lung;
RA   Strausberg R.;
RL   Submitted (APR-2002) to the EMBL/GenBank/DDBJ databases.
DR   EMBL; BC027867; AAH27867.1; -.
DR   InterPro; IPR007110; Ig-like.
DR   PROSITE; PS50835; IG_LIKE; 1.
SQ   SEQUENCE   296 AA;  32581 MW;  E85D277192494EEC CRC64;

  Query Match             76.1%;  Score 1349;  DB 4;  Length 296;
  Best Local Similarity   100.0%;  Pred. No. 5.3e-119;
  Matches  257;  Conservative    0;  Mismatches    0;  Indels    0;  Gaps    0;

Qy           1 MAGSPTCLTLIYILWQLTGSAASGPVKELVGSVGGAVTFPLKSKVKQVDSIVWTFNTTPL 60
                ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db           1 MAGSPTCLTLIYILWQLTGSAASGPVKELVGSVGGAVTFPLKSKVKQVDSIVWTFNTTPL 60

Qy          61 VTIQPEGGTIIVTQNRNRERVDFPDGGYSLKLSKLKKNDSGIYYVGIYSSSLQQPSTQEY 120
                ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db          61 VTIQPEGGTIIVTQNRNRERVDFPDGGYSLKLSKLKKNDSGIYYVGIYSSSLQQPSTQEY 120

Qy         121 VLHVYEHLSKPKVTMGLQSNKNGTCVTNLTCCMEHGEEDVIYTWKALGQAANESHNGSIL 180
                ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db         121 VLHVYEHLSKPKVTMGLQSNKNGTCVTNLTCCMEHGEEDVIYTWKALGQAANESHNGSIL 180

Qy         181 PISWRWGESDMTFICVARNPVSRNFSSPILARKLCEGAADDPDSSMVLLCLLLVPLLLSL 240
                ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db         181 PISWRWGESDMTFICVARNPVSRNFSSPILARKLCEGAADDPDSSMVLLCLLLVPLLLSL 240

Qy         241 FVLGLFLWFLKRERQEE 257
                |||||||||||||||||
Db         241 FVLGLFLWFLKRERQEE 257


RESULT 5
Q8ND32
ID   Q8ND32      PRELIMINARY;      PRT;   228 AA.
AC   Q8ND32;
DT   01-OCT-2002 (TrEMBLrel. 22, Created)
DT   01-OCT-2002 (TrEMBLrel. 22, Last sequence update)
DT   01-OCT-2003 (TrEMBLrel. 25, Last annotation update)
DE   Hypothetical protein.
GN   DKFZP667F126.
OS   Homo sapiens (Human).
OC   Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC   Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
OX   NCBI_TaxID=9606;
RN   [1]
RP   SEQUENCE FROM N.A.
RC   TISSUE=Lymph node;
RA   Bloecker H., Boecher M., Brandt P., Mewes H.W., Weil B., Wiemann S.;
RL   Submitted (JUL-2002) to the EMBL/GenBank/DDBJ databases.
DR   EMBL; AL834424; CAD39085.1; -.
DR   InterPro; IPR007110; Ig-like.
DR   PROSITE; PS50835; IG_LIKE; 1.
KW   Hypothetical protein.
SQ   SEQUENCE   228 AA;  25831 MW;  2B01DB70E7BBFC14 CRC64;
```

```
  Query Match             65.5%;  Score 1160.5;  DB 4;  Length 228;
  Best Local Similarity   68.1%;  Pred. No. 2.4e-101;
  Matches  228;  Conservative    0;  Mismatches    0;  Indels  107;  Gaps    1;

Qy          1 MAGSPTCLTLIYILWQLTGSAASGPVKELVGSVGGAVTFPLKSKVKQVDSIVWTFNTTPL 60
              ||||||||||||||||||
Db          1 MAGSPTCLTLIYILWQLT---------------------------------------- 18

Qy         61 VTIQPEGGTIIVTQNRNRERVDFPDGGYSLKLSKLKKNDSGIYYVGIYSSSLQQPSTQEY 120

Db         19 ------------------------------------------------------------ 18

Qy        121 VLHVYEHLSKPKVTMGLQSNKNGTCVTNLTCCMEHGEEDVIYTWKALGQAANESHNGSIL 180
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db         19 -----EHLSKPKVTMGLQSNKNGTCVTNLTCCMEHGEEDVIYTWKALGQAANESHNGSIL 73

Qy        181 PISWRWGESDMTFICVARNPVSRNFSSPILARKLCEGAADDPDSSMVLLCLLLVPLLLSL 240
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db         74 PISWRWGESDMTFICVARNPVSRNFSSPILARKLCEGAADDPDSSMVLLCLLLVPLLLSL 133

Qy        241 FVLGLFLWFLKRERQEEYIEEKKRVDICRETPNICPHSGENTEYDTIPHTNRTILKEDPA 300
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        134 FVLGLFLWFLKRERQEEYIEEKKRVDICRETPNICPHSGENTEYDTIPHTNRTILKEDPA 193

Qy        301 NTVYSTVEIPKKMENPHSLLTMPDTPRLFAYENVI 335
              |||||||||||||||||||||||||||||||||||
Db        194 NTVYSTVEIPKKMENPHSLLTMPDTPRLFAYENVI 228
```

RESULT 6
Q8BHK6
ID Q8BHK6 PRELIMINARY; PRT; 333 AA.
AC Q8BHK6;
DT 01-MAR-2003 (TrEMBLrel. 23, Created)
DT 01-MAR-2003 (TrEMBLrel. 23, Last sequence update)
DT 01-OCT-2003 (TrEMBLrel. 25, Last annotation update)
DE Similar to 19A24 protein homolog.
GN 4930560D03RIK.
OS Mus musculus (Mouse).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus.
OX NCBI_TaxID=10090;
RN [1]
RP SEQUENCE FROM N.A.
RC STRAIN=Aorta;
RX MEDLINE=22354683; PubMed=12466851;
RA The FANTOM Consortium,
RA the RIKEN Genome Exploration Research Group Phase I & II Team;
RT "Analysis of the mouse transcriptome based on functional annotation of
RT 60,770 full-length cDNAs.";
RL Nature 420:563-573(2002).
DR EMBL; AK030135; BAC26801.1; -.
DR EMBL; AK030148; BAC26810.1; -.
DR EMBL; AK040678; BAC30665.1; -.
DR PIR; PT0566; PT0566.
DR MGD; MGI:1922595; 4930560D03Rik.
DR InterPro; IPR007110; Ig-like.
DR PROSITE; PS50835; IG_LIKE; 1.
SQ SEQUENCE 333 AA; 37217 MW; 0CC9A0AAFEACD46E CRC64;

```
  Query Match             46.1%;  Score 817;  DB 11;  Length 333;
  Best Local Similarity   49.6%;  Pred. No. 1.2e-68;
  Matches  168;  Conservative   59;  Mismatches  102;  Indels   10;  Gaps    4;

Qy          1 MAGSPTCLTLIYILWQLTGSAASGPVKELVGSVGGAVTFPLKSKVKQVDSIVWTFNTTPL 60
              ||   | :    :| ||| :|||| :|:: |:: |:||| |     :|| :||||||  |
Db          1 MARFSTYIIFTSVLCQLTVTAASGTLKKVAGALDGSVTFTLNITEIKVDYVVWTFNTFFL 60

Qy         61 VTIQPEGGTIIVTQNRNRERVDFPDGGYSLKLSKLKKNDSGIYYVGIYSSSLQQPSTQEY 120
                :: :|   : :|: |:||: |||| ||:|||:||||||| |   |||:| |    |||
Db         61 AMVKKDG---VTSQSSNKERIVFPDGLYSMKLSQLKKNDSGAYRAEIYSTSSQASLIQEY 117

Qy        121 VLHVYEHLSKPKVTMGLQSNKNGTCVTNLTCCMEHGEEDVIYTWKALGQAANESHNGSIL 180
              |||||:|||:||||:  |||||||| |||| :   |:| |:|||:||  |: |:|: |
Db        118 VLHVYKHLSRPKVTIDRQSNKNGTCVINLTCSTDQDGENVTYSWKAVGQGDNQFHDGATL 177

Qy        181 PISWRWGESDMTFICVARNPVSRNFSSPILARKLCEGAADDPDSSMVLLCLLLVPLLLSL 240
              |:|| || |    |:|||||| :||:|:  :|||| || |  |   :| :|    :| |
Db        178 SIAWRSGEKDQALTCMARNPVSNSFSTPVFPQKLCEDAATDLTSLRGILYILCFSAVLIL 237

Qy        241 F--VLGLF--LWFLKRERQEEYIEEKKRVDICRETPNICPHSGENTEYDTIPHTNRTILK 296
              |  :| :|  :|  | :  |   |:|||||  :| |::|||  || :|||||:| :   :
Db        238 FAVLLTIFHTMWIKKGKGCE---EDKKRVDRHQEMPDLCPHLEENADYDTIPYTEKRRPE 294

Qy        297 EDPANTVYSTVEIPKKMENPHSLLTMPDTPRLFAYENVI 335
              ||  || ||||:||| :::| ||   |  ||  ::||||
Db        295 EDAPNTFYSTVQIPKVVKSPSSLPAKPLVPRSLSFENVI 333
```

RESULT 7
Q8CJ64
ID Q8CJ64 PRELIMINARY; PRT; 335 AA.
AC Q8CJ64;
DT 01-MAR-2003 (TrEMBLrel. 23, Created)
DT 01-MAR-2003 (TrEMBLrel. 23, Last sequence update)
DT 01-OCT-2003 (TrEMBLrel. 25, Last annotation update)
DE Leukocyte cell-surface antigen.
GN 4930560D03RIK.
OS Mus musculus (Mouse).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus.
OX NCBI_TaxID=10090;
RN [1]
RP SEQUENCE FROM N.A.
RC STRAIN=BALB/c; TISSUE=Thymus;
RX MEDLINE=22226696; PubMed=12242590;
RA Tovar V., Del Valle J., Zapater N., Martin M., Romero X., Pizcueta P.,
RA Bosch J., Terhorst C., Engel P.;
RT "Mouse novel Ly9: a new member of the expanding CD150 (SLAM) family of
RT leukocyte cell-surface receptors.";
RL Immunogenetics 54:394-402(2002).
DR EMBL; AF467910; AAN63159.1; -.
DR PIR; PT0566; PT0566.
DR MGD; MGI:1922595; 4930560D03Rik.
DR InterPro; IPR007110; Ig-like.
DR PROSITE; PS50835; IG_LIKE; 1.
SQ SEQUENCE 335 AA; 37590 MW; 85F00ABDFC8B90A0 CRC64;

```
  Query Match             43.9%;  Score 778.5;  DB 11;  Length 335;
  Best Local Similarity   48.8%;  Pred. No. 5.3e-65;
  Matches  161;  Conservative   55;  Mismatches  101;  Indels   13;  Gaps    4;

Qy          1 MAGSPTCLTLIYILWQLTGSAASGPVKELVGSVGGAVTFPLKSKVKQVDSIVWTFNTTPL 60
              ||   | :    :| ||| :|||| :|:: |:: |:||| |     :|| :||||||  |
Db          1 MARFSTYIIFTSVLCQLTVTAASGTLKKVAGALDGSVTFTLNITEIKVDYVVWTFNTFFL 60

Qy         61 VTIQPEGGTIIVTQNRNRERVDFPDGGYSLKLSKLKKNDSGIYYVGIYSSSLQQPSTQEY 120
                :: :|   : :|: |:||: |||| ||:|||:||||||| |   |||:| |    |||
Db         61 AMVKKDG---VTSQSSNKERIVFPDGLYSMKLSQLKKNDSGAYRAEIYSTSSQASLIQEY 117

Qy        121 VLHVYEHLSKPKVTMGLQSNKNGTCVTNLTCCMEHGEEDVIYTWKALGQAANESHNGSIL 180
              |||||:|||:||||:  |||||||| |||| :   |:| |:|||:||  |: |:|: |
Db        118 VLHVYKHLSRPKVTIDRQSNKNGTCVINLTCSTDQDGENVTYSWKAVGQGDNQFHDGATL 177

Qy        181 PISWRWGESDMTFICVARNPVSRNFSSPILARKLCEGAADDPDSSMVLLCLLLVPLLLSL 240
              |:|| || |    |:|||||| :||:|:  :|||| || |  |   :| :|    :| |
Db        178 SIAWRSGEKDQALTCMARNPVSNSFSTPVFPQKLCEDAATDLTSLRGILYILCFSAVLIL 237

Qy        241 FVLGLFL----WFLKRERQEEYIEEKKRVDICRETPNICPHSGENTEYDTIPHTNRTILK 296
              | : | :    |  ||:  |   |:|||||  :| |::|||  || :|||||:| :   :
Db        238 FAVLLTIFHTTWIKKRKGCE---EDKKRVDRHQEMPDLCPHLEENADYDTIPYTEKRRPE 294

Qy        297 EDPANTVYSTVEIPKKMEN---PHSLLTMP 323
              ||  || ||||:||| : :    | |   |
Db        295 EDAPNTFYSTVQIPKVVRSCPAEHHLTCQP 324
```

```
RESULT 8
Q8BTL2
ID   Q8BTL2      PRELIMINARY;      PRT;   335 AA.
AC   Q8BTL2;
DT   01-MAR-2003 (TrEMBLrel. 23, Created)
DT   01-MAR-2003 (TrEMBLrel. 23, Last sequence update)
DT   01-OCT-2003 (TrEMBLrel. 25, Last annotation update)
DE   Similar to 19A24 protein homolog.
GN   4930560D03RIK.
OS   Mus musculus (Mouse).
OC   Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC   Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus.
OX   NCBI_TaxID=10090;
RN   [1]
RP   SEQUENCE FROM N.A.
RC   STRAIN=C57BL/6J;
RX   MEDLINE=22354683; PubMed=12466851;
RA   The FANTOM Consortium,
RA   the RIKEN Genome Exploration Research Group Phase I & II Team;
RT   "Analysis of the mouse transcriptome based on functional annotation of
RT   60,770 full-length cDNAs.";
RL   Nature 420:563-573(2002).
DR   EMBL; AK089525; BAC40914.1; -.
DR   PIR; PT0566; PT0566.
DR   MGD; MGI:1922595; 4930560D03Rik.
DR   InterPro; IPR007110; Ig-like.
DR   PROSITE; PS50835; IG_LIKE; 1.
SQ   SEQUENCE   335 AA;  37521 MW;  99E8802E55A98A03 CRC64;

  Query Match             43.7%;  Score 773.5;  DB 11;  Length 335;
  Best Local Similarity   48.8%;  Pred. No. 1.6e-64;
  Matches  161;  Conservative   56;  Mismatches  100;  Indels   13;  Gaps    5;

Qy          1 MAGSPTCLTLIYILWQLTGSAASGPVKELVGSVGGAVTFPLKSKVKQVDSIVWTFNTTPL 60
              ||    | :    :| ||| :|||| :|:: |:: |:||| |     :|| :||||||  |
Db          1 MARFSTYIIFTSVLCQLTVTAASGTLKKVAGALDGSVTFTLNITEIKVDYVVWTFNTFFL 60

Qy         61 VTIQPEGGTIIVTQNRNRERVDFPDGGYSLKLSKLKKNDSGIYYVGIYSSSLQQPSTQEY 120
                :: :|   : :|: |:||: |||| ||:|||:|||||| |   |||:| |    |||
Db         61 AMVKKDG---VTSQSSNKERIVFPDGLYSMKLSQLKKNDSGAYRAEIYSTSSQASLIQEY 117

Qy        121 VLHVYEHLSKPKVTMGLQSNKNGTCVTNLTCCMEHGEEDVIYTWKALGQAANESHNGSIL 180
              |||||:|||:||||:  |||||||||| ||||  :   |:| |:|||:||  |: |:|: |
Db        118 VLHVYKHLSRPKVTIDRQSNKNGTCVINLTCSTDQDGENVTYSWKAVGQGDNQFHDGATL 177

Qy        181 PISWRWGESDMTFICVARNPVSRNFSSPILARKLCEGAADDPDSSMVLLCLLLVPLLLSL 240
               |:|| || |    |:|||||| :||:|:  :|||| || |  |   :| :|    :| |
Db        178 SIAWRSGEKDQALTCMARNPVSNSFSTPVFPQKLCEDAATDLTSLRGILYILCFSAVLIL 237

Qy        241 F--VLGLF--LWFLKRERQEEYIEEKKRVDICRETPNICPHSGENTEYDTIPHTNRTILK 296
              |  :| :|  :|  | :  |   |:|||||  :| |::|||  || :|||||:| :   :
Db        238 FAVLLTIFHTMWIKKGKGCE---EDKKRVDRHQEMPDLCPHLEENADYDTIPYTEKRRPE 294

Qy        297 EDPANTVYSTVEIPKKMEN---PHSLLTMP 323
              ||  ||-||||:||| : :    | |   |
Db        295 EDAPNTFYSTVQIPKVVRSCPAEHHLTCQP 324


RESULT 9
Q8CJ65
ID   Q8CJ65      PRELIMINARY;      PRT;   335 AA.
AC   Q8CJ65;
DT   01-MAR-2003 (TrEMBLrel. 23, Created)
DT   01-MAR-2003 (TrEMBLrel. 23, Last sequence update)
DT   01-OCT-2003 (TrEMBLrel. 25, Last annotation update)
DE   Leukocyte cell-surface antigen.
GN   4930560D03RIK.
OS   Mus musculus (Mouse).
OC   Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC   Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus.
OX   NCBI_TaxID=10090;
RN   [1]
RP   SEQUENCE FROM N.A.
RC   STRAIN=C57BL/6J; TISSUE=Thymus;
RX   MEDLINE=22226696; PubMed=12242590;
RA   Tovar V., Del Valle J., Zapater N., Martin M., Romero X., Pizcueta P.,
RA   Bosch J., Terhorst C., Engel P.;
RT   "Mouse novel Ly9: a new member of the expanding CD150 (SLAM) family of
RT   leukocyte cell-surface receptors.";
RL   Immunogenetics 54:394-402(2002).
DR   EMBL; AF467909; AAN63158.1; -.
DR   PIR; PT0566; PT0566.
DR   MGD; MGI:1922595; 4930560D03Rik.
DR   InterPro; IPR007110; Ig-like.
DR   PROSITE; PS50835; IG_LIKE; 1.
SQ   SEQUENCE   335 AA;  37493 MW;  C210E9CEADC8F3EB CRC64;

  Query Match             43.4%;  Score 769.5;  DB 11;  Length 335;
  Best Local Similarity   48.5%;  Pred. No. 3.7e-64;
  Matches  160;  Conservative   56;  Mismatches  101;  Indels   13;  Gaps    5;

Qy          1 MAGSPTCLTLIYILWQLTGSAASGPVKELVGSVGGAVTFPLKSKVKQVDSIVWTFNTTPL 60
              ||    | :    :| ||| :|||| :|:: |:: |:||| |     :|| :||||||  |
Db          1 MARFSTYIIFTSVLCQLTVTAASGTLKKVAGALDGSVTFTLNITEIKVDYVVWTFNTFFL 60

Qy         61 VTIQPEGGTIIVTQNRNRERVDFPDGGYSLKLSKLKKNDSGIYYVGIYSSSLQQPSTQEY 120
                :: :|   : :|: |:||: |||| ||:|||:|||||| |   |||:| |    |||
Db         61 AMVKKDG---VTSQSSNKERIVFPDGLYSMKLSQLKKNDSGAYRAEIYSTSSQASLIQEY 117

Qy        121 VLHVYEHLSKPKVTMGLQSNKNGTCVTNLTCCMEHGEEDVIYTWKALGQAANESHNGSIL 180
              |||||:|||:||||:  |||||||||| ||||  :   |:| |:|||:||  |: |:|: |
Db        118 ALHVYKHLSRPKVTIDRQSNKNGTCVINLTCSTDQDGENVTYSWKAVGQGDNQFHDGATL 177

Qy        181 PISWRWGESDMTFICVARNPVSRNFSSPILARKLCEGAADDPDSSMVLLCLLLVPLLLSL 240
               |:|| || |    |:|||||| :||:|:  :|||| || |  |   :| :|    :| |
Db        178 SIAWRSGEKDQALTCMARNPVSNSFSTPVFPQKLCEDAATDLTSLRGILYILCFSAVLIL 237

Qy        241 F--VLGLF--LWFLKRERQEEYIEEKKRVDICRETPNICPHSGENTEYDTIPHTNRTILK 296
              |  :| :|  :|  | :  |   |:|||||  :| |::|||  || :|||||:| :   :
Db        238 FAVLLTIFHTMWIKKGKGCE---EDKKRVDRHQEMPDLCPHLEENADYDTIPYTEKRRPE 294

Qy        297 EDPANTVYSTVEIPKKMEN---PHSLLTMP 323
              ||  ||-||||:||| : :    | |   |
Db        295 EDAPNTFYSTVQIPKVVRSCPAEHHLTCQP 324


RESULT 10
Q8CJ63
ID   Q8CJ63      PRELIMINARY;      PRT;   300 AA.
AC   Q8CJ63;
DT   01-MAR-2003 (TrEMBLrel. 23, Created)
DT   01-MAR-2003 (TrEMBLrel. 23, Last sequence update)
DT   01-OCT-2003 (TrEMBLrel. 25, Last annotation update)
DE   Leukocyte cell-surface antigen isoform s.
GN   4930560D03RIK.
OS   Mus musculus (Mouse).
OC   Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC   Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus.
OX   NCBI_TaxID=10090;
RN   [1]
RP   SEQUENCE FROM N.A.
RC   STRAIN=BALB/c; TISSUE=Thymus;
RX   MEDLINE=22226696; PubMed=12242590;
RA   Tovar V., Del Valle J., Zapater N., Martin M., Romero X., Pizcueta P.,
RA   Bosch J., Terhorst C., Engel P.;
RT   "Mouse novel Ly9: a new member of the expanding CD150 (SLAM) family of
RT   leukocyte cell-surface receptors.";
RL   Immunogenetics 54:394-402(2002).
DR   EMBL; AF467911; AAN63160.1; -.
DR   PIR; PT0566; PT0566.
DR   MGD; MGI:1922595; 4930560D03Rik.
DR   InterPro; IPR007110; Ig-like.
DR   PROSITE; PS50835; IG_LIKE; 1.
SQ   SEQUENCE   300 AA;  33332 MW;  9948108710BEBC3D CRC64;
```

```
  Query Match             36.7%;  Score 651;  DB 11;  Length 300;
  Best Local Similarity   42.4%;  Pred. No. 5.1e-53;
  Matches  140;  Conservative   50;  Mismatches   92;  Indels   48;  Gaps    4;

Qy          1 MAGSPTCLTLIYILWQLTGSAASGPVKELVGSVGGAVTFPLKSKVKQVDSIVWTFNTTPL 60
              ||    | :    :| ||| :|||| :|:: |:: |:||| |      :|| :||||||  |
Db          1 MARFSTYIIFTSVLCQLTVTAASGTLKKVAGALDGSVTFTLNITEIKVDYVVWTFNTFFL 60

Qy         61 VTIQPEGGTIIVTQNRNRERVDFPDGGYSLKLSKLKKNDSGIYYVGIYSSSLQQPSTQEY 120
                :: :|   : :|: |:||: |||| ||:|||:|||||||  |   |||:| |    |||
Db         61 AMVKKDG---VTSQSSNKERIVFPDGLYSMKLSQLKKNDSGAYRAEIYSTSSQASLIQEY 117

Qy        121 VLHVYEHLSKPKVTMGLQSNKNGTCVTNLTCCMEHGEEDVIYTWKALGQAANESHNGSIL 180
              |||||:|||:||||:  |||||||||| |||| :   |:| |:|||:||  |: |:|: |
Db        118 VLHVYKHLSRPKVTIDRQSNKNGTCVINLTCSTDQDGENVTYSWKAVGQGDNQFHDGATL 177

Qy        181 PISWRWGESDMTFICVARNPVSRNFSSPILARKLCEGAADDPDSSMVLLCLLLVPLLLSL 240
               |:|| || |    |:|||||| :||:|:  :|||| || |  |   :| :|    :| |
Db        178 SIAWRSGEKDQALTCMARNPVSNSFSTPVFPQKLCEDAATDLTSLRGILYILCFSAVLIL 237

Qy        241 FVLGLFL----WFLKRERQEEYIEEKKRVDICRETPNICPHSGENTEYDTIPHTNRTILK 296
              | : | :    |  | ::: :
Db        238 FAVLLTIFHTTWIKKGKKRRP-----------------------------------E 259

Qy        297 EDPANTVYSTVEIPKKMEN---PHSLLTMP 323
              || .|| ||||:||| : :    | | |
Db        260 EDAPNTFYSTVQIPKVVRSCPAEHHLTCQP 289


RESULT 11
Q91XA0
ID   Q91XA0      PRELIMINARY;      PRT;   294 AA.
AC   Q91XA0;
DT   01-DEC-2001 (TrEMBLrel. 19, Created)
DT   01-DEC-2001 (TrEMBLrel. 19, Last sequence update)
DT   01-OCT-2003 (TrEMBLrel. 25, Last annotation update)
DE   Similar to 19A24 protein.
GN   4930560D03RIK.
OS   Mus musculus (Mouse).
OC   Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC   Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus.
OX   NCBI_TaxID=10090;
RN   [1]
RP   SEQUENCE FROM N.A.
RC   TISSUE=Salivary gland;
RA   Strausberg R.;
RL   Submitted (JUL-2001) to the EMBL/GenBank/DDBJ databases.
DR   EMBL; BC011154; AAH11154.1; -.
DR   MGD; MGI:1922595; 4930560D03Rik.
DR   InterPro; IPR007110; Ig-like.
DR   PROSITE; PS50835; IG_LIKE; 1.
SQ   SEQUENCE   294 AA;  32782 MW;  F4C88BC4CFAA1AFB CRC64;

  Query Match             36.0%;  Score 637.5;  DB 11;  Length 294;
  Best Local Similarity   45.6%;  Pred. No. 9.4e-52;
  Matches  139;  Conservative   50;  Mismatches   95;  Indels   21;  Gaps    6;

Qy          1 MAGSPTCLTLIYILWQLTGSAASGPVKELVGSVGGAVTFPLKSKVKQVDSIVWTFNTTPL 60
              ||    | :    :| ||| :|||| :|:: |:: |:||| |      :|| :||||||  |
Db          1 MARFSTYIIFTSVLCQLTVTAASGTLKKVAGALDGSVTFTLNITEIKVDYVVWTFNTFFL 60

Qy         61 VTIQPEGGTIIVTQNRNRERVDFPDGGYSLKLSKLKKNDSGIYYVGIYSSSLQQPSTQEY 120
                :: :|   : :|: |:||: |||| ||:|||:|||||||  |   |||:| |    |||
Db         61 AMVKKDG---VTSQSSNKERIVFPDGLYSMKLSQLKKNDSGAYRAEIYSTSSQASLIQEY 117

Qy        121 VLHVYEHLSKPKVTMGLQSNKNGTCVTNLTCCMEHGEEDVIYTWKALGQAANESHNGSIL 180
              |||||:|||:||||:  |||||||||| |||| :   |:| |:|||:||  |: |:|: |
Db        118 VLHVYKHLSRPKVTIDRQSNKNGTCVINLTCSTDQDGENVTYSWKAVGQGDNQFHDGATL 177

Qy        181 PISWRWGESDMTFICVARNPVSRNFSSPILARKLCEGAADDPDSSMVLLCLLLVPLLLSL 240
               |:|| || |    |:|||||| :||:|:  :|||| || |  |   :| :|    :| |
Db        178 SIAWRSGEKDQALTCMARNPVSNSFSTPVFPQKLCEDAATDLTSLRGILYILCFSAVLIL 237

Qy        241 FVLGLFL----WFLKRERQEEYIEEKKRVDICRETPNI---C--PHSGENTEYDTIPHTN 291
              | : | :    |  ||       :|||    |  | :|   |  | ||: ::       |
Db        238 FAVLLTIFHTTWIKKR-------KEKKTRRRC--TKHILFHCADPQSGKESQLPACKATR 288

Qy        292 RTILK 296
                ::|
Db        289 AKVIK 293


RESULT 12
O15430
ID   O15430      PRELIMINARY;      PRT;   328 AA.
AC   O15430;
DT   01-JAN-1998 (TrEMBLrel. 05, Created)
DT   01-JAN-1998 (TrEMBLrel. 05, Last sequence update)
DT   01-OCT-2003 (TrEMBLrel. 25, Last annotation update)
DE   Leukocyte antigen CD84.
GN   CD84.
OS   Homo sapiens (Human).
OC   Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC   Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
OX   NCBI_TaxID=9606;
RN   [1]
RP   SEQUENCE FROM N.A.
RX   MEDLINE=97454416; PubMed=9310491;
RA   De la Fuente M.A., Pizcueta P., Nadal M., Bosch J., Engel P.;
RT   "CD84 leukocyte antigen is a new member of the Ig superfamily.";
RL   Blood 90:2398-2405(1997).
RN   [2]
RP   SEQUENCE FROM N.A.
RA   Krause S.W., Rehli M., Heinz S., Ebner R., Andreesen R.;
RT   "Molecular cloning of MAX.3 antigen, a glycoprotein expressed on
RT   macrophages, platelets and megacaryocytes.";
RL   Submitted (FEB-1998) to the EMBL/GenBank/DDBJ databases.
RN   [3]
RP   SEQUENCE FROM N.A.
RX   MEDLINE=86188202; PubMed=3008886;
RA   Andreesen R., Bross K.J., Osterholz J., Emmrich F.;
RT   "Human macrophage maturation and heterogeneity: analysis with a newly
RT   generated set of monoclonal antibodies to differentiation antigens.";
RL   Blood 67:1257-1264(1986).
RN   [4]
RP   SEQUENCE FROM N.A.
RA   Palou E., Sole J., Pirotto F., Gaya A.;
RL   Submitted (MAR-1998) to the EMBL/GenBank/DDBJ databases.
DR   EMBL; U82988; AAB84364.1; -.
DR   EMBL; AJ223324; CAA11264.1; -.
DR   EMBL; AF054815; AAF21721.1; -.
DR   GO; GO:0005887; C:integral to plasma membrane; TAS.
DR   GO; GO:0006952; P:defense response; TAS.
DR   GO; GO:0007156; P:homophilic cell adhesion; TAS.
DR   InterPro; IPR003599; Ig.
DR   InterPro; IPR007110; Ig-like.
DR   SMART; SM00409; IG; 1.
DR   PROSITE; PS50835; IG_LIKE; 1.
KW   Signal.
SQ   SEQUENCE   328 AA;  36871 MW;  6C9A89206A6D0344 CRC64;

  Query Match             20.5%;  Score 362.5;  DB 4;  Length 328;
  Best Local Similarity   31.5%;  Pred. No. 1.1e-25;
  Matches  107;  Conservative   55;  Mismatches  143;  Indels   35;  Gaps   10;

Qy         14 LWQL-----TGSAASGPVKELV---GSVGGAVTFPLK-SKVKQVDSIVWTFNTTPLVTIQ 64
              || |     |   |:|   |:    | :| :|||:   : :||  | ||  |:
Db          6 LWILLLCLQTWPEAAGKDSEIFTVNGILGESVTFPVNIQEPRQVKIIAWTSKTSVAYVTP 65

Qy         65 PEGGT---IIVTQNRNRERVDFPDGGYSLKLSKLKKNDSGIYYVGIYSSSLQQPSTQEYV 121
                :  |   : ||       ||:     |:| :| |:  |:| |   | : :   :|: |
Db         66 GDSETAPVVTVTHRNYYERIHALGPNYNLVISDLRMEDAGDYKADINTQADPYTTTKRYN 125

Qy        122 LHVYEHLSKPKVTMGLQSNKNGTCVTNLTCCMEHGEEDVIYTWKALGQAANESHNGSILP 181
              | :|  | |||:|  | :: | ||   ||| :|  |::| | |  ||:       |::|
```

```
Db        126 LQIYRRLGKPKITQSLMASVNSTCNVTLTCSVEKEEKNVTYNWSPLGE------EGNVLQ 179

Qy        182 ISWRWGESDMTFICVARNPVSRNFSSPILARKLCEGAADDPDS------SMVLLCLLLVP 235
              |      : ::|: | |:|||| | |  | ||:||    |     :       |:: :  |||
Db        180 IFQTPEDQELTYTCTAQNPVSNN-SDSISARQLCADIAMGFRTHHTGLLSVLAMFFLLVL 238

Qy        236 LLLSLFVLGLFLWFLKRERQEEYIEEKKRVDICRETPNICPHSGENTEYDTIPHTNRTIL 295
              :| |:|:  ||      :|:::   :|       : |  |   |:  || |  :
Db        239 ILSSVFLFRLF------KRRQDAASKKTIYTYIMASRNTQP--AESRIYDEILQSKVLPS 290

Qy        296 KEDPANTVYSTVEIPKKMENPHSLLTMPDTPRLFAYENVI 335
              ||:| |||||  |:   ||    :  : |  |   :|| ||
Db        291 KEEPVNTVYSEVQFADKMGKASTQDSKP--PGTSSYEIVI 328


RESULT 13
Q8WLP1
ID   Q8WLP1      PRELIMINARY;      PRT;   328 AA.
AC   Q8WLP1;
DT   01-MAR-2002 (TrEMBLrel. 20, Created)
DT   01-MAR-2002 (TrEMBLrel. 20, Last sequence update)
DT   01-OCT-2003 (TrEMBLrel. 25, Last annotation update)
DE   CD84 antigen (Leukocyte antigen).
OS   Homo sapiens (Human).
OC   Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC   Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
OX   NCBI_TaxID=9606;
RN   [1]
RP   SEQUENCE FROM N.A.
RC   TISSUE=Lymphoma;
RA   Strausberg R.;
RL   Submitted (DEC-2001) to the EMBL/GenBank/DDBJ databases.
DR   EMBL; BC020063; AAH20063.1; -.
DR   InterPro; IPR007110; Ig-like.
DR   PROSITE; PS50835; IG_LIKE; 1.
SQ   SEQUENCE   328 AA;  36871 MW;  6C9A89206A6D0344 CRC64;

  Query Match             20.5%;  Score 362.5;  DB 7;  Length 328;
  Best Local Similarity   31.5%;  Pred. No. 1.1e-25;
  Matches  107;  Conservative   55;  Mismatches  143;  Indels   35;  Gaps   10;

Qy         14 LWQL-----TGSAASGPVKELV---GSVGGAVTFPLK-SKVKQVDSIVWTFNTTPLVTIQ 64
              || |     |   |:|   |:    | :| :|||:   : :||  | ||  |:
Db          6 LWILLLCLQTWPEAAGKDSEIFTVNGILGESVTFPVNIQEPRQVKIIAWTSKTSVAYVTP 65

Qy         65 PEGGT---IIVTQNRNRERVDFPDGGYSLKLSKLKKNDSGIYYVGIYSSSLQQPSTQEYV 121
               :  |   : ||     ||:      |:| :| |:  |:|  |  | :  :    :|: |
Db         66 GDSETAPVVTVTHRNYYERIHALGPNYNLVISDLRMEDAGDYKADINTQADPYTTTKRYN 125

Qy        122 LHVYEHLSKPKVTMGLQSNKNGTCVTNLTCCMEHGEEDVIYTWKALGQAANESHNGSILP 181
              | :|  | |||:|  | :: | ||   ||| :|  |::| | |  ||:       |::|
Db        126 LQIYRRLGKPKITQSLMASVNSTCNVTLTCSVEKEEKNVTYNWSPLGE------EGNVLQ 179

Qy        182 ISWRWGESDMTFICVARNPVSRNFSSPILARKLCEGAADDPDS------SMVLLCLLLVP 235
              |      : ::|: | |:|||| | |  | ||:||    |     :       |:: :  |||
Db        180 IFQTPEDQELTYTCTAQNPVSNN-SDSISARQLCADIAMGFRTHHTGLLSVLAMFFLLVL 238

Qy        236 LLLSLFVLGLFLWFLKRERQEEYIEEKKRVDICRETPNICPHSGENTEYDTIPHTNRTIL 295
              :| |:|:  ||      :|:::   :|       : |  |   |:  || |  :
Db        239 ILSSVFLFRLF------KRRQDAASKKTIYTYIMASRNTQP--AESRIYDEILQSKVLPS 290

Qy        296 KEDPANTVYSTVEIPKKMENPHSLLTMPDTPRLFAYENVI 335
              ||:| |||||  |:   ||    :  : |  |   :|| ||
Db        291 KEEPVNTVYSEVQFADKMGKASTQDSKP--PGTSSYEIVI 328


RESULT 14
Q9Z178
ID   Q9Z178      PRELIMINARY;      PRT;   329 AA.
AC   Q9Z178;
DT   01-MAY-1999 (TrEMBLrel. 10, Created)
DT   01-MAY-1999 (TrEMBLrel. 10, Last sequence update)
DT   01-OCT-2003 (TrEMBLrel. 25, Last annotation update)
DE   CD84 leukocyte antigen.
GN   CD84.
OS   Mus musculus (Mouse).
OC   Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC   Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus.
OX   NCBI_TaxID=10090;
RN   [1]
RP   SEQUENCE FROM N.A.
RC   TISSUE=Peritoneum;
RX   MEDLINE=99180614; PubMed=10079287;
RA   de la Fuente M.A., Tovar V., Pizcueta P., Nadal M., Bosch J.,
RA   Engel P.;
RT   "Molecular cloning, characterization, and chromosomal localization of
RT   the mouse homologue of CD84, a member of the CD2 family of cell
RT   surface molecules.";
RL   Immunogenetics 49:249-255(1999).
DR   EMBL; AF043445; AAD02273.1; -.
DR   MGD; MGI:1336885; Cd84.
DR   InterPro; IPR003599; Ig.
DR   InterPro; IPR007110; Ig-like.
DR   SMART; SM00409; IG; 1.
DR   PROSITE; PS50835; IG_LIKE; 1.
SQ   SEQUENCE   329 AA;  37345 MW;  43BB1AA5AF1989E0 CRC64;

  Query Match             20.5%;  Score 362.5;  DB 11;  Length 329;
  Best Local Similarity   30.5%;  Pred. No. 1.1e-25;
  Matches  105;  Conservative   62;  Mismatches  136;  Indels   41;  Gaps   14;

Qy         11 IYILWQLTGSAASGPVKELV---GSVGGAVTFPLK-SKVKQVDSIVWTFNTTPLVTIQP- 65
              |: |    | | |:|   : |   | :| :||| |   : |::|:| || : : :  |:|
Db          8 IWFLCLQTWSEAAGKDADPVVMNGILGESVTFLLNIQEPKKIDNIAWT-SQSSVAFIKPG 66

Qy         66 -EGGTIIVTQNRNRERVDFPDGGYSLKLSKLKKNDSGIYYVGIYSSSLQQPSTQEYVLHV 124
                 : :||   : |::  |  | | :  |:  |:| |    |   : ::  |: | ||:
Db         67 VNKAEVTITQGTYKGRIEIIDQKYDLVIRDLRMEDAGTYKADINEEN-EETITKIYYLHI 125

Qy        125 YEHLSKPKVTMGLQSNKNGTCVTNLTCCMEHGEEDVIYTWKALGQAANESHNGSILPISW 184
              |  |  ||:|  | |: | ||   ||| :|  |:|| |:|   |: :|      :| |
Db        126 YRRLKTPKITQSLISSLNNTCNITLTCSVEKEEKDVTYSWSPFGEKSN------VLQIVH 179

Qy        185 RWGESDMTFICVARNPVSRNFSSPILARKLCEGA-------ADDPDSSMVLLCLLLVPLL 237
                :  :|: | |:|||| | |  :  :: |           |   |    ||  |:|:|:|
Db        180 SPMDQKLTYTCTAQNPVS-NSSDSVTVQQPCTDTPSFHPRHAVLPGGLAVLFLLILIPML 238

Qy        238 LSLFVLGLFLWFLKRERQEEYIEEKKRVDICRETP-NICPHSGENTE---YDTIPHTNRT 293
                || |      || |    :|     |: ::|   :   : : ||   || || :
Db        239 AFLFRL------YKRRRDRIVLEAD---DVSKKTVYAVVSRNAQPTESRIYDEIPQSKML 289

Qy        294 ILKEDPANTVYSTVEIPKKMENPHSLLTMPD--TPRLFAYENVI 335
               |:||  |:||:|:: :||:  :    | |   |:    | |:
Db        290 SCKKDPVTTIYSSVQLSEKMKETN----MKDRSLPKALGNEIVV 329


RESULT 15
Q8WWI8
ID   Q8WWI8      PRELIMINARY;      PRT;   339 AA.
AC   Q8WWI8;
DT   01-MAR-2002 (TrEMBLrel. 20, Created)
DT   01-MAR-2002 (TrEMBLrel. 20, Last sequence update)
DT   01-OCT-2003 (TrEMBLrel. 25, Last annotation update)
DE   Leukocyte differentiation antigen CD84 precursor.
OS   Homo sapiens (Human).
OC   Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC   Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
OX   NCBI_TaxID=9606;
RN   [1]
RP   SEQUENCE FROM N.A.
RA   Gaya A.;
RL   Submitted (APR-1997) to the EMBL/GenBank/DDBJ databases.
DR   EMBL; Y12632; CAA73181.1; -.
DR   InterPro; IPR003599; Ig.
DR   InterPro; IPR007110; Ig-like.
DR   SMART; SM00409; IG; 1.
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DR   PROSITE; PS50835; IG_LIKE; 1.
KW   Signal.
FT   SIGNAL        1     21       POTENTIAL.
FT   CHAIN        22    339       LEUKOCYTE DIFFERENTIATION ANTIGEN CD84.
SQ   SEQUENCE   339 AA;  38082 MW;  E78D6D5CAC8D3604 CRC64;

  Query Match             20.3%;  Score 359;  DB 4;  Length 339;
  Best Local Similarity   31.6%;  Pred. No. 2.4e-25;
  Matches  111;  Conservative   51;  Mismatches  143;  Indels   46;  Gaps   12;

Qy         14 LWQL-----TGSAASGPVKELV---GSVGGAVTFPLK-SKVKQVDSIVWTFNTTPLVTIQ 64
              || |     |   |:|   |:    | :| :||||:   : :||  | ||  |:
Db          6 LWILLLCLQTWPEAAGKDSEIFTVNGILGESVTFPVNIQEPRQVKIIAWTSKTSVAYVTP 65

Qy         65 PEGGT---IIVTQNRNRERVDFPDGGYSLKLSKLKKNDSGIYYVGIYSSSLQQPSTQEYV 121
              :  |   : ||     ||:      |:| :| |:  |:| |   | : :    :|: |
Db         66 GDSETAPVVTVTHRNYYERIHALGPNYNLVISDLRMEDAGDYKADINTQADPYTTTKRYN 125

Qy        122 LHVYEHLSKPKVTMGLQSNKNGTCVTNLTCCMEHGEEDVIYTWKALGQAANESHNGSILP 181
              | :|  | |||:|  | :: | ||   ||| :|  |::| | |  ||:       |::|
Db        126 LQIYRRLGKPKITQSLMASVNSTCNVTLTCSVEKEEKNVTYNWSPLGE------EGNVLQ 179

Qy        182 ISWRWGESDMTFICVARNPVSRNFSSPILARKLCEGAADDPDSSM-------VLLCLLLV 234
              |     : ::|: | |:|||| | |  | ||:||       | :|       || :| :
Db        180 IFQTPEDQELTYTCTAQNPVSNN-SDSISARQLC------ADIAMGFRTHHTGLLSVLAM 232

Qy        235 PLLLSLFVLGLFLWFLKRERQ---------EEYIEEKKRV-DICRETPNICPHSGENTEY 284
              || | :  :||: | : ||          |   || :      : |  |   |:  |
Db        233 FFLLVLILSSVFLFRLFKRRQGSCLNTFTKNPYAASKKTIYTYIMASRNTQP--AESRIY 290

Qy        285 DTIPHTNRTILKEDPANTVYSTVEIPKKMENPHSLLTMPDTPRLFAYENVI 335
              | |  :     ||:| ||||| |:   ||    :  : |  |   :|| ||
Db        291 DEILQSKVLPSKEEPVNTVYSEVQFADKMGKASTQDSKP--PGTSSYEIVI 339


Search completed: August 18, 2004, 15:52:28
Job time : 46 secs
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GenCore version 5.1.6

OM protein - protein search, using sw model

Run on: August 18, 2004, 15:43:31 ; Search time 47 Seconds
(without alignments)
2237.566 Million cell updates/sec

Title: US-10-063-549-46
Perfect score: 1772
Sequence: 1 MAGSPTCLTLIYILWQLTGS.....PHSLLTMPDTPRLFAYENVI 335

Scoring table: BLOSUM62
Gapop 10.0 , Gapext 0.5

Searched: 1292805 seqs, 313927144 residues

Total number of hits satisfying chosen parameters: 1292805

Minimum DB seq length: 0
Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%
Maximum Match 100%
Listing first 700 summaries

Database : Published_Applications_AA:*
1: /cgn2_6/ptodata/2/pubpaa/US07_PUBCOMB.pep:*
2: /cgn2_6/ptodata/2/pubpaa/PCT_NEW_PUB.pep:*
3: /cgn2_6/ptodata/2/pubpaa/US06_NEW_PUB.pep:*
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Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	% Query Match	Length	DB	ID	Description
1	1772	100.0	335	9	US-09-732-524-2	Sequence 2, Appli
2	1772	100.0	335	9	US-09-989-722-253	Sequence 253, App
3	1772	100.0	335	9	US-09-989-723-253	Sequence 253, App
4	1772	100.0	335	9	US-09-989-279-253	Sequence 253, App
5	1772	100.0	335	9	US-09-989-727-253	Sequence 253, App
6	1772	100.0	335	9	US-09-989-731-253	Sequence 253, App
7	1772	100.0	335	9	US-09-989-732-253	Sequence 253, App
8	1772	100.0	335	9	US-09-745-605-4	Sequence 4, Appli
9	1772	100.0	335	9	US-09-991-073-253	Sequence 253, App
10	1772	100.0	335	9	US-09-990-442-253	Sequence 253, App
11	1772	100.0	335	9	US-09-991-163-253	Sequence 253, App
12	1772	100.0	335	9	US-09-993-604-253	Sequence 253, App
13	1772	100.0	335	9	US-09-990-456-253	Sequence 253, App
14	1772	100.0	335	9	US-09-989-721-253	Sequence 253, App
15	1772	100.0	335	9	US-09-992-598-253	Sequence 253, App
16	1772	100.0	335	9	US-09-989-293A-253	Sequence 253, App
17	1772	100.0	335	9	US-09-989-735-253	Sequence 253, App
18	1772	100.0	335	9	US-09-990-444-253	Sequence 253, App
19	1772	100.0	335	9	US-09-991-181-253	Sequence 253, App
20	1772	100.0	335	9	US-09-989-730-253	Sequence 253, App
21	1772	100.0	335	9	US-09-990-436-253	Sequence 253, App
22	1772	100.0	335	9	US-09-993-687-253	Sequence 253, App
23	1772	100.0	335	10	US-09-989-734-253	Sequence 253, App
24	1772	100.0	335	10	US-09-997-653-253	Sequence 253, App
25	1772	100.0	335	10	US-09-993-667-253	Sequence 253, App
26	1772	100.0	335	10	US-09-997-428-253	Sequence 253, App
27	1772	100.0	335	10	US-09-997-666-253	Sequence 253, App
28	1772	100.0	335	10	US-09-990-438-253	Sequence 253, App
29	1772	100.0	335	10	US-09-990-562-253	Sequence 253, App
30	1772	100.0	335	10	US-09-990-711-253	Sequence 253, App
31	1772	100.0	335	10	US-09-989-726-253	Sequence 253, App
32	1772	100.0	335	10	US-09-998-156-253	Sequence 253, App
33	1772	100.0	335	10	US-09-990-437-253	Sequence 253, App
34	1772	100.0	335	10	US-09-991-157-253	Sequence 253, App
35	1772	100.0	335	10	US-09-997-514-253	Sequence 253, App
36	1772	100.0	335	10	US-09-997-573-253	Sequence 253, App
37	1772	100.0	335	10	US-09-991-172-253	Sequence 253, App
38	1772	100.0	335	10	US-09-990-726-253	Sequence 253, App
39	1772	100.0	335	10	US-09-997-559-253	Sequence 253, App
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41	1772	100.0	335	10	US-09-990-443-253	Sequence 253, App
42	1772	100.0	335	10	US-09-991-854-253	Sequence 253, App
43	1772	100.0	335	10	US-09-997-628-253	Sequence 253, App
44	1772	100.0	335	10	US-09-997-683-253	Sequence 253, App
45	1772	100.0	335	10	US-09-989-729A-253	Sequence 253, App
46	1772	100.0	335	10	US-09-997-349-253	Sequence 253, App
47	1772	100.0	335	10	US-09-997-440-253	Sequence 253, App
48	1772	100.0	335	10	US-09-990-440-253	Sequence 253, App
49	1772	100.0	335	10	US-09-993-469-253	Sequence 253, App
50	1772	100.0	335	10	US-09-997-542-253	Sequence 253, App
51	1772	100.0	335	10	US-09-993-748-253	Sequence 253, App
52	1772	100.0	335	10	US-09-990-439-253	Sequence 253, App
53	1772	100.0	335	10	US-09-990-427-253	Sequence 253, App
54	1772	100.0	335	10	US-09-989-328-253	Sequence 253, App
55	1772	100.0	335	10	US-09-993-583-253	Sequence 253, App
56	1772	100.0	335	10	US-09-941-992-253	Sequence 253, App
57	1772	100.0	335	10	US-09-992-521-253	Sequence 253, App
58	1772	100.0	335	10	US-09-997-333-253	Sequence 253, App
59	1772	100.0	335	10	US-09-997-384-253	Sequence 253, App
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61	1772	100.0	335	10	US-09-997-585-253	Sequence 253, App
62	1772	100.0	335	10	US-09-997-614-253	Sequence 253, App
63	1772	100.0	335	10	US-09-989-862-253	Sequence 253, App
64	1772	100.0	335	10	US-09-997-529-253	Sequence 253, App
65	1772	100.0	335	10	US-09-989-725-253	Sequence 253, App
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67	1772	100.0	335	11	US-09-992-643-253	Sequence 253, App
68	1772	100.0	335	12	US-10-206-915-192	Sequence 192, App
69	1772	100.0	335	12	US-10-199-670-192	Sequence 192, App
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83	1772	100.0	335	12	US-10-063-569-46	Sequence 46, Appl
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642	1772	100.0	335	14	US-10-202-475-192	Sequence 192, App
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678	1772	100.0	335	14	US-10-063-650-46	Sequence 46, Appl
679	1772	100.0	335	14	US-10-063-652-46	Sequence 46, Appl
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688	1772	100.0	335	14	US-10-063-587-46	Sequence 46, Appl
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694	1772	100.0	335	14	US-10-063-611-46	Sequence 46, Appl
695	1772	100.0	335	14	US-10-063-614-46	Sequence 46, Appl
696	1772	100.0	335	14	US-10-063-639-46	Sequence 46, Appl
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698	1772	100.0	335	14	US-10-063-646-46	Sequence 46, Appl
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ALIGNMENTS

RESULT 1
US-09-732-524-2
; Sequence 2, Application US/09732524
; Patent No. US20020004193A1
; GENERAL INFORMATION:
; APPLICANT: Khodadoust, Mehran
; TITLE OF INVENTION: NOVEL MP-7 PROTEIN AND NUCLEIC ACID MOLECULES
; TITLE OF INVENTION: AND USES THEREOF
; NUMBER OF SEQUENCES: 7
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: LAHIVE & COCKFIELD, LLP
; STREET: 28 State Street
; CITY: Boston
; STATE: Massachusetts
; COUNTRY: USA
; ZIP: 02109
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Floppy disk
; COMPUTER: IBM PC compatible
; OPERATING SYSTEM: PC-DOS/MS-DOS
; SOFTWARE: PatentIn Release #1.0, Version #1.25
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/09/732,524
; FILING DATE:
; CLASSIFICATION:
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: 09/261,759
; FILING DATE:
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: 60/090,579
; FILING DATE: 1998-JUN-25
; ATTORNEY/AGENT INFORMATION:
; NAME: Mandragouras, Amy E.
; REGISTRATION NUMBER: 36,207
; REFERENCE/DOCKET NUMBER: MNI-048CP
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: (617)227-7400
; TELEFAX: (617)742-4214
; INFORMATION FOR SEQ ID NO: 2:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 335 amino acids
; TYPE: amino acid
; TOPOLOGY: linear
; MOLECULE TYPE: protein
US-09-732-524-2

Query Match 100.0%; Score 1772; DB 9; Length 335;
Best Local Similarity 100.0%; Pred. No. 9.8e-168;
Matches 335; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

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Db        121 VLHVYEHLSKPKVTMGLQSNKNGTCVTNLTCCMEHGEEDVIYTWKALGQAANESHNGSIL 180

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Db        181 PISWRWGESDMTFICVARNPVSRNFSSPILARKLCEGAADDPDSSMVLLCLLLVPLLLSL 240

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Qy        301 NTVYSTVEIPKKMENPHSLLTMPDTPRLFAYENVI 335
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Db        301 NTVYSTVEIPKKMENPHSLLTMPDTPRLFAYENVI 335
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RESULT 2
US-09-989-722-253
; Sequence 253, Application US/09989722
; Patent No. US20020072067A1
; GENERAL INFORMATION:
; APPLICANT: Ashkenazi,Avi J.
; APPLICANT: Baker,Kevin P.
; APPLICANT: Botstein,David
; APPLICANT: Desnoyers,Luc
; APPLICANT: Eaton,Dan L.
; APPLICANT: Ferrara,Napoleone
; APPLICANT: Fong,Sherman
; APPLICANT: Gerber,Hanspeter
; APPLICANT: Gerritsen,Mary E.
; APPLICANT: Goddard,Audrey
; APPLICANT: Godowski,Paul J.
; APPLICANT: Grimaldi,J.Christopher
; APPLICANT: Gurney,Austin L.
; APPLICANT: Kljavin,Ivar J.
; APPLICANT: Napier,Mary A.
; APPLICANT: Pan,James
; APPLICANT: Paoni,Nicholas F.
; APPLICANT: Roy, Margaret Ann
; APPLICANT: Stewart, Timothy A.
; APPLICANT: Tumas, Daniel
; APPLICANT: Watanabe, Colin K.
; APPLICANT: Williams, P. Mickey
; APPLICANT: Wood, William I.
; APPLICANT: Zhang, Zemin
; TITLE OF INVENTION: Secreted and Transmembrane Polypeptides and Nucleic
; TITLE OF INVENTION: Acids Encoding the Same
; FILE REFERENCE: P2730P1C63
; CURRENT APPLICATION NUMBER: US/09/989,722
; CURRENT FILING DATE: 2001-11-19
; PRIOR APPLICATION NUMBER: 60/049787
; PRIOR FILING DATE: 1997-06-16
; PRIOR APPLICATION NUMBER: 60/062250
; PRIOR FILING DATE: 1997-10-17

; PRIOR APPLICATION NUMBER: 60/065186
; PRIOR FILING DATE: 1997-11-12
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; PRIOR FILING DATE: 1998-07-07
; PRIOR APPLICATION NUMBER: 60/091982
; PRIOR FILING DATE: 1998-07-07
; PRIOR APPLICATION NUMBER: 60/092182
; PRIOR FILING DATE: 1998-07-09

Query Match 100.0%; Score 1772; DB 9; Length 335;
Best Local Similarity 100.0%; Pred. No. 9.8e-168;
Matches 335; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

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Db          1 MAGSPTCLTLIYILWQLTGSAASGPVKELVGSVGGAVTFPLKSKVKQVDSIVWTFNTTPL 60

Qy         61 VTIQPEGGTIIVTQNRNRERVDFPDGGYSLKLSKLKKNDSGIYYVGIYSSSLQQPSTQEY 120
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Db         61 VTIQPEGGTIIVTQNRNRERVDFPDGGYSLKLSKLKKNDSGIYYVGIYSSSLQQPSTQEY 120

Qy        121 VLHVYEHLSKPKVTMGLQSNKNGTCVTNLTCCMEHGEEDVIYTWKALGQAANESHNGSIL 180
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        121 VLHVYEHLSKPKVTMGLQSNKNGTCVTNLTCCMEHGEEDVIYTWKALGQAANESHNGSIL 180

Qy        181 PISWRWGESDMTFICVARNPVSRNFSSPILARKLCEGAADDPDSSMVLLCLLLVPLLLSL 240
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Db        181 PISWRWGESDMTFICVARNPVSRNFSSPILARKLCEGAADDPDSSMVLLCLLLVPLLLSL 240

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Db        241 FVLGLFLWFLKRERQEEYIEEKKRVDICRETPNICPHSGENTEYDTIPHTNRTILKEDPA 300

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Db        301 NTVYSTVEIPKKMENPHSLLTMPDTPRLFAYENVI 335
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RESULT 3
US-09-989-723-253
; Sequence 253, Application US/09989723
; Patent No. US20020072092A1
; GENERAL INFORMATION:
; APPLICANT: Ashkenazi,Avi J.
; APPLICANT: Baker,Kevin P.
; APPLICANT: Botstein,David
; APPLICANT: Desnoyers,Luc
; APPLICANT: Eaton,Dan L.
; APPLICANT: Ferrara,Napoleone
; APPLICANT: Fong,Sherman
; APPLICANT: Gerber,Hanspeter
; APPLICANT: Gerritsen,Mary E.
; APPLICANT: Goddard,Audrey
; APPLICANT: Godowski,Paul J.
; APPLICANT: Grimaldi,J.Christopher
; APPLICANT: Gurney,Austin L.
; APPLICANT: Kljavin,Ivar J.
; APPLICANT: Napier,Mary A.
; APPLICANT: Pan,James
; APPLICANT: Paoni,Nicholas F.
; APPLICANT: Roy, Margaret Ann
; APPLICANT: Stewart, Timothy A.
; APPLICANT: Tumas, Daniel
; APPLICANT: Watanabe, Colin K.
; APPLICANT: Williams, P. Mickey
; APPLICANT: Wood, William I.
; APPLICANT: Zhang, Zemin
; TITLE OF INVENTION: Secreted and Transmembrane Polypeptides and Nucleic
; TITLE OF INVENTION: Acids Encoding the Same
; FILE REFERENCE: P2730P1C62
; CURRENT APPLICATION NUMBER: US/09/989,723
; CURRENT FILING DATE: 2001-11-19
; PRIOR APPLICATION NUMBER: 60/049787
; PRIOR FILING DATE: 1997-06-16
; PRIOR APPLICATION NUMBER: 60/062250
; PRIOR FILING DATE: 1997-10-17
; PRIOR APPLICATION NUMBER: 60/065186
; PRIOR FILING DATE: 1997-11-12
; PRIOR APPLICATION NUMBER: 60/065311
; PRIOR FILING DATE: 1997-11-13
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; PRIOR FILING DATE: 1998-02-25
; PRIOR APPLICATION NUMBER: 60/078910
; PRIOR FILING DATE: 1998-03-20
; PRIOR APPLICATION NUMBER: 60/083322
; PRIOR FILING DATE: 1998-04-28
; PRIOR APPLICATION NUMBER: 60/084600
; PRIOR FILING DATE: 1998-05-07
; PRIOR APPLICATION NUMBER: 60/087106
; PRIOR FILING DATE: 1998-05-28
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; PRIOR FILING DATE: 1998-06-04
; PRIOR APPLICATION NUMBER: 60/088025
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; PRIOR FILING DATE: 1998-06-05
; PRIOR APPLICATION NUMBER: 60/088202
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; PRIOR FILING DATE: 1998-07-07
; PRIOR APPLICATION NUMBER: 60/092182
; PRIOR FILING DATE: 1998-07-09

Query Match 100.0%; Score 1772; DB 9; Length 335;
Best Local Similarity 100.0%; Pred. No. 9.8e-168;
Matches 335; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

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Qy        181 PISWRWGESDMTFICVARNPVSRNFSSPILARKLCEGAADDPDSSMVLLCLLLVPLLLSL 240
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RESULT 4
US-09-989-279-253
; Sequence 253, Application US/09989279
; Patent No. US20020072496A1
; GENERAL INFORMATION:
; APPLICANT: Ashkenazi,Avi J.
; APPLICANT: Baker,Kevin P.
; APPLICANT: Botstein,David
; APPLICANT: Desnoyers,Luc
; APPLICANT: Eaton,Dan L.
; APPLICANT: Ferrara,Napoleone
; APPLICANT: Fong,Sherman

; APPLICANT: Gerber,Hanspeter
; APPLICANT: Gerritsen,Mary E.
; APPLICANT: Goddard,Audrey
; APPLICANT: Godowski,Paul J.
; APPLICANT: Grimaldi,J.Christopher
; APPLICANT: Gurney,Austin L.
; APPLICANT: Kljavin,Ivar J.
; APPLICANT: Napier,Mary A.
; APPLICANT: Pan,James
; APPLICANT: Paoni,Nicholas F.
; APPLICANT: Roy, Margaret Ann
; APPLICANT: Stewart, Timothy A.
; APPLICANT: Tumas, Daniel
; APPLICANT: Watanabe, Colin K.
; APPLICANT: Williams, P. Mickey
; APPLICANT: Wood, William I.
; APPLICANT: Zhang, Zemin
; TITLE OF INVENTION: Secreted and Transmembrane Polypeptides and Nucleic
; TITLE OF INVENTION: Acids Encoding the Same
; FILE REFERENCE: P2730P1C56
; CURRENT APPLICATION NUMBER: US/09/989,279
; CURRENT FILING DATE: 2001-11-19
; PRIOR APPLICATION NUMBER: 60/049787
; PRIOR FILING DATE: 1997-06-16
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; PRIOR FILING DATE: 1998-07-07
; PRIOR APPLICATION NUMBER: 60/092182
; PRIOR FILING DATE: 1998-07-09

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Matches 335; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

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Qy        121 VLHVYEHLSKPKVTMGLQSNKNGTCVTNLTCCMEHGEEDVIYTWKALGQAANESHNGSIL 180
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RESULT 5
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; Patent No. US20020072497A1
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; APPLICANT: Baker,Kevin P.
; APPLICANT: Botstein,David
; APPLICANT: Desnoyers,Luc
; APPLICANT: Eaton,Dan L.
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; APPLICANT: Kljavin,Ivar J.
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; APPLICANT: Paoni,Nicholas F.
; APPLICANT: Roy, Margaret Ann
; APPLICANT: Stewart, Timothy A.
; APPLICANT: Tumas, Daniel
; APPLICANT: Watanabe, Colin K.
; APPLICANT: Williams, P. Mickey
; APPLICANT: Wood, William I.
; APPLICANT: Zhang, Zemin
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; TITLE OF INVENTION: Acids Encoding the Same
; FILE REFERENCE: P2730P1C65
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; CURRENT FILING DATE: 2001-11-19
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; PRIOR APPLICATION NUMBER: 60/090435
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; PRIOR FILING DATE: 1998-07-02
; PRIOR APPLICATION NUMBER: 60/091633
; PRIOR FILING DATE: 1998-07-02
; PRIOR APPLICATION NUMBER: 60/091978
; PRIOR FILING DATE: 1998-07-07
; PRIOR APPLICATION NUMBER: 60/091982
; PRIOR FILING DATE: 1998-07-07
; PRIOR APPLICATION NUMBER: 60/092182
; PRIOR FILING DATE: 1998-07-09

Query Match 100.0%; Score 1772; DB 9; Length 335;
Best Local Similarity 100.0%; Pred. No. 9.8e-168;
Matches 335; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

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Qy          1 MAGSPTCLTLIYILWQLTGSAASGPVKELVGSVGGAVTFPLKSKVKQVDSIVWTFNTTPL 60
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Db          1 MAGSPTCLTLIYILWQLTGSAASGPVKELVGSVGGAVTFPLKSKVKQVDSIVWTFNTTPL 60

Qy         61 VTIQPEGGTIIVTQNRNRERVDFPDGGYSLKLSKLKKNDSGIYYVGIYSSSLQQPSTQEY 120
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Db         61 VTIQPEGGTIIVTQNRNRERVDFPDGGYSLKLSKLKKNDSGIYYVGIYSSSLQQPSTQEY 120

Qy        121 VLHVYEHLSKPKVTMGLQSNKNGTCVTNLTCCMEHGEEDVIYTWKALGQAANESHNGSIL 180
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Db        121 VLHVYEHLSKPKVTMGLQSNKNGTCVTNLTCCMEHGEEDVIYTWKALGQAANESHNGSIL 180
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Qy        181 PISWRWGESDMTFICVARNPVSRNFSSPILARKLCEGAADDPDSSMVLLCLLLVPLLLSL 240
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Db        181 PISWRWGESDMTFICVARNPVSRNFSSPILARKLCEGAADDPDSSMVLLCLLLVPLLLSL 240

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Qy        301 NTVYSTVEIPKKMENPHSLLTMPDTPRLFAYENVI 335
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Db        301 NTVYSTVEIPKKMENPHSLLTMPDTPRLFAYENVI 335
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RESULT 6
US-09-989-731-253
; Sequence 253, Application US/09989731
; Patent No. US20020103125A1
; GENERAL INFORMATION:
; APPLICANT: Ashkenazi,Avi J.
; APPLICANT: Baker,Kevin P.
; APPLICANT: Botstein,David
; APPLICANT: Desnoyers,Luc
; APPLICANT: Eaton,Dan L.
; APPLICANT: Ferrara,Napoleone
; APPLICANT: Fong,Sherman
; APPLICANT: Gerber,Hanspeter
; APPLICANT: Gerritsen,Mary E.
; APPLICANT: Goddard,Audrey
; APPLICANT: Godowski,Paul J.
; APPLICANT: Grimaldi,J.Christopher
; APPLICANT: Gurney,Austin L.
; APPLICANT: Kljavin,Ivar J.
; APPLICANT: Napier,Mary A.
; APPLICANT: Pan,James
; APPLICANT: Paoni,Nicholas F.
; APPLICANT: Roy, Margaret Ann
; APPLICANT: Stewart, Timothy A.
; APPLICANT: Tumas, Daniel
; APPLICANT: Watanabe, Colin K.
; APPLICANT: Williams, P. Mickey
; APPLICANT: Wood, William I.
; APPLICANT: Zhang, Zemin
; TITLE OF INVENTION: Secreted and Transmembrane Polypeptides and Nucleic
; TITLE OF INVENTION: Acids Encoding the Same
; FILE REFERENCE: P2730P1C70
; CURRENT APPLICATION NUMBER: US/09/989,731
; CURRENT FILING DATE: 2001-11-20
; PRIOR APPLICATION NUMBER: 60/049787
; PRIOR FILING DATE: 1997-06-16
; PRIOR APPLICATION NUMBER: 60/062250
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; PRIOR FILING DATE: 1998-07-02
; PRIOR APPLICATION NUMBER: 60/091978
; PRIOR FILING DATE: 1998-07-07
; PRIOR APPLICATION NUMBER: 60/091982
; PRIOR FILING DATE: 1998-07-07
; PRIOR APPLICATION NUMBER: 60/092182
; PRIOR FILING DATE: 1998-07-09

Query Match 100.0%; Score 1772; DB 9; Length 335;
Best Local Similarity 100.0%; Pred. No. 9.8e-168;

Matches 335; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

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Qy          1 MAGSPTCLTLIYILWQLTGSAASGPVKELVGSVGGAVTFPLKSKVKQVDSIVWTFNTTPL 60
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Qy         61 VTIQPEGGTIIVTQNRNRERVDFPDGGYSLKLSKLKKNDSGIYYVGIYSSSLQQPSTQEY 120
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Db         61 VTIQPEGGTIIVTQNRNRERVDFPDGGYSLKLSKLKKNDSGIYYVGIYSSSLQQPSTQEY 120

Qy        121 VLHVYEHLSKPKVTMGLQSNKNGTCVTNLTCCMEHGEEDVIYTWKALGQAANESHNGSIL 180
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Db        121 VLHVYEHLSKPKVTMGLQSNKNGTCVTNLTCCMEHGEEDVIYTWKALGQAANESHNGSIL 180

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Qy        241 FVLGLFLWFLKRERQEEYIEEKKRVDICRETPNICPHSGENTEYDTIPHTNRTILKEDPA 300
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RESULT 7
US-09-989-732-253
; Sequence 253, Application US/09989732
; Patent No. US20020123463A1
; GENERAL INFORMATION:
; APPLICANT: Ashkenazi,Avi J.
; APPLICANT: Baker,Kevin P.
; APPLICANT: Botstein,David
; APPLICANT: Desnoyers,Luc
; APPLICANT: Eaton,Dan L.
; APPLICANT: Ferrara,Napoleone
; APPLICANT: Fong,Sherman
; APPLICANT: Gerber,Hanspeter
; APPLICANT: Gerritsen,Mary E.
; APPLICANT: Goddard,Audrey
; APPLICANT: Godowski,Paul J.
; APPLICANT: Grimaldi,J.Christopher
; APPLICANT: Gurney,Austin L.
; APPLICANT: Kljavin,Ivar J.
; APPLICANT: Napier,Mary A.
; APPLICANT: Pan,James
; APPLICANT: Paoni,Nicholas F.
; APPLICANT: Roy, Margaret Ann
; APPLICANT: Stewart, Timothy A.
; APPLICANT: Tumas, Daniel
; APPLICANT: Watanabe, Colin K.
; APPLICANT: Williams, P. Mickey
; APPLICANT: Wood, William I.
; APPLICANT: Zhang, Zemin
; TITLE OF INVENTION: Secreted and Transmembrane Polypeptides and Nucleic
; TITLE OF INVENTION: Acids Encoding the Same
; FILE REFERENCE: P2730P1C57
; CURRENT APPLICATION NUMBER: US/09/989,732
; CURRENT FILING DATE: 2001-11-19
; PRIOR APPLICATION NUMBER: 60/049787
; PRIOR FILING DATE: 1997-06-16
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; PRIOR FILING DATE: 1998-02-25

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;  PRIOR APPLICATION NUMBER: 60/091626
;  PRIOR FILING DATE: 1998-07-02
;  PRIOR APPLICATION NUMBER: 60/091633
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;  PRIOR APPLICATION NUMBER: 60/091978
;  PRIOR FILING DATE: 1998-07-07
;  PRIOR APPLICATION NUMBER: 60/091982
;  PRIOR FILING DATE: 1998-07-07
;  PRIOR APPLICATION NUMBER: 60/092182
;  PRIOR FILING DATE: 1998-07-09

  Query Match           100.0%;  Score 1772;  DB 9;  Length 335;
  Best Local Similarity  100.0%;  Pred. No. 9.8e-168;
  Matches  335;  Conservative    0;  Mismatches    0;  Indels    0;  Gaps    0;

Qy          1 MAGSPTCLTLIYILWQLTGSAASGPVKELVGSVGGAVTFPLKSKVKQVDSIVWTFNTTPL 60
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Db          1 MAGSPTCLTLIYILWQLTGSAASGPVKELVGSVGGAVTFPLKSKVKQVDSIVWTFNTTPL 60

Qy         61 VTIQPEGGTIIVTQNRNRERVDFPDGGYSLKLSKLKKNDSGIYYVGIYSSSLQQPSTQEY 120
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Db         61 VTIQPEGGTIIVTQNRNRERVDFPDGGYSLKLSKLKKNDSGIYYVGIYSSSLQQPSTQEY 120

Qy        121 VLHVYEHLSKPKVTMGLQSNKNGTCVTNLTCCMEHGEEDVIYTWKALGQAANESHNGSIL 180
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Db        121 VLHVYEHLSKPKVTMGLQSNKNGTCVTNLTCCMEHGEEDVIYTWKALGQAANESHNGSIL 180

Qy        181 PISWRWGESDMTFICVARNPVSRNFSSPILARKLCEGAADDPDSSMVLLCLLLVPLLLSL 240
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Db        181 PISWRWGESDMTFICVARNPVSRNFSSPILARKLCEGAADDPDSSMVLLCLLLVPLLLSL 240

Qy        241 FVLGLFLWFLKRERQEEYIEEKKRVDICRETPNICPHSGENTEYDTIPHTNRTILKEDPA 300
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Db        241 FVLGLFLWFLKRERQEEYIEEKKRVDICRETPNICPHSGENTEYDTIPHTNRTILKEDPA 300

Qy        301 NTVYSTVEIPKKMENPHSLLTMPDTPRLFAYENVI 335
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RESULT 8
US-09-745-605-4
; Sequence 4, Application US/09745605
; Patent No. US20020123617A1
; GENERAL INFORMATION:
;  APPLICANT: Starling, Gary C.
;  APPLICANT:  Finger, Joshua N.
;  TITLE OF INVENTION: NOVEL IMMUNOGLOBIN SUPERFAMILY MEMBERS APEX-1, APEX-2,
;  TITLE OF INVENTION:  AND APEX-3 AND USES THEREOF
;  FILE REFERENCE: DB13NP
;  CURRENT APPLICATION NUMBER: US/09/745,605
;  CURRENT FILING DATE:  2000-12-22
;  PRIOR APPLICATION NUMBER: 60/172,025
;  PRIOR FILING DATE: 1999-12-23
;  NUMBER OF SEQ ID NOS: 44
;  SOFTWARE: PatentIn Ver. 2.0
; SEQ ID NO 4
;   LENGTH: 335
;   TYPE: PRT
;   ORGANISM: Homo sapiens
US-09-745-605-4

  Query Match           100.0%;  Score 1772;  DB 9;  Length 335;
  Best Local Similarity  100.0%;  Pred. No. 9.8e-168;
  Matches  335;  Conservative    0;  Mismatches    0;  Indels    0;  Gaps    0;

Qy          1 MAGSPTCLTLIYILWQLTGSAASGPVKELVGSVGGAVTFPLKSKVKQVDSIVWTFNTTPL 60
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Qy         61 VTIQPEGGTIIVTQNRNRERVDFPDGGYSLKLSKLKKNDSGIYYVGIYSSSLQQPSTQEY 120
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Qy        121 VLHVYEHLSKPKVTMGLQSNKNGTCVTNLTCCMEHGEEDVIYTWKALGQAANESHNGSIL 180
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Db        121 VLHVYEHLSKPKVTMGLQSNKNGTCVTNLTCCMEHGEEDVIYTWKALGQAANESHNGSIL 180

Qy        181 PISWRWGESDMTFICVARNPVSRNFSSPILARKLCEGAADDPDSSMVLLCLLLVPLLLSL 240
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Db        181 PISWRWGESDMTFICVARNPVSRNFSSPILARKLCEGAADDPDSSMVLLCLLLVPLLLSL 240

Qy        241 FVLGLFLWFLKRERQEEYIEEKKRVDICRETPNICPHSGENTEYDTIPHTNRTILKEDPA 300
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Db        241 FVLGLFLWFLKRERQEEYIEEKKRVDICRETPNICPHSGENTEYDTIPHTNRTILKEDPA 300

Qy        301 NTVYSTVEIPKKMENPHSLLTMPDTPRLFAYENVI 335
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RESULT 9
US-09-991-073-253
; Sequence 253, Application US/09991073
; Patent No. US20020127576A1
; GENERAL INFORMATION:
;  APPLICANT: Ashkenazi,Avi J.
;  APPLICANT:  Baker,Kevin P.
;  APPLICANT:  Botstein,David
;  APPLICANT:  Desnoyers,Luc
;  APPLICANT:  Eaton,Dan L.
;  APPLICANT:  Ferrara,Napoleone
;  APPLICANT:  Fong,Sherman
;  APPLICANT:  Gerber,Hanspeter
;  APPLICANT:  Gerritsen,Mary E.
;  APPLICANT:  Goddard,Audrey
;  APPLICANT:  Godowski,Paul J.
;  APPLICANT:  Grimaldi,J.Christopher
;  APPLICANT:  Gurney,Austin L.
;  APPLICANT:  Kljavin,Ivar J.
;  APPLICANT:  Napier,Mary A.
;  APPLICANT:  Pan,James
;  APPLICANT:  Paoni,Nicholas F.
;  APPLICANT:  Roy, Margaret Ann
;  APPLICANT:  Stewart, Timothy A.
;  APPLICANT:  Tumas, Daniel
;  APPLICANT:  Watanabe, Colin K.
;  APPLICANT:  Williams, P. Mickey
;  APPLICANT:  Wood, William I.
;  APPLICANT:  Zhang, Zemin
;  TITLE OF INVENTION: Secreted and Transmembrane Polypeptides and Nucleic
;  TITLE OF INVENTION:  Acids Encoding the Same
;  FILE REFERENCE: P2730P1C15
;  CURRENT APPLICATION NUMBER: US/09/991,073
;  CURRENT FILING DATE:  2001-11-14
;  PRIOR APPLICATION NUMBER: 60/049787
;  PRIOR FILING DATE: 1997-06-16
;  PRIOR APPLICATION NUMBER: 60/062250
;  PRIOR FILING DATE: 1997-10-17
;  PRIOR APPLICATION NUMBER: 60/065186
;  PRIOR FILING DATE: 1997-11-12
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;  PRIOR FILING DATE: 1997-11-13
;  PRIOR APPLICATION NUMBER: 60/066770
;  PRIOR FILING DATE: 1997-11-24
;  PRIOR APPLICATION NUMBER: 60/075945
;  PRIOR FILING DATE: 1998-02-25
;  PRIOR APPLICATION NUMBER: 60/078910
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;  PRIOR APPLICATION NUMBER: 60/083322
;  PRIOR FILING DATE: 1998-04-28
;  PRIOR APPLICATION NUMBER: 60/084600
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;  PRIOR APPLICATION NUMBER: 60/087106
;  PRIOR FILING DATE: 1998-05-28
;  PRIOR APPLICATION NUMBER: 60/087607
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; PRIOR FILING DATE: 1998-07-02
; PRIOR APPLICATION NUMBER: 60/091978
; PRIOR FILING DATE: 1998-07-07
; PRIOR APPLICATION NUMBER: 60/091982
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;  PRIOR FILING DATE: 1998-07-09

  Query Match             100.0%;  Score 1772;  DB 9;  Length 335;
  Best Local Similarity   100.0%;  Pred. No. 9.8e-168;
  Matches  335;  Conservative    0;  Mismatches    0;  Indels    0;  Gaps    0;

Qy          1 MAGSPTCLTLIYILWQLTGSAASGPVKELVGSVGGAVTFPLKSKVKQVDSIVWTFNTTPL 60
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Db          1 MAGSPTCLTLIYILWQLTGSAASGPVKELVGSVGGAVTFPLKSKVKQVDSIVWTFNTTPL 60

Qy         61 VTIQPEGGTIIVTQNRNRERVDFPDGGYSLKLSKLKKNDSGIYYVGIYSSSLQQPSTQEY 120
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Db         61 VTIQPEGGTIIVTQNRNRERVDFPDGGYSLKLSKLKKNDSGIYYVGIYSSSLQQPSTQEY 120

Qy        121 VLHVYEHLSKPKVTMGLQSNKNGTCVTNLTCCMEHGEEDVIYTWKALGQAANESHNGSIL 180
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Db        121 VLHVYEHLSKPKVTMGLQSNKNGTCVTNLTCCMEHGEEDVIYTWKALGQAANESHNGSIL 180

Qy        181 PISWRWGESDMTFICVARNPVSRNFSSPILARKLCEGAADDPDSSMVLLCLLLVPLLLSL 240
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        181 PISWRWGESDMTFICVARNPVSRNFSSPILARKLCEGAADDPDSSMVLLCLLLVPLLLSL 240

Qy        241 FVLGLFLWFLKRERQEEYIEEKKRVDICRETPNICPHSGENTEYDTIPHTNRTILKEDPA 300
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Db        241 FVLGLFLWFLKRERQEEYIEEKKRVDICRETPNICPHSGENTEYDTIPHTNRTILKEDPA 300

Qy        301 NTVYSTVEIPKKMENPHSLLTMPDTPRLFAYENVI 335
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RESULT 10
US-09-990-442-253
; Sequence 253, Application US/09990442
; Patent No. US20020132252A1
; GENERAL INFORMATION:
;  APPLICANT: Ashkenazi,Avi J.
;  APPLICANT:  Baker,Kevin P.
;  APPLICANT:  Botstein,David
;  APPLICANT:  Desnoyers,Luc
;  APPLICANT:  Eaton,Dan L.
;  APPLICANT:  Ferrara,Napoleone
;  APPLICANT:  Fong,Sherman
;  APPLICANT:  Gerber,Hanspeter
;  APPLICANT:  Gerritsen,Mary E.
;  APPLICANT:  Goddard,Audrey
;  APPLICANT:  Godowski,Paul J.
;  APPLICANT:  Grimaldi,J.Christopher
;  APPLICANT:  Gurney,Austin L.
;  APPLICANT:  Kljavin,Ivar J.
;  APPLICANT:  Napier,Mary A.
;  APPLICANT:  Pan,James
;  APPLICANT:  Paoni,Nicholas F.
;  APPLICANT:  Roy, Margaret Ann
;  APPLICANT:  Stewart, Timothy A.
;  APPLICANT:  Tumas, Daniel
;  APPLICANT:  Watanabe, Colin K.
;  APPLICANT:  Williams, P. Mickey
;  APPLICANT:  Wood, William I.
;  APPLICANT:  Zhang, Zemin
;  TITLE OF INVENTION: Secreted and Transmembrane Polypeptides and Nucleic
;  TITLE OF INVENTION:  Acids Encoding the Same
;  FILE REFERENCE: P2730P1C8
;  CURRENT APPLICATION NUMBER: US/09/990,442
;  CURRENT FILING DATE:  2001-11-14
;  PRIOR APPLICATION NUMBER: 60/049787
;  PRIOR FILING DATE: 1997-06-16
;  PRIOR APPLICATION NUMBER: 60/062250
;  PRIOR FILING DATE: 1997-10-17
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; PRIOR FILING DATE: 1998-07-02
; PRIOR APPLICATION NUMBER: 60/091633
; PRIOR FILING DATE: 1998-07-02
; PRIOR APPLICATION NUMBER: 60/091978
; PRIOR FILING DATE: 1998-07-07
; PRIOR APPLICATION NUMBER: 60/091982
; PRIOR FILING DATE: 1998-07-07
; PRIOR APPLICATION NUMBER: 60/092182
; PRIOR FILING DATE: 1998-07-09

Query Match 100.0%; Score 1772; DB 9; Length 335;
Best Local Similarity 100.0%; Pred. No. 9.8e-168;
Matches 335; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

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Db        121 VLHVYEHLSKPKVTMGLQSNKNGTCVTNLTCCMEHGEEDVIYTWKALGQAANESHNGSIL 180

Qy        181 PISWRWGESDMTFICVARNPVSRNFSSPILARKLCEGAADDPDSSMVLLCLLLVPLLLSL 240
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Db        181 PISWRWGESDMTFICVARNPVSRNFSSPILARKLCEGAADDPDSSMVLLCLLLVPLLLSL 240

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RESULT 11
US-09-991-163-253
; Sequence 253, Application US/09991163
; Patent No. US20020132253A1
; GENERAL INFORMATION:
; APPLICANT: Ashkenazi,Avi J.
; APPLICANT: Baker,Kevin P.
; APPLICANT: Botstein,David
; APPLICANT: Desnoyers,Luc
; APPLICANT: Eaton,Dan L.
; APPLICANT: Ferrara,Napoleone
; APPLICANT: Fong,Sherman
; APPLICANT: Gerber,Hanspeter
; APPLICANT: Gerritsen,Mary E.
; APPLICANT: Goddard,Audrey
; APPLICANT: Godowski,Paul J.
; APPLICANT: Grimaldi,J.Christopher
; APPLICANT: Gurney,Austin L.
; APPLICANT: Kljavin,Ivar J.
; APPLICANT: Napier,Mary A.
; APPLICANT: Pan,James
; APPLICANT: Paoni,Nicholas F.
; APPLICANT: Roy, Margaret Ann
; APPLICANT: Stewart, Timothy A.
; APPLICANT: Tumas, Daniel
; APPLICANT: Watanabe, Colin K.
; APPLICANT: Williams, P. Mickey
; APPLICANT: Wood, William I.
; APPLICANT: Zhang, Zemin

; TITLE OF INVENTION: Secreted and Transmembrane Polypeptides and Nucleic
; TITLE OF INVENTION: Acids Encoding the Same
; FILE REFERENCE: P2730P1C17
; CURRENT APPLICATION NUMBER: US/09/991,163
; CURRENT FILING DATE: 2001-11-14
; PRIOR APPLICATION NUMBER: 60/049787
; PRIOR FILING DATE: 1997-06-16
; PRIOR APPLICATION NUMBER: 60/062250
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; PRIOR FILING DATE: 1998-07-02
; PRIOR APPLICATION NUMBER: 60/091978
; PRIOR FILING DATE: 1998-07-07
; PRIOR APPLICATION NUMBER: 60/091982
; PRIOR FILING DATE: 1998-07-07
; PRIOR APPLICATION NUMBER: 60/092182
; PRIOR FILING DATE: 1998-07-09

Query Match 100.0%; Score 1772; DB 9; Length 335;
Best Local Similarity 100.0%; Pred. No. 9.8e-168;
Matches 335; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

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Qy         61 VTIQPEGGTIIVTQNRNRERVDFPDGGYSLKLSKLKKNDSGIYYVGIYSSSLQQPSTQEY 120
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Qy        121 VLHVYEHLSKPKVTMGLQSNKNGTCVTNLTCCMEHGEEDVIYTWKALGQAANESHNGSIL 180
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RESULT 12
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; Patent No. US20020137075A1
; GENERAL INFORMATION:
; APPLICANT: Ashkenazi,Avi J.
; APPLICANT: Baker,Kevin P.
; APPLICANT: Botstein,David
; APPLICANT: Desnoyers,Luc
; APPLICANT: Eaton,Dan L.
; APPLICANT: Ferrara,Napoleone
; APPLICANT: Fong,Sherman
; APPLICANT: Gerber,Hanspeter
; APPLICANT: Gerritsen,Mary E.
; APPLICANT: Goddard,Audrey
; APPLICANT: Godowski,Paul J.
; APPLICANT: Grimaldi,J.Christopher
; APPLICANT: Gurney,Austin L.
; APPLICANT: Kljavin,Ivar J.
; APPLICANT: Napier,Mary A.
; APPLICANT: Pan,James
; APPLICANT: Paoni,Nicholas F.
; APPLICANT: Roy, Margaret Ann
; APPLICANT: Stewart, Timothy A.
; APPLICANT: Tumas, Daniel
; APPLICANT: Watanabe, Colin K.
; APPLICANT: Williams, P. Mickey
; APPLICANT: Wood, William I.
; APPLICANT: Zhang, Zemin
; TITLE OF INVENTION: Secreted and Transmembrane Polypeptides and Nucleic
; TITLE OF INVENTION: Acids Encoding the Same
; FILE REFERENCE: P2730P1C25
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; CURRENT FILING DATE: 2001-11-14
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; PRIOR FILING DATE: 1997-06-16
; PRIOR APPLICATION NUMBER: 60/062250
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; PRIOR FILING DATE: 1998-07-07
; PRIOR APPLICATION NUMBER: 60/092182
; PRIOR FILING DATE: 1998-07-09

Query Match 100.0%; Score 1772; DB 9; Length 335;
Best Local Similarity 100.0%; Pred. No. 9.8e-168;
Matches 335; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

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RESULT 13
US-09-990-456-253
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; Patent No. US20020137890A1
; GENERAL INFORMATION:
; APPLICANT: Ashkenazi,Avi J.
; APPLICANT: Baker,Kevin P.
; APPLICANT: Botstein,David
; APPLICANT: Desnoyers,Luc
; APPLICANT: Eaton,Dan L.
; APPLICANT: Ferrara,Napoleone
; APPLICANT: Fong,Sherman
; APPLICANT: Gerber,Hanspeter
; APPLICANT: Gerritsen,Mary E.
; APPLICANT: Goddard,Audrey
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; APPLICANT: Stewart, Timothy A.
; APPLICANT: Tumas, Daniel
; APPLICANT: Watanabe, Colin K.
; APPLICANT: Williams, P. Mickey
; APPLICANT: Wood, William I.
; APPLICANT: Zhang, Zemin
; TITLE OF INVENTION: Secreted and Transmembrane Polypeptides and Nucleic
; TITLE OF INVENTION: Acids Encoding the Same
; FILE REFERENCE: P2730P1C22
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;  PRIOR APPLICATION NUMBER: 60/091978
;  PRIOR FILING DATE: 1998-07-07
;  PRIOR APPLICATION NUMBER: 60/091982
;  PRIOR FILING DATE: 1998-07-07
;  PRIOR APPLICATION NUMBER: 60/092182
;  PRIOR FILING DATE: 1998-07-09

  Query Match           100.0%;  Score 1772;  DB 9;  Length 335;
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RESULT 14
US-09-989-721-253
; Sequence 253, Application US/09989721
; Patent No. US20020142961A1
; GENERAL INFORMATION:
;  APPLICANT: Ashkenazi,Avi J.
;  APPLICANT:  Baker,Kevin P.
;  APPLICANT:  Botstein,David
;  APPLICANT:  Desnoyers,Luc
;  APPLICANT:  Eaton,Dan L.
;  APPLICANT:  Ferrara,Napoleone
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;  APPLICANT:  Stewart, Timothy A.
;  APPLICANT:  Tumas, Daniel
;  APPLICANT:  Watanabe, Colin K.
;  APPLICANT:  Williams, P. Mickey
;  APPLICANT:  Wood, William I.
;  APPLICANT:  Zhang, Zemin
;  TITLE OF INVENTION: Secreted and Transmembrane Polypeptides and Nucleic
;  TITLE OF INVENTION:  Acids Encoding the Same
;  FILE REFERENCE: P2730P1C55
;  CURRENT APPLICATION NUMBER: US/09/989,721
;  CURRENT FILING DATE:  2001-11-19
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RESULT 15
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;  APPLICANT: Ashkenazi,Avi J.
;  APPLICANT:  Baker,Kevin P.
;  APPLICANT:  Botstein,David
;  APPLICANT:  Desnoyers,Luc
;  APPLICANT:  Eaton,Dan L.
;  APPLICANT:  Ferrara,Napoleone
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;  APPLICANT:  Tumas, Daniel
;  APPLICANT:  Watanabe, Colin K.
;  APPLICANT:  Williams, P. Mickey
;  APPLICANT:  Wood, William I.
;  APPLICANT:  Zhang, Zemin
;  TITLE OF INVENTION: Secreted and Transmembrane Polypeptides and Nucleic
;  TITLE OF INVENTION:  Acids Encoding the Same
;  FILE REFERENCE: P2730P1C20
;  CURRENT APPLICATION NUMBER: US/09/992,598
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